mle

A Programming Language for Building Likelihood Models

Version 2.1

Volume 1. User's Manual

Darryl J. Holman

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Suggested citation: Holman, Darryl J. (2003) *mle*: *A Programming Language for Building Likelihood Models.* Version 2.1. Vol. 1: User's Manual. http://faculty.washington.edu/~djholman/mle.

mle** List:* There is an email list for ***mle users to receive update and bug notices. To subscribe, send an email message to majordomo@pop.psu.edu with the text "subscribe mle" as the body of the email message.

Preface

mle is the culmination of years of tinkering, punctuated by occasional bursts of concentrated activity that began in 1991. At the time, I was a graduate student in biological anthropology and demography working on several projects that used parametric survival analysis. Some of the parametric models I was working with—a bivariate normal, and a negative exponential distribution with lognormally distributed frailty and an immune fraction—were not available in software I had at hand. Instead, I pieced together a series of numerical routines, some translated from FORTRAN to Pascal, into a special-purpose program for my needs. Ken Weiss suggested that there was a need for a general-purpose program for specifying and solving likelihood models. That suggestion and encouragement from Jim Wood and Robert Jones led me to develop *mle*.

Since then, I have progressively added language features, functions, probability density functions, and numerical methods to the program. For a spell, I was obsessed with collecting probability density functions the way some people collect shoes—many will never be used for serious work, but I can peer into the wardrobe and take great satisfaction in seeing them tidily arranged. During another compulsive period, I decided that *mle* ought to recognize a plethora of number formats, including dates, times, angular formats, numbers in arbitrary bases, numbers with metric and computation suffixes, and Roman numerals. Eventually, the language was generalized to recognize and work with different variable types, including integer, real, complex, boolean, character, string and file types. This led to a preoccupation with adding predefined mathematical, boolean, and string functions.

Recent additions to *mle* have included full programming language capabilities. The language was largely modeled after Pascal, with some major differences. First, I jettisoned most punctuation—those pesky semicolons that separate statements, and the commas and semicolons that separate lists of arguments. In *mle*, commas are always optional where they make sense. Sometimes they are helpful for appearance or to separate an argument beginning with a negative sign [so that (*a, -b*) is treated as two arguments and not the algebraic expression (*a – b*)].

In an important way, the *mle* programming language breaks sacred rules from the halls of Computer Science: variables can be automatically declared when first encountered in an assignment statement. The pitfalls of permitting this, in my opinion, are offset by ease of use in a statistical programming language. Formal declarations are intimidating to the occasional programmer (although I insist on writing the ***mle*** interpreter in a language that strictly enforces variable declaration). The suite of programming features was completed with the addition of user-defined procedures and functions.

Currently, *mle* is embodied as about 25,000 lines of Pascal. Earlier DOS versions of the *mle* interpreter were compiled in Borland Pascal version 7. I still use the Borland environment for most development and

debugging. The most recent release is compiled using the Free Pascal Compiler, FPC (Van Canneyt, 2000), which benchmarks at three to six time faster than the Borland compiler, with slightly smaller code size. FPC has also relaxed the small data set limitation as data variables and arrays can now be allocated larger than 64 Ki. With FPC, I can now release versions for Linux (ELF binaries), Windows 95/98/2000/NT, and, in the off chance that there is demand, OS/2, FreeBSD, Solaris/Intel, Commodore Amiga, and Atari ST. The Unix version of *mle* has traditionally been Solaris for the Sun Sparc architecture. This version was created by translating Pascal into c using the p2c translator (Gillespie 1989), and then compiling the result with a c compiler. An old version of *mle* (2.0.10) is still available for Solaris/Sparc, but I have made the agonizing decision to restrict future development to architectures supported by FPC.

For the first-time user of *mle*, I would like to offer this encouragement. Many of the uninitiated find the ideas behind maximum likelihood estimation completely foreign. Yet, the principles, once grasped, are utterly straightforward and fundamental. A Zen-like attitude really helps—empty your mind of traditional statistical teachings. Learning the *mle* language for doing likelihood estimation essentially involves thinking about the likelihood of an observation, and specifying the likelihood for that observation in a way that is useful to the computer. Once you begin thinking in this mindset, the rest is straightforward hard work.

Many people have contributed their ideas, insights, criticisms, and bug reports. Other's have given me time or space for development, datasets, interesting analytical challenges, or have given of his or her time in reading or testing. I thank Ken Bennett, Adam Connor, Henry Harpending, Dennis Hogan, Robert E. Jones, George Kephart, Goeff Kushnick, Lyle Konigsberg, Arindam Mukherjee, Kathleen O'Connor, Paul Riggs, David Steven, Bethany Usher, Kenneth Weiss, and James Wood. Their encouragement and interest are deeply appreciated.

I suspect that few software manuals come complete with dedications. But, it is with great pleasure I dedicate this manual to my undergraduate advisor, the late Dr. Robert E. Miller. Dr. Miller was an anthropologist, a South Asianist, a futurists, and an ardent advocate of systems thinking. He taught with an enthusiasm that was both infectious and inspiring. I suspect that my career as an anthropologist has been motivated (subconsciously) by the words that ended a number of our philosophical debates, "Darryl, you simply can't quantify love!" If Dr. Miller's conjecture is ever disproven, I am sure that likelihood will have played a pivotal role.

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Chapter 1
Introduction to *mle*

mle is a simple programming language for building and estimating parameters of likelihood models. The language was originally intended for building and estimating the parameters of survival models, but it has evolved to be general enough to estimate parameters for many other types of likelihood models. Indeed, the language attempts to be a general-purpose tool for likelihood estimation.

This chapter provides an overview of *mle*. The basic concepts of the programming language are introduced and some examples are given. Additional examples of *mle* programs and program fragments are sprinkled throughout this chapter, the rest of this *User's manual* and the *Reference manual*.

The mechanics of running *mle* from DOS or Unix is given in Chapter 2. Formal descriptions of the *mle* programming language are saved for later chapters. Another later chapter is devoted to examples of different type of likelihood models.

Preliminaries

This manual gives only a superficial treatment of topics like probability theory, probability models, stochastic modeling, and maximum likelihood estimation. In order to write *mle* programs, you will need a basic understanding of these topics. Some helpful, generally applied, introductions to statistical modeling and maximum likelihood estimation can be found in Burnham and Anderson (1998), Cullen and Frey (1999), Edwards (1972), Hilborn and Mangel (1997), Holman and Jones (1998), King (1998), Nelson (1982), Morgan (2000), Pickles (1985), Royall (1999) and Wood et al. (1992). Guttorp (1995) and Morgan (2000) give accessible introduction to stochastic modeling.

Programs written in *mle* are, in many respects, similar to those written in SAS, S+, SPSS, BMDP, or other statistical programming languages. The language consists of keywords like `MODEL`, `END`, `DATA`, and so on. Like all languages, *mle* has rules of syntax that must be strictly followed to produce a valid program. The resulting *mle* program is translated into actions (like parameter estimation) by the *mle* interpreter.[1]

The *mle* interpreter typically works with three files: the *mle* program file, the data file, and the output file. The next three sections discuss these files in more detail.

[1] Notice that *mle* has two distinct meanings in this document. First, it is a programming language for building likelihoods described herein. Second, it is the name of the computer program that interprets the language and finds maximum likelihood estimates of model parameters.

The Program File

The program file contains a program written in the *mle* programming language. The first line of this file begins with the word `MLE` and the program ends with a matching `END`. The program—consisting of a set of zero or more statements—falls between the `MLE` and the `END`.

Most programs will have statements that name the data file and the output file, a `DATA` statement describing how to read (and possibly transform) observations from a data file, and specifications of one or more likelihood models along with parameters to find. Parameter estimates are then found by an iterative search that maximizes the likelihood given a set of observations. The resulting parameter estimates are then written to the output file.

The *mle* program file is created as an ordinary text file using almost any editor. You can create and edit the *mle* program using *Notepad* (in Windows), the *EDIT* command (in DOS), *vi*, *pico*, or *Emacs* (in Unix), or any other editor that will read and write a file as ASCII text. Word processors, such as Microsoft *MSWord*, can be used as well, but you must remember to save your work using the "*text (with line breaks)*" option.

The Data File

The data file contains lines of *observations*. The observations are read, and perhaps transformed, when the *mle* program is run. The observations are then used with the likelihood function (specified in the *mle* program file) to find parameter estimates. Data files are standard ASCII text files. Typically, one line in the file represents one observation (although a single observation can span more than one line). Within each observation is a series of *fields* that are separated by spaces, tabs, commas, or some other user-specified delimiter. Numeric fields can be read into *mle variables*.

The Output File

The output file is where results are usually written. The name of the output file is specified in the *mle* program file. The program file also specifies what kind of result will be written to the output file, and how much of the details will be included.

You can also specify that *mle* write partial results and messages to the screen (or standard output as it is called). This is helpful for monitoring progress while estimation is taking place.

Skeleton of an *mle* Program

An *mle* program begins with the word `MLE` and ends with a matching `END`. A typical program includes four types of statements between the `MLE` and `END`.

- A `DATA` statement describes the format of the input data file, and provides simple data transformations and mechanisms to drop observations.

- A `MODEL` statement defines the likelihood function along with the parameters to be estimated. A second part of each `MODEL` statement contains the keyword `RUN` that specifies how the model is to be estimated.

- Assignment statements define variables and change the values of the variables, including some that affect the behavior of the `DATA` and `MODEL` statements.

- Procedure statements, like `DATAFILE()` and `OUTFILE()`, take a list of arguments and performs some predefined action. `DATAFILE()`, for example, names and opens up the file read in by the `DATA` statement.

The following code fragment shows the skeleton of a typical *mle* program. The first two statements are procedure calls that define the data file and the output file. The `DATA` statement comes next, followed by a `MODEL` statement. Omitted sections of code are specified <*like this*>.

```
MLE
  DATAFILE("mydatafile.dat")  {for example}
  OUTFILE("myoutfile.out")
  TITLE = "..."
  MAXITER = 100

  DATA
    <Data specification>
  END

  MODEL
    <Expression>
  RUN
    <Run specification>
  END

END
```

An Example

Figure 1 is an example of an *mle* program that estimates the parameters of a likelihood. The problem at hand is to estimate the distribution of gestational ages at birth given for the observations shown in Figure 2. These observations are counts of gestational ages at birth that were (mostly) recorded two within one week. We will use survival analysis to estimate the parameters (μ and σ) for the best-fitting normal distribution.

This is an example of survival analysis with interval censored observations. In this example, each line in the data file represents multiple observations. The number of observations on each line is given as frequencies within each interval.

```
MLE
  TITLE = "Distribution of gestational age" {Data are from Hammes
                                             and Treloar(1970) Am J Pub
                                             Health 60:1496-1505}
  MAXITER = 50                              {Maximum number of iterations allowed}
  EPSILON = 0.0000001                       {Criterion for convergence of the model}
  DATAFILE("hammes.dat")                    {Opens the input data file}
  OUTFILE("hammes.out")                     {Opens the output file}

  DATA {This is the data statement}
       {Data are interval censored and are
        in units of days as per Table 2 of Hammes and Treloar}
    topen     FIELD 1                       {time at opening the interval}
    tclose    FIELD 2                       {time at closing the interval}
    frequency FIELD 3                       {Frequency from Menstrual History Program}
  END  {data}

  MODEL
    DATA                                    {function to loop through all observations}
      PDF NORMAL(topen, tclose)             {Define the parametric distribution}
        PARAM    mean      LOW = 100  HIGH = 400 START = 270 END
        PARAM    stdev     LOW = 0.1  HIGH = 100 START = 20  END
      END  {pdf}
    END  {data}
  RUN
    FULL                                    {run the model with both parameters free}
  END  {model}

END  {mle}
```

Figure 1. Program to estimate parameters for the distribution of gestational ages at birth.

Program Constants and Variables

A number of variables and constants (e.g. `MAXITER`) are pre-defined in *mle*. Frequently, you will want to change the value of these variables in order to fine tune the behavior of the program, change the type of output produced, etc. `MAXITER` is a pre-defined variable that changes the maximum number of iterations permitted in estimating the model parameters. In this example, the value of `MAXITER` is changed from the default value of 100 to a maximum of 50.

The `TITLE` variable is also assigned to a string variable (i.e. a series of characters). The `TITLE` variable is simply written to the output file. The variable `EPSILON` is assigned a value as well. This variable determines how precisely the parameters are to be found: normal convergence occurs when the change in the log-likelihood from one iteration to the next falls below this value.

Comments

Comments can be placed throughout the body of a program by enclosing the text in curly brackets `{` and `}`. Likewise, the curly brackets can be used to effectively remove large sections of code. A second way to comment out all or part of a single line is to put a pound sign (`#`) at the point where you want the comment to begin. *mle* ignores all text from the pound sign to the end of the line.

Reading Data

The data file called `hammes.dat`, is shown in Figure 2. Data files are standard ASCII text files of numbers. The numbers are organized into a series of fields. Each field is usually delimited by white space (tabs or spaces as used in Figure 2) or commas. You can specify your own list of field delimiters, for example, if your data are separated by colons or semicolons. This is done by changing the value of the variable called `DELIMITERS` (see the `DATA` chapter for details).

The data in Figure 2 are structured as three columns of numbers. The first field is the last observed gestational age prior to birth. The second field is the observed gestational age after a birth was

observed. These two times form an interval within which the birth occurred (i.e. the birth occurred at some unknown time within this interval). The third field is the number of births that were observed within the interval.

```
0         141        0
141       196        9
197       217       11
218       224        2
225       231       12
232       238       17
239       245       22
246       252       40
253       259       69
260       266      134
267       273      324
274       280      653
281       287      724
288       294      382
295       301      125
302       308       47
309       315       26
316       322       10
323       329        1
329       -1         6
```

Figure 2. Data file read by the program in Figure 1. Column 1 is the minimum gestational age in a category, column 2 is the maximum gestational age in a category. Together they define a birth weight interval. The -1 in the last row denotes an open birth weight interval (i.e. a weight of 329+). Column 3 is the frequency of births in each birth weight interval.

The `DATA` statement given in Figure 1 specifies how the data file is to be read. The three variables, `topen`, `tclose`, and `frequency` that come between `DATA` and its matching `END` are read in for each observation (i.e. each line in Figure 2). In fact, each of these variables will be created as an array, each having twenty elements, each element corresponding to one line in the data file.

The variable name `frequency` is special. *mle* treats variables with the name `frequency` (and `freq` as well) as a count of repeated observations. The likelihood is "adjusted" for the number of observations so that the contribution will be the same as if multiple identical observations been read in from the file.

Likelihood Model

The next part of the program is the `MODEL` statement. The `MODEL` statement consists of two parts: an expression that comes between the `MODEL` and `RUN` that defines the likelihood, and a list of one or more specifications between the `RUN` and `END`, each giving some details of how parameters are to be estimated.

`Model. . . Run` *Part of the Model Statement*

Within the `MODEL...RUN` part of the statement is a single function that defines the likelihood. In this example, we specify the likelihood:

(1)
$$L(\mu,\sigma) = \prod_{i=1}^{N}\left[S(t_{open_i}|\mu,\sigma) - S(t_{close_i}|\mu,\sigma)\right]^{frequency_i}$$

where *N* is the number of age categories (i.e. the number of lines of observations), *frequency* is the frequency of observations per age category, S() is a survival density function for the normal distribution, t_{open} and t_{close} are the two times read from the data file into the variables `topen` and `tclose`, and μ and σ are the parameters that will be found by maximizing the likelihood.

The first part of the likelihood expression is a `DATA...END` function. This function specifies that observations are to be "fed" to the likelihood one at a time, corresponding to the product (Π) shown in the likelihood above. Do not confuse the `DATA` *function* (found within the `MODEL` statement) with the `DATA` *statement* (discussed above). The `DATA` *function* loops through all observations that were

previously read in by the DATA *statement.* Within the DATA...END function comes the rest of the likelihood, which is shown to the right of the $\prod$ in likelihood (1).

Within the DATA...END function is the *individual likelihood.* As parameter estimates are being found, the individual likelihood is evaluated for each observation, and the log of that likelihood is taken. Each individual loglikelihood is multiplied by the frequency of the current observation and added to the total likelihood.

In short, the DATA...END function takes a series of *observations* and an expression for an *individual likelihood*. It computes and returns the *total log-loglikelihood.*

The individual likelihood for this example (specified within the DATA function) consists of a PDF function. A NORMAL distribution is specified with two arguments (topen, tclose). These times denote the time interval within which births occur. Because the arguments (which were read from column 1 and 2 of the data file) differ from each other, the PDF function returns the area under a normal PDF between topen, and tclose. The area corresponds to the probability of observing a birth within that interval. If, instead, we had specified one argument to the PDF function (or if topen was equal to tclose), the PDF function would have returned the probability density at that point, corresponding to exact ages at birth.

Within the PDF NORMAL function call are two PARAM functions. These functions define parameters that will be changed in order to maximize the likelihood. Naturally, you can specify limits, starting values, etc. for these parameters.

Run. . . End *Part of the Model Statement*

Between the RUN and the END part of a MODEL statement comes a list specifying how to run the model. The full model is run by specifying FULL; all parameters defined in the model will be estimated. Various reduced forms of the model can be run by specifying a REDUCE command. More details on this are given below and in a later chapter.

```
Distribution of gestational age
Parameter file: hammes.mle
Input data file name: hammes.dat
Output file name: hammes.out
    3 variables read.

18 lines read from file hammes.dat
18 Observations kept and 0 observations dropped for each variable.

ROW         topen      tclose   frequency
MEAN   258.722222  253.555556  144.111111
VAR    5338.56536  6032.37908  51267.3987
STDEV  73.0654868  77.6683918  226.423052
MIN    0.00000000  -1.0000000  0.00000000
MAX    329.000000  329.000000  724.000000
Model 1 Run 1 : Distribution of gestational age

METHOD = DIRECT
Maximum Iterations MAXITER = 50
Maximum function evaluations MAXEVALS = 100000
Convergence at EPSILON = 0.0000001000
LogLikelihood: -6459.238 AIC: 12922.476 Del(LL): 0.0000000000
Iterations: 3 Function evaluations: 146 Converged normally

PDF NORMAL with 2 free parameters
      Name Form     Estimate         Std Error         t           against
      mean          279.1204377949   0.370066272387    754.244465444   0.0
     stdev          23.02007362180   0.365987430388    62.8985361530   0.0
Variance/covariance matrix:
0.13694904596  -0.0586570132
-0.0586570132  0.13394679920

Likelihood CI Results:
  Log Likelihood = -5915.1352 after 4 iterations.  Delta(LL)=0.00000000
PDF NORMAL with 2 free parameters
         Name Form       Estimate          Lower CI          Upper CI
         mean          279.7654969512   279.1863052702    280.3447034638
        stdev          13.04605798312   12.64289497881    13.47052893809
```

Figure 3. Output generated by the program in Figure 1.

The *mle* program is run by typing the line `mle hammes.mle` at the command line prompt (see Chapter 2 for details). The results written to the output file are shown in Figure 3. The first section of the output provides summary statistics for each of the variables read from the data file. The parameter estimates are given in two ways: once with estimated standard errors (including a *t*-test of the hypothesis that the estimate is zero) and once with likelihood confidence intervals.

A Note About Parameters

The ultimate goal of putting together a likelihood model is to estimate one or more *parameters* of the model. In *mle*, the `PARAM...END` function defines parameters to be estimated. This use of the word "parameter" can be confusing, so lets clear up the issue. In any mathematical language, we can refer to a function's arguments as "parameters". For example, in the statement $a = \sin(b)$, sin() is a function with one "parameter", *b*. This manual will avoid the word "parameter" in this general sense. Instead, the word *argument* will be used to refer to the arguments of a function in this general sense. So, the sin() function has the *argument b*.

As used in this manual, the word *parameter* in *mle* refers to an unknown quantity of a probability model whose value is to be estimated.[2] Parameters, in this sense, are frequently arguments to functions, but not all arguments are parameters.

[2] A more accurate definition of a parameter is an unknown quantity whose distribution of values is to be estimated. The standard errors or confidence intervals provide information about the distribution of possible parameter values.

Parameters are sometimes the constants defined within a function. For example, in the equation for the slope of a line, $y = mx + b$, we would call m and b the parameters of the equation, and x the argument. This is clearer when we rewrite the equation for a slope as $f(x \mid m, b) = mx + b$, which is read, "f of x given m and b. . . ." This function has a single argument x, and the parameters are m and b. Typically a series of x values are known, and the goal is to find the best values for parameters m and b. By "best", of course, we mean the best in some statistical sense. In *mle*, m and b would be called parameters if and only if they were quantities to be estimated.

The one exception to this usage of *parameter* is for the built-in probability density functions in *mle*, where we refer to *intrinsic parameters*. For example, the normal distribution, $f(t|\mu, \sigma)$, has two intrinsic parameters, μ and σ. Typically we wish to estimate these intrinsic parameters. If so, the intrinsic parameters μ and σ are also model parameters.

As described later, most probability density functions take four argument for t. Combinations of these arguments allow you to specify

- The probability density function (1 argument, or 2 identical arguments).
- The cumulative density function (2 arguments: the 1st argument ≤ minimum range of the PDF).
- The survival density function (2 arguments: the 2nd argument is ≥ maximum range, or the 2nd argument < the 1st argument).
- An area under the probability density function (2 arguments within the range of the PDF).
- The hazard function (3 identical arguments).
- Any of the above with right and left truncation of the distribution. (The 3rd and 4th arguments define the left and right truncation points).

Thus, in the syntax of *mle* , there is a natural delineation between arguments and intrinsic parameters. Consider the following function call: `PDF NORMAL(0, 4, 0, 40) 10, 20 END`. This function call has the four "time" arguments 0, 4, 0, and 40. Together they specify a normal distribution truncated over the range 0 and 40, with the area between 0 and 4 returned. The two intrinsic parameters of the normal are passed as $\mu = 10$ and $\sigma = 20$. There are no model "parameters" in this example, simply because there are no `PARAM` functions specified.

Writing *mle* Programs

This section gives additional details needed to write *mle* programs. The simplest way to create a new *mle* program is to modify a working program (like that given in Figure 1) to make it do the task at hand.

Style Conventions

mle is a free format language. That is, a program can be written on a single line, or spaced across multiple lines. Indenting, spacing within a line, and spacing across lines is never done for the computer. Rather, the use of indentation is solely for the benefit of human readers.

Good programming practices can greatly aid in reading, understanding and debugging a program. Good formatting consists of selecting and consistently using indentation to reflect logical levels and blocks within a program. Comments are indispensable for making a program understandable.

Throughout this manual, *mle* programs use indentation to show, for example, the matching `MODEL` and `END`. This manual uses two spaces to indent each natural "level". Keywords that are a part of *mle* are always upper-case letters and user-defined words are lower-case (this is not required since *mle* is not case sensitive). Finally, each matching `END` is usually followed by a comment denoting what key-word the `END` matches. This last convention is helpful in complex programs that involve many nested functions.

Typographic Conventions

Typographic conventions are used in this manual to distinguish between *mle* language components and English text.

- Keywords in *mle* are shown in a fixed-pitch font as uppercase words: `MODEL END`, `DATA END`, and `DEFAULTOUTNAME`.

- User-defined variables and identifiers are shown in a fixed-pitch font as lowercase words: `y = slope + intercept*x`.

- Within programs, items placed in < and > and italicized are used to denote an omitted or unspecified parts of the code. For example, *<Statements>* denotes a list of program statements that have been omitted. Other commonly used phrases are *<expr>* to denote an expression, *<v>* to denote an identifier, *<rexpr>* to denote an expression of type `REAL`, *<iexpr>* to denote an `INTEGER` expression, *<bexpr>* to denote a `BOOLEAN` expression, *<sexpr>* to denote a string expression. Here is an example: `WHILE` *<bexpr>* `DO` *<statements>* `END`.

- When syntax diagrams are shown, items shown within *[]* are optional arguments. Note that the brackets are italicized. Un-italicized `[]` are part of the language (used for arrays). For example, `WRITELN`*[* `(` *[*`fexpr`*,]]* *<expr>* *[[,]* *<expr>* *...]* `)` *]* shows that the `WRITELN` statements has an optional set of arguments enclosed within parenthesis. The first argument can optionally be a file expression. At least one expression must be enclosed within the parentheses. Commas separating the expressions are optional.

- Ellipses (. . .) are used in two ways. First, they denote that a pattern can be repeated an unlimited number of times. Hence, in the previous point, the ellipses indicate that an unlimited number of expressions can be placed within the `WRITELN` statement. The second use denotes that parts of a statement or function are not shown. For example, `MODEL...END` uses ellipses in this way.

- A list of alternatives are separated by the vertical bar (|). For example, the `DATA` function has a series of optional forms specified this way:

```
DATA [ FORM = SUMLL | SUMMATION | SUM | PRODUCT | PROD ]
  <expr>
END
```

What is a Statement?

Every program begins with the word `MLE` and ends with the matching word `END`. Any text after the final `END` is ignored. Between the `MLE` and its matching `END` comes the body of an *mle* program as a series of *statements.* The most basic outline of an *mle* program looks like this:

```
MLE
  <Statement 1>
  <Statement 2>
  <Statement 3>
  .
  .
  .
END
```

A statement is a single complete instruction. When a program is run, each statement is executed in turn. Here are some things statements do:

- Print messages to the screen (`WRITELN` statement)
- Create data sets (`DATA` statement)
- Find maximum likelihood estimates (`MODEL` statement)
- Define variables (assignment statement)
- Assign or change the value of a variable (assignment statement)
- Define a data file (a call to the `DATAFILE` procedure)
- Loop through a series of statements (`FOR`, `WHILE`, or `REPEAT` statements)
- Conditionally execute one series of statements over of another (`IF` statement)
- Create user-defined procedures or functions (`PROCEDURE` or `FUNCTION` statements)
- Call a user-defined procedure (procedure call)

Each type of statement is briefly discussed below.

Assignment Statement

Assignment statement serves two purposes. The primary purpose is to assign values to variables. A secondary purpose is to define new variables. A great number of pre-defined variables are available to change or fine-tune the behavior of *mle*, and the values of these variables can be changed with assignment statements.

Assignment statements may be placed anywhere within the body of the *mle* program—that is, between the `MLE` and its matching `END`.[3] Some examples are:

[3] Normally assignment statements do not occur within the `DATA...END` and `MODEL...END` statements. Assignment-like statements occur within the `DATA` statement for transformations. Additionally, the `PREASSIGN` and `POSTASSIGN` functions allow a list of one or more assignment (or other) statements to be used. Finally, the `PARAM...END` statement uses assignment-like statements, like to define start, highest, and lowest values of parameters.

```
MAXITER = 100         {Set the maximum number of iterations}
EPSILON = 0.0000001   {Set the criterion for convergence}
PRINT_OBS = TRUE      {print all observations after transformations}
```

The simplest assignment statement is generically defined in this way: <*variable name*> = <*expression*>. The <*variable name*> name can be a preexisting variable (e.g. MAXITER, EPSILON), or a user-defined variable. The <*expression*> that follows the equal sign can be a simple constant, another variable, or a mathematical expression. Details of the syntax and functions that can be used to make up expressions are given in a later chapter. The following are some examples of assignment statements using expressions:

```
pie      = PI
bmi_max  = weight_max/height_max^2
total    = e1_count + e2_count + e3_count + e4_count
last_age = IF linear THEN max_age ELSE SQRT(max_age) END
area     = PDF NORMAL(-2, 2) 1, 3 END        {gives area from -2 to 2 for N(1, 3)}
one      = SIN(total)^2 + COS(total)^2
```

Variable Names

You can create new variables for the purpose of holding values. A few rules must be observed for naming variable (and other identifiers, such as user-defined procedure and function names).

- A variable name must begin with a letter.
- After the initial letter, any combination of letters, numbers, the underscore character (_) and the period (.) character may be embedded in the name. Punctuation other than a period and underscore character is not permitted.
- Variable names in *mle* are insensitive to case: the variable GGG is the same as ggg, Ggg, and gGg.
- Variable names cannot be identical to *mle* keywords, such as PROCEDURE, DATA, FOR, etc. Also, a variable cannot take on the name of an intrinsic procedure (READLN, SEED, OUTFILE, etc.).
- Variable names *can* be the same as an intrinsic function. You are discouraged from doing this—it can become extremely confusing. If you do define variable with the same name as a function, the function will no longer be available for use by the program.

Here are some examples of valid variable names:

```
a  = 1
A  = 2                 {identical identifier: a is the same as A}
a_ = 1
a_long_variable_name = 1
a23 = 1
measure.left = 1
United_States.Wisconsin.Madison.longitude = 40.1388333

{ Here are some legal names that are of questionable value }

a________ = 1      {legal, if odd, name}
a........ = 3      {ditto}
sin = 4            {bad name -- could be confused with the sin() function}
a...b = 3          {confusing name.  Looks like a subrange of some sort}
O.123E23 = 2       {confusing legal name.  The leading oh looks like a zero}
l423     = 4       {confusing legal name.  The leading el looks like a 1}
Here are some examples of improper variable names:
{Bad variable names}

test = 2       {TEST is an mle reserve word}
model = 2      {MODEL is an mle reserve word}
writeln = 6    {WRITELN is an mle intrinsic procedure}
2days = 2      {doesn't begin with a letter}
_now = 2       {doesn't begin with a letter}
sib's_name     {embedded punctuation}
school number  {embedded space}
```

Variable Types

Most examples so far have shown assignments using *real numbers* and *integers*. There are, in fact, seven different *types* supported by *mle*: `REAL`, `INTEGER`, `COMPLEX`, `BOOLEAN`, `STRING`, `CHAR` (character), and `FILE`.

A variable's *type* refers to the domain of values that the variable can take on. For example, `INTEGER` variables can take on a limited range of integer values, `BOOLEAN` variables can only take on the values `TRUE` and `FALSE`. Variables can be defined for each of the seven types; expressions always take on one of these types. Here is an explanation of each:

- ***Real*** variables represent the continuous real number line.[4] Many mathematical functions like `GAMMA()`, `BETA()`, and `BESSELI()` return real values, and so the variable to which these functions are assigned must be type `REAL` as well. Integer variables and functions can always be assigned to real variables—they are automatically converted to real values on assignment. On the other hand, you must use the `ROUND()` or `TRUNC()` functions to convert a real number into an integer value for assignment to an integer varuable.

- ***Integer*** variables take on whole number values over a machine-dependent range of numbers. For most versions of *mle* this range is [-2,147,483,648 to 2,147,483,647]. Arguments to some functions *require* `INTEGER` type variables, like `IDIV()`.

- ***Complex*** variables include a real number part and an imaginary part. Complex numbers are specified by expressions such as `1.2 + 0.4i`. Most mathematical functions are defined for complex types. For example, `SQRT(-1 + 0i)` returns `0.000+1.000i`. There is no natural ordering for complex variables, so that the comparisons `<`, `<=`, `>`, and `>=` are undefined.

Boolean variables take on one of two states: `TRUE` or `FALSE`. No other value is allowed or recognized. Boolean expressions are frequently used to test conditions. For example, the `IF...THEN...ELSE...END` function evaluates the first expression (between the `IF` and `THEN`) to

[4] Be aware, however, that the computer representation for real numbers is not strictly continuous. Occasionally difficulties arise with round-off error because of the discrete computer representation of real numbers.

either TRUE or FALSE and decides which of the remaining two expressions will be evaluated and returned. An example of a boolean expression is this: `3.5 == 4.5`, which returns the value FALSE.

- ***String*** variables hold a sequence of character constants. A string written as a constant is a sequence of characters, enclosed within quotes ("). The single quote character (') can be used as well for strings greater than one character (see *Character* below for an explanation). String variables are typically used to assign file names, titles, etc. Some functions take on string (or character) variables, other functions return strings. For example, the `CONCAT(s1, s2)` function will add together two string variables and return it as a longer string.

- ***Character*** variables take on the value of a single character. When written as a constant in a program, character constants consist of a single character enclosed within single quotes ('). Character constants are not typically used within a user's program, but are available if needed. Usually, character constants and variables can be used anywhere string variables are allowed.

- ***File*** variables are used to reference files. Most of the time, file variables are transparent, and you need not explicitly define or manipulate file variables. This is because *mle* defines and does the bookkeeping for the data file, the output file, the plot file, and the screen (or standard output) file. File variables can be created should you wish to create and manipulate other files.

When a variable is first used in an assignment statement, its *type* will be determined by the *type* returned from the expression on the right-hand side. Here are some examples to illustrate the point:

```
large_data = N_OBS > 5000                    {large_data will be type BOOLEAN}
subtitle   = "Analysis: " + DEFAULTOUTNAME   {subtitle will be type STRING}
nine       = 3 * 3.0                         {nine will be REAL}
five       = 2 + 3                           {five will be INTEGER}
```

You can explicitly define the *type* for a variable when it is first referenced in an assignment statement. Here are some examples:

```
c:STRING  = 'x'      {c would default to CHAR, but is explicitly defined as a STRING variable}
nine:REAL = 3 * 3    {nine would default to INTEGER, but will be a REAL variable}
t:BOOLEAN = TRUE     {t is explicitly declared as Boolean, although this is the default}
ang:REAL = SIN(2*pi) {ang is explicitly declared as real, although this is the default}
```

Array Variables

Multidimensional arrays and matrices of all *types* are supported by *mle*. Array variables must be explicitly defined the first time the variable is mentioned in the program. The format is <*var*> : <*type*>[<*min1*> TO <*max1*>, <*min2*> TO <*max2*>, . . .]. Some examples of declarations are:

```
s : STRING[1 TO 5]                    {Defines a one-dimensional array of strings}
r : REAL[1 TO 10, 1 TO 10]            {Defines a 10 x 10 matrix}
b : BOOLEAN[0 TO 1, 0 TO 1, 0 TO 1]   {Defines a 3 dimensional BOOLEAN array}
```

Values within an array variable are accessed using brackets to denote subscripts. The following example creates an array of radian angles for integral degree angles, and prints out a table of sine values:

```
r : REAL[0 TO 359]
FOR i = 0 TO 359 DO
  r[i] = DTOR(i)                        {assignment to element i of array r}
  writeln("Sin(" i ") = " SIN(r[i]) )   {access the ith element of array r}
END
```

Initialized Array Variables

Arrays can be initialized in the same time they are defined. There are three ways to initialize an array. First, the value of a constant can be assigned to the array. Examples are:

```
s : STRING[1 TO 5] = ""        {Defines s and initializes all values to an empty string}
r : REAL[1 TO 10, 1 TO 10] = 0 {Defines a 10 x 10 matrix and initializes everything to 0}
```

An array can be used to initialize another array, provided that the arrays are identically defined. That is, they must have the same number of subscripts and the same subscript ranges. Here is an example:

```
a : REAL[1 TO 20]
FOR x = 1 TO 5 DO
  a2[x] = x
END  {for}
b : REAL[1 TO 5] = a2
```

Arrays can also be initialized with a list of values, one per element. A special function is defined that that is enclosed within brackets ([]), and within the function, brackets are used to nest the values to different levels. Here is an example:

```
a : REAL[1 TO 5, 1 TO 2]  =  [[1.1  1.2]
                              [2.1  2.2]
                              [3.1  3.2]
                              [4.1  4.2]
                              [5.1  5.2]]

FOR x = 1 TO 5 DO
  FOR y = 1 TO 2 DO
    WRITE(' a[' x ',' y ']=' a[x, y])
  END  {for y}
  WRITELN
END  {for x}
```

Here are the results of running this example:

```
 a[1,1]=1.1000000000 a[1,2]=1.2000000000
 a[2,1]=2.1000000000 a[2,2]=2.2000000000
 a[3,1]=3.1000000000 a[3,2]=3.2000000000
 a[4,1]=4.1000000000 a[4,2]=4.2000000000
 a[5,1]=5.1000000000 a[5,2]=5.2000000000
```

Data Statement

Most *mle* programs include a DATA...END statement. The purpose of a DATA *statement* is to create a series of observations, which will be used to compute likelihoods. The DATA...END statement defines the format of the data file, defines variables to be read in, provides a way of transforming variables, and provides a way of selecting and dropping observations. Only an overview of the DATA statement is given here. Details are given in chapter three.

Formats for the DATA statement are:

```
DATA
  <variable>  FIELD x                                              {reads variable from field>
  <variable>  FIELD x LINE y                                       {multiline version}
  <variable>  FIELD x [LINE y] = <expr>                            {reads and transforms}
  <variable>  FIELD x [LINE y] [DROPIF <expr> | KEEPIF <expr> ...] {generic from with FIELD}
  <variable>  = <expr>                                             {creates from an expressions}
  <variable>  = <expr>  [DROPIF <expr> | KEEPIF <expr> ...]        {creates and conditionally keeps}
  <variable> [FIELD x [LINE y]] = <expr>  [DROPIF <expr> | KEEPIF <expr> ...]
   ...
END
```

A description of each field follows:

- <*variable*> is the name of the variable being defined. The variable must not already exist. All variables created by the DATA statement are defined to be type real. Integer values will be read in from the data file and converted to real numbers. Text strings can exist within a fields of a text file, but must not be assigned to a variable.

- FIELD refers to which column within an input file a variable is found in. In the hammes.dat file, four fields (or columns) existed in the input file. The field specifier must be a positive integer constant.

- LINE provides a way to read observations spread across multiple lines in the data file. When the LINE keyword is used, the maximum number of lines specified (e.g. 2 for LINE 2) is taken as the number of lines for all observations. If observations each take but one line, the statement LINE 1 may be dropped—one line per observation is assumed as a default. The line specifier must be a positive integer constant.

- <= *expr*> defines a data transformation expression. The expression may refer to the variable being read, or any variables defined prior to the current variable. The line newvar FIELD 3 = newvar^2 will read newvar from field three of the data file; the value of newvar is then squared and assigned back to newvar.

- DROPIF provides a mechanism to drop observations. The expression following DROPIF will evaluate to TRUE or FALSE. If TRUE, the observation is dropped. The line newvar FIELD 3 DROPIF newvar <= 0 will drop all observations when the variable in field three is not positive.

- KEEPIF provides another mechanism to drop observations. The expression following KEEPIF must evaluate to TRUE or FALSE. If FALSE, the observation is dropped (that is, not kept). The line newvar FIELD 3 KEEPIF newvar > 0 will drop all observations for which the variable in field three is not positive. KEEPIF and DROPIF expressions can be far more complex, but must return TRUE or FALSE.

Usually, data are read from a data file. The DATAFILE() procedure defines and opens this file. Here is an example:

```
DATAFILE("test.dat")
DATA
  o_time      FIELD 1  = o_time*365.25
                         DROPIF (o_time > 1000)
  c_time      FIELD 3  = IF c_time = -1 THEN c_time ELSE c_time*365.25 END
  height      FIELD 6  DROPIF height <= 0
  heightsq    = height^2
  missing     FIELD 4  DROPIF missing_data <> 1
  frequency   FIELD 5  DROPIF frequency <= 0
END
```

The variable names FREQUENCY or FREQ are taken as frequencies for each observation. (If both variable names are used, FREQUENCY is taken as the frequency variable). The frequency of each observation is used to compute a proper likelihood as if multiple lines of identical observations were read. If the FREQUENCY or FREQ keywords are missing, a frequency of one is assumed for each observation.

The DATA *statement* is used in conjunction with the DATA *function*. Within a MODEL statement, you can use the DATA *function* to evaluate the likelihood, one observation at a time. Do not be confused by the fact that there is both a DATA statement and a DATA function. They complement each other. Simply remember that a DATA statement is used as a statement, and there is typically one such

statement per program. The DATA function can only be used as part of an expression—typically only within the likelihood expression of a MODEL statement.

Model Statement

The MODEL...RUN...END statement defines the underlying probability model used by *mle*, defines the parameters to be found for the model, and defines constraints under which parameters are to be estimated. Only an overview of the MODEL statement is given here. An entire chapter is devoted to the MODEL statement, including some details for specifying likelihoods.

The basic structure of the MODEL statement looks like this:

```
MODEL
  <expression>
RUN
  <run specifications>
END
```

Between MODEL and RUN is a single expression that is the likelihood. Within the likelihood is one or more PARAM...END functions. These define the parameters, whose values will be found so that the likelihood is maximized. One of the most important aspects of learning *mle* is the design and construction of the expression for the likelihood.

A list of <*run specifications*> is given between the RUN and the END part of the MODEL statement, this provides a way of evaluating the full model as well as a series of nested or reduced models. If all of the parameters (defined by PARAM...END functions) are to be found, a simple FULL command is placed between the RUN and its matching END. Reduced models, where one or more parameters are constrained to a constant or another parameter, are specified as REDUCE followed with a list of one or more "reductions". For example, you might constrain a parameter called mean to be zero and only allow the parameter called stdev to be found. Then you would put REDUCE mean = 0 between the RUN and the END. Any number of REDUCE commands (along with one FULL) can be used in a single model. The various forms of the model will be evaluated in turn.

Intrinsic Procedures

Intrinsic procedures are predefined, single word statements that perform a specific task on a list of zero or more arguments. When called, a procedure executes a series of actions using the arguments. (Procedures do not return a value the way a function does). For example, the statement DATAFILE("hammes.dat") found in the earlier example defines and opens the file used by the DATA statement. A list of all procedures, with examples, can be found in a later chapter. Here are some example procedure statements:

```
SEED(9734)                          {Seeds the random number generator}
HALT                                {stops a program from running further}
WRITELN("Final value is ", total)   {Writes text to the screen}
DATAFILE("hammes.dat")              {Defines and opens a data file}
OUTFILE("hammes.out")               {defines and opens an output file}
```

User-defined Procedures

mle provides capabilities for users-defined procedures (and functions). A procedure is a single-word command that takes a list of zero or more arguments; when called, a procedure executes a series of statements and returns to the place whence called. User-defined procedures are something like subroutines in FORTRAN; they are very similar to Pascal's user-defined procedures. User-defined procedures must be understood as two components: the procedure definition and a call to the procedure.

A user-defined procedure must be defined prior to being invoked (called). By convention, user-defined procedures (and functions) are usually placed near the beginning of the program. Here is an example of a user-defined procedure being defined and later called.

```
MLE
  a : STRING = "Hello world"

  PROCEDURE myproc (a:INTEGER b:REAL c:STRING)     {Define the procedure here}
    msg = "    a is "
    WRITELN("  In myproc: a = ", a, " b = ", b, " c = ",  c)
    IF a < 10 THEN
      WRITELN(msg "< 10")
      a = a + ROUND(b)
    ELSE
      WRITELN(msg "> 10 ")
    END  {if}
    WRITELN('  Exit myproc with a = ', a)
  END  {procedure}                                 {End of user-defined procedure definition}

  t = 4
  WRITELN('Call myproc with t = ' t)
  myproc(t, 4.2, a)     {Here is a call to the user-defined procedure}
  WRITELN('Back from myproc with t = ' t)

END
```

The definition begins with the word `PROCEDURE` and ends with the corresponding `END`. The word following `PROCEDURE` is the name of the procedure, in this case `myproc`. The name is followed by a list of 0 or more arguments that are formally defined—that is, a name and type must be specified for each argument. In this example three arguments (`a`, `b`, and `c`) are defined. The argument names and all of the variables defined within the procedure (like `msg`) are "private" to the procedure. Names of preexisting variables (like `a`) are not affected by and do not affect declarations outside of the procedure.

The procedure definition does not actually do any (visible) work in a program. The work comes when a procedure is called, as in the line `myproc(t, 4.2, a)`. Once called, each argument is evaluated and a copy of the result is assigned to the formal argument defined in the heading of the procedure. The statements within the procedure are executed, and control is passed back to the main program. Here are results from the sample program:

```
Call myproc with t = 4
  In myproc: a = 4 b = 4.2000000000 c = Hello world
    a is < 10
  Exit myproc with a = 8
Back from myproc with t = 4
```

A careful examination reveals an interesting behavior in this example: the arguments passed from outside the procedure are not affected by any manipulation within the procedure. Specifically, `t` in the call was not changed by the assignment to a in the procedure. The reason is that a *copy* of each argument is passed to the procedure. This behavior prevents accidental *side-effects* (outside of the procedure) resulting from manipulations within procedures. Additionally, this permits *recursive* calls to a procedure (i.e. a procedure that calls itself).

Sometimes it is helpful to permit the procedure to change the variables back in the main program (or calling procedure). It is possible to pass a variable to a procedure so that its value can be manipulated within the procedure. This is done by preceding the variable in the formal argument list of the procedure by the name `VAR`. (This mechanism is almost identical to variable arguments in Pascal and Modula.) Suppose we rewrite the previous example by adding `VAR` before the formal declaration of variable `a`:

```
 PROCEDURE myproc (VAR a:INTEGER b:REAL c:STRING)
   msg = "    a is "
   . . .
```

Now, any changes to variable a within the procedure will be reflected in changes to variable t outside of the procedure.

```
Call myproc with t = 4
  In myproc: a = 4 b = 4.2000000000 c = Hello world
    a is < 10
  Exit myproc with a = 8
Back from myproc with t = 8
```

Here are some other notes about user-defined procedures

- VAR arguments require that variables be passed (instead of constants), since the variable may be modified
- Arrays can only be passed as VAR arguments
- Procedures can be defined and called within a procedure (but will not be available outside that procedure)
- Procedures can "overwrite" the name of intrinsic procedures

User-defined Functions

mle provides capabilities for user-defined functions. A function is a single-word command that takes a list of zero or more arguments, performs some operation, and returns a result. User-defined functions in *mle* are very similar to Pascal's user-defined functions. They must be understood as two components: the function definition and a call to the function.

A user-defined function must be defined prior to being called. By convention, they are usually placed near the beginning of the program. Here is an example of a user-defined function being defined and later used.

```
MLE
  FUNCTION int_power(a:REAL j:INTEGER):REAL
    { -- raises a to integer power j}
    RETURN = 1.0
    WHILE j > 0 DO
      IF ISODD(j) THEN
        RETURN = RETURN*a
      END  {if}
      a = a*a
      j = j DIV 2
    END  {while}
  END  {int_power}

  WRITELN(
          int_power(SQRT(4), 2), ' ',
          int_power(4.5, 2), ' ',
          int_power(10/2, 3)
         )
END
```

The definition begins with the word FUNCTION and ends with the corresponding END. The word following FUNCTION is the name of the function, in this case int_power. The name is followed by a list of 0 or more arguments that are formally defined—that is, a name and type must be specified for each argument. In this example two arguments (a and j) are defined. The argument names and all of the variables defined within the function are "private" to that function.

The function declaration does not actually do any work in a program. The work comes when the function is called, as in the WRITELN line that calls the function. Once called, each argument is

evaluated and a copy is assigned to the formal argument defined in the heading of the function. The statements within the function are executed, and the result is passed back to the expression.

Within a function, the variable `RETURN` is automatically declared. `RETURN` can be used as an ordinary variable. When the function exits, the value stored in `RETURN` is passed back to the calling expression. Here is what this example produces:

```
4.0000000000 20.250000000 125.00000000
```

Here are some other notes about user-defined functions

- Like procedures, `VAR` arguments can be defined
- Arrays can only be passed as `VAR` arguments to user-defined functions
- Functions and procedures can be defined and called within a function (but will not be available outside that function)
- User-defined functions can "overwrite" the name of intrinsic functions

BEGIN...END Statement

The `BEGIN...END` statement provides a means of providing multiple statements in contexts where only a single statement is allowed. The format is

```
BEGIN
  <statements>
END
```

The most important use for this statement is with the `PREASSIGN...END` and `POSTASSIGN...END` functions discussed in a later chapter.

FOR Statement

The `FOR` statement provides a means of looping through statements. The formats are

```
FOR <v> = <expr> TO <expr> DO                  {form 1}
  <statements>
END
FOR <v> = <expr> TO <expr> STEP <expr> DO      {form 2}
  <statements>
END
FOR <v> = <expr> TO <expr> STEPS <iexpr> DO    {form 3}
  <statements>
END
FOR <v> = <array> DO                           {form 4}
  <statements>
END
```

Form 1 is a simple looping statement. The variable <*v*> must either not be previously defined or, if it already exists, it must be an integer or real variable. Its value will change as the `FOR` statement is executed. The first <*expr*> will be executed once and will define the starting value of <*v*>. The second <*expr*> will be executed once and will define the last value of <*v*>. Every iteration through the loop, the value of <*v*> will be incremented by 1.

Here is an example that will print sine and cosine tables in one degree increments as well as creating a table of radians for each degree:

```
r : REAL[0 TO 359]
FOR x = 0 TO 359 DO
  r[x] = DTOR(x)
  WRITELN(x " degrees (" r[x] " radians): SIN()=" SIN(r[x]) ", COS()=" COS(r[x]))
END
```

Form 2 of the FOR statement is like form 1 except that the <*expr*> after STEP will be used as the increment (or decrement) value instead of one. The step size can be any real or integer value. If the value is positive, then <*statements*> will not be executed unless the start <*expr*> is less than or equal to the TO <*expr*>. Likewise, if the step size is less than zero, then the start <*expr*> should be greater than or equal to the TO <*expr*>.

Form 3 of the FOR statement performs the loop in a fixed number of steps, defined by the <*expr*> after STEPS, in equally spaced values from the start <*expr*> to the TO <*expr*>. The variable <*v*> is declared as type REAL (or must be REAL if it is already defined). Here is a simple example that goes from 0 to 1 in 100 steps: `FOR x = 0 TO 1 STEPS 101 DO ... END`.

Form 4 of the FOR statement takes an array variable (or a dataarray) and loops through the array from its lowest bound to its highest bound. The index variable may be any type and must match the type of the array elements. Here is an example using a dataarray: `FOR x = [TRUE FALSE FALSE TRUE TRUE] DO ... END`.

REPEAT Statement

The REPEAT statement loops through statements until some condition is met. The format is

```
REPEAT
  <statements>
UNTIL <bexpr>
```

The <*statements*> are executed and then the Boolean expression<*bexpr*> is evaluated. If the result is FALSE, the loop repeats and <*statements*> are executed again. When <*bexpr*> evaluates to TRUE, the loop terminates. A REPEAT statement always executes the <*statements*> at least once.

WHILE Statement

The WHILE statement loops through statements while some condition is true. The format is

```
WHILE <bexpr> DO
  <statements>
END
```

The Boolean expression <*bexpr*> is executed first. If the value is TRUE, the <*statements*> are executed once and <*bexpr*> is evaluated again. The sequence continues until <*bexpr*> evaluates to FALSE. That is, when <*bexpr*> is FALSE, the loop terminates. Unlike the REPEAT statements, the statements will not be executed once if the condition initially fails.

IF Statement

The IF statement provides a means of conditionally executing statements. The following types of IF statements are available:

```
IF <bexpr> THEN
  <statements>
END
```

This form will conditionally execute the <*statements*> only if <*bexpr*> evaluates to TRUE. An ELSE clause can be added to the statement so that one of two sets of statements will always be executed:

```
IF <bexpr> THEN
  <statements>
ELSE
  <statements>
END
```

In addition, one or more ELSEIF clauses can be added to the statement to allow multiple conditions to be tested:

```
IF <bexpr> THEN
  <statements>
ELSEIF <bexpr> THEN
  <statements>
ELSEIF <bexpr> THEN
  <statements>
ELSE
  <statements>
END
```

Here is an example of an IF statement:

```
IF SYSTEM = "MS-DOS" THEN
  PRINTLN("Run from an MS-DOS system")
  SEP = '\'
  DATAFILE("C:" + SEP + DIR + SEP + NAME)
ELSE
  PRINTLN("Run on a unix system")
  SEP = '/'
  DATAFILE(DIR + SEP + NAME)
END
```

The Break Statement

The BREAK statement works within loop statements (WHILE, REPEAT, and FOR). When a BREAK statement is encountered, the loop is immediately exited. The behavior of a BREAK statement outside of a loop causes the current "scope" to be exited. This means that within the main program (outside of a user-defined procedure or function) a BREAK acts like a HALT statement. Within a user-defined procedure or function, the procedure or function is exited.

The Continue Statement

The CONTINUE statement works within loop statements (WHILE, REPEAT, and FOR). When a CONTINUE statement is encountered, all further statements are skipped until the end of the current loop.

The Exit Statement

The EXIT statement immediately exits the current procedure or function. When an EXIT statement is encountered outside of a procedure or function, the program exits.

Differences Between Version 2.0 and Version 2.1

Version 2.1 offers improved speed, greater memory capacity, and the addition of some significant new capabilities. With one minor exception (FOR loops using DOWNTO), version 2.0 programs should work without change in version 2.1. Here is a list of the most important changes:

- User-defined procedures and functions are now available.

- BREAK, CONTINUE, and EXIT statements have been added.

- DOS/Windows versions of *mle* execute from two to five times faster.

- Versions are now available for Linux (and other) operating systems. New versions are not available for Solaris/SPARC systems.

- The 64 ki limit on user-defined arrays and DATA variables in DOS/Windows versions has been lifted.

- The dataarray structure for defining arrays (single or multidimensional) [<expr>, <expr>, ...] has been added for assigning initial values to array variables.

- Array variables can be assigned to other array variables of identical size.

- Complex numbers are now supported. Many functions have been extended to return complex numbers. Complex numbers are specified as the expression, for example, 2.7 - 3.4i.

- The REAL2STR function has been modified to provide for many new formats.

- Some predefined files are now flushed (i.e. buffered data are written) before the program exits

- SYMBOLICINFIN is a new Boolean variable that, when TRUE (the default) writes oo and -oo for infinity. When false, it prints a number. This is useful when writing output to be used by other programs. Also, the value of infinity can be changed by assigning a new value to INFINITY.

- The default width of real numbers is controlled by the REALWIDTH and the default number of decimal places is controlled by the REALDECIMALS variables. Likewise, the default width and decimal places for complex numbers is controlled by COMPLEXWIDTH and COMPLEXDECIMALS.

- Plotting routines have been added for generating *GNUPLOT* output: PLOT, CURVE, and MULTIPLOT. Also the MODEL statement has been modified to plot estimated distributions (with confidence intervals) and likelihood surfaces. See the **PLOTTING** chapter in the *Users manual* for details.

- The FOR statement has been greatly enhanced. The STEP keyword provides for different step sizes. The looping index variable can be either real or integer. The STEPS keyword specifies the number of steps to loop over between the two limits. Finally, the FOR statement can take a dataarray or an array variable and loop over each element of the array (of any type). Since a step size of -1 can be used, the DOWNTO statement is no longer supported.

- A great number of intrinsic functions have been added: CLOCKSEED, EXEC(<*cmd*>,<*args*>), PLOTFILE(), NORMAL(x), NORMALCDF(x), CHISQ(x,df), STUDENTT(x,df), INVSTUDENTT(p,df), FDIST(x,df1,df2), INVFDIST(p,df1,df2), INVBETA(p,v,w), DIREXISTS, FILESIZE(), ENVCOUNT, ENVSTRING(), ARGCOUNT, ARGSTRING(), GETDIR, ZETA(), SETRANSFORM(<*expr*>).

- Added some new procedures. Among them: `ERASE`, `EXEC(<cmd>,<args>)`, `RENAME(n1, n2)`, `CHDIR(n1)`, `MKDIR(n1)`, `RMDIR(n1)`, `GETDATE()`, `GETTIME()`, `WRITEPLOTLN()`, `WRITEPLOT()`, `PLOTFILE()`, `PTRANSFORM()`, `FINISHPLOT`. Additionally, `INC(x)` and `DEC(x)` are defined as both procedures and functions.

- New predefined PDFs: `ZIPF`, `BETABINOMIAL`, `THOMAS`, `POLYAEGGENBERGER`.

- A restart file option has been added assist in rerunning programs. The `-sw` writes updated parameter `START` values to the file <*name* ><*model_number*>.<*run_number*> each iteration. The `-sr` option on the command line instructs *mle* to read parameter `START` values from the file.

- A termination file option has been added. When the `-t` is given, the program will periodically check for the file <*name*>.TRM. If the file exists, the program will terminate.

- The `RUN` part of the `MODEL` statement can now take a `WITH` clause in addition to `FULL` and `REDUCE`. A list of parameter names follow the `WITH` keyword. The model will be run using only those parameters. Other parameters will be set to the `TEST` value set in the `PARAM` function. Additionally, one or more parameter names can be enclosed in parentheses following the `WITH` keyword. All possible models (2^N for N parameters) that include and exclude these parameters will be formed.

- A Bayesian model selection report is now available. Setting `AIC_SELECT=TRUE` will produce a report based on Akaike's information criterion (AIC). Setting `AICC_SELECT=TRUE` will produce a report based on a sample-size corrected Akaike's information criterion (AICC). Setting `BIC_SELECT=TRUE` will produce a report based on Bayesian information criterion (BIC). For each report, the most parsimonious model is selected. Parameters for the selected model are reported with new estimates of standard errors that include model selection uncertainty. The variable `IC_SAMPLE_SIZE` can be set to the effective sample size for a set of observations used for AICC and BIC report.

- The `RUN` part of the `MODEL` statement now takes on a `THEN` <*statements*> `END` clause. The statements are executed after each sub-model is solved. Likewise `THEN` <*statements*> `END` can be used after each `FULL`, `REDUCE`, and `WITH` clause to run statements after the model.

Differences Between Version 1 and Version 2

Changes and New Features in Version 2

There are a number of syntax differences and other changes between *mle* version 1 and version 2. Here is a summary of the most important changes:

- General algebraic expressions are now recognized. Standard operators include: `+`, `-`, `*`, `/`, `^`, `AND`, `OR`, `XOR`, `NOT`, `MOD`, `DIV`, `SHL`, `SHR`, `>`, `<`, `<>`, `=`, `==`, `>=`, `<=`. These operators can be used to build algebraic and Boolean expressions of nearly unlimited complexity. Both = and == are allowed for specifying Boolean comparisons. The standard operator precedence, common to most programming languages, is recognized by *mle*:

Operator(s)	Precedence	Category

- + NOT	High	Uniary operators
^		Exponent operator
* / DIV MOD AND SHL SHR		Multiplying operators
+ - OR XOR		Adding operators
= (or ==) <> < > <= >=	low	Relational operators

The expression `-23+4*-2^3` is equivalent to `ADD(NEGATE(23), MULTIPLY(4, POWER(NEGATE(2), 3)))` which returns `-55`. Parenthesis can be used to override operator precedence. For example, `2*5 + 3*7` will evaluate each multiplication before the addition. Addition can be forced to occur first with parenthesis as in `2*(5 + 3)*7`.

- The `DATA` statement has been rewritten to have a more intuitive transformation mechanism. The transformation looks like an assignment statement following the `FIELD` and `LINE` specification (if any). A list of `DROPIF` <expr> and `KEEPIF` <expr> statements can then be specified (replacing the old `DROP` and `KEEP` statements). Here are some examples:

```
DATA
  age     FIELD 1 = age*365.25 + 270  {convert to days since conception}
  weight  FIELD 2 = weight * 1000  DROPIF weight <= 0
  height  FIELD 3   KEEPIF height > 0
  bmi             = height/weight^2
END {data}
```

The formal specification for each variable is this

<*var*> [`FIELD` x [`LINE` y]] [= <*expr*>] [`DROPIF` <*bexpr*> | `KEEPIF` <*bexpr*> ...]

The first example above reads a value in the first field of the data file and assigns the value to the variable `age`. After that, the expression `age*365.25 + 270` is evaluated and the result assigned to the variable `age`. The second example reads the second field and assigns the value to the variable `weight`. Following that, the expression `weight*1000` is evaluated and assigned to the variable `weight`. Then the expression `weight <= 0` is evaluated. If `TRUE`, the observation is dropped. If not, the observation is kept.

- Observations can now be simulated or otherwise created within *mle*, without reference to a data file. This is done by setting `CREATE_OBS` to some positive value. The following example will create 100 uniform random observations:

```
CREATE_OBS = 100
DATA
  v1      FIELD 1 = RAND
END {data}
```

- A number of useless functions that were used with the old data transformations have been eliminated, e.g.: `ONE`, `SECOND`, `ONEIF`, `RESPONSE`, etc.

- A number of new functions have been added, e.g.: `DEFAULTOUTNAME`, `FISHER`, `ISODD`, `STRING2REAL`, `INT2STR`, `EOF`, `EOLN`. A fairly complete set of functions are now available to work with calendar dates. A full list of simple functions can be generated by typing `mle -h functions`.

- The `PREASSIGN` and `POSTASSIGN` functions have been generalized so that any single statement is allowed in the statement part of the function. By using a `BEGIN ... END` block, more than one statement can be used in the assignment part of the functions. For example:

```
PREASSIGN
  BEGIN  {This is the statement part}
    r : REAL[0 TO 359]
    FOR i = 0 TO 359 DO
      r[i] = DTOR(i)
    END {for}
  END {begin – this is the end of the statement part of the PREASSIGN}
  PDF NORMAL(a, b) c, d END  {This is the function returned by PREASSIGN}
END {preassign}
```

- The conditional expressions in the `IF THEN ELSE END` and `LEVEL` functions take a Boolean expression of any complexity, e.g., `IF (a = b) AND (c^2 + 2 <= 23) OR (d > 1) THEN ... ELSE ... END`.

- The `IF...THEN...ELSE...END` function has been generalized so that multiple `ELSEIF...THEN...` conditions may be added. The following assignment is an example:

```
status = IF height < 48 THEN
           -1
         ELSEIF (height >= 48) and (height <= 60) THEN
           0
         ELSE
           1
         END {if}
```

- Types can be optionally defined for variables when they are first encountered. Valid types are `INTEGER`, `REAL`, `CHAR`, `STRING`, `BOOLEAN`, and `FILE`. For example:

```
x : REAL = 23   {x would be integer, but is defined to be real}
c : STRING = '!'   {c would be char, but is defined to be string}
```

- In general, types are handled better. Adding two integers variables together, for example, returns an integer value. The `IF...THEN...ELSE...END` function can return any type, but the type after the `THEN` must match the type after the `ELSE`.

- Multidimensional arrays are supported for all types. Subscripted values are accessed as, for example, `z[i, j, k]`. Arrays are declared as

```
a : REAL[1 TO 5, -1 TO 1]  = 0   {Declare and initialize matrix a}
b : INTEGER[-4 TO 4, 0 TO 1]     {Declare but no assignment}
```

- A new `DERIVATIVE` function numerically finds the value of a derivative at a specified point along some function. For example, `DERIVATIVE x = 2, 3*x^2 + 2*x + 4 END`, which is the derivative of $3x^2 + 2x + 4$ evaluated at $x = 2$, returns `14.0`.

- The new `FINDMIN` function finds the value that minimizes a bounded function. An example is `FINDMIN x (0, 2*PI) COS(x) END`, which finds a minimum of the function cosine(x) between 0 and 2π. It returns `3.1415925395570` (π is an exact solution). The accuracy of the solution may be specified as a third argument within the parenthesis.

- The new `FINDZERO` function finds the value of an argument for which the function goes to zero. An example is `FINDZERO x (0, PI) COS(x) END`, which finds a value of x for which cosine(x) is zero. It returns `1.5707963267949` (which is close to the exact solution of $\pi/2$). The accuracy of the solution may be specified.

- An important syntactical change is that every `PARAM` function must have a matching `END`.

- The default FORM for the PARAM function is NUMBER if no covariates are specified and LOGLIN if one or more covariates are specified.

- The COVAR specification part of the PARAM function has been generalized to COVAR <*expr*> <*expr*>. A typical specification is

```
PARAM x  LOW=0  HIGH=100 START=25
  COVAR z PARAM beta_z LOW=-5 HIGH=5 START=0 END
END
```

Nevertheless, other expressions are legal. For example

```
PARAM x LOW=0 HIGH=100 START=25
  COVAR z 1
END {param}
```

- The PARAM options HIGH, LOW, START, and TEST are treated like assignment statements which are evaluated just prior to maximization. The right-hand side of the assignment can be any valid expression. For example,

```
PARAM a LOW = IF y > 3 THEN 0 ELSE 3  HIGH = x^2 + 2x - 4  START = y - 1 END
```

- The CONST part of the MODEL statement is longer supported.

- A number of procedures have been added that can be used wherever a statement is allowed, including

```
OPENAPPEND(,) {Opens a file for appending}
OPENREAD(,)   {Opens a file for reading}
OPENWRITE(,)  {Opens a file for writing}
WRITE()       {writes to standard output}
WRITELN()     {writes a line to the standard output}
READ()        {Reads variables from the standard input}
READLN()      {Reads one line of variables from the standard input}
PRINT()       {writes to the output file}
PRINTLN()     {writes a line to the output file}
CLOSE()       {Closes a file}
SEED()        {seeds the random number generator}
DATAFILE()    {defines the data file}
OUTFILE()     {defines the output file}
HALT          {halts the program}
```

- A variety of statements have been added that can be used wherever a statement is allowed, including

```
IF <bexpr> THEN <statements> ELSEIF . . . ELSE <statements> END
FOR <v> = <expr> TO <expr> DO <statements> END
BEGIN <statements> END
WHILE <bexpr> DO <statements> END
REPEAT <statements> UNTIL <bexpr>
BREAK          {exits the current WHILE, REPEAT, FOR loop, or BEGIN...END block}
CONTINUE       {Skips to the next iteration of a WHILE, REPEAT, or FOR loop}
```

- A new QUANTILE function returns the value that gives the *q*th quantile of any of the predefined pdfs. For example, the median (where $q = 0.5$) can be found for the RANDOMWALK pdf, with arguments 2 and 3, as: `QUANTILE RANDOMWALK(0.5) 2, 3 END`. It returns `7.4595847118228`. The function uses algebraic solutions for many pdfs. When no closed for solution is known, an iterative solution is found.

- Fundamental physical constants have been updated to the most recent recommend values provided in Mohr and Taylor (1999).

- Strings can be delimited by either " or ', except that a one-character sequence using ' is a character constant.

Converting Version 1 Programs to Version 2

Programs written in earlier versions of *mle* can be converted into later versions without much difficulty. The most important things to change are given below.

- Change all `INFILE = "mydata.dat"` statements to `DATAFILE("mydata.dat")` procedure calls.

- Change all `OUTFILE = "results.out"` statements to `OUTFILE("results.dat")` procedure calls.

- Change all `SEED = 5352` statements to `SEED(5352)` procedure calls.

- Eliminate all `CONST` blocks that may have been used at the beginning of `MODEL` statements. Instead, define the constant outside of the `MODEL` statement. Alternatively, use a `PREASSIGN` function within the `MODEL` statement to create temporary variables within that statement.

- Add an `END` after all `PARAM` functions.

- Some older versions of *mle* did not have or allow the `DATA...END` function within the `MODEL` statement. In more recent versions, a `DATA...END` function is almost always required to cycle through all observations in the data set. `MODEL` statements should usually look like this:

```
MODEL
  DATA
        {the rest of the likelihood goes here}
  END   {data}
RUN
  FULL
END     {model}
```

- Some older versions of *mle* used the keyword `FREQ` followed by a variable name *within* a `PDF` function to denote the a frequency variable. These must be deleted. The special variable names `FREQ` and `FREQUENCY` should be used in the `DATA` statement to denote frequencies of observations.

- The method of transforming variables within the `DATA` statement has changed in version 2. All transformations must be re-coded following the new syntax (described earlier in this chapter and in a later chapter). Additionally, the method of dropping or keeping variables within the `DATA` statement has changed. An example of the old syntax is

```
DATA
  v1  FIELD 1  DROP < 0
  v2  FIELD 2  ADD 10 MULTIPLY 2
  v3  FIELD 3  KEEP >= 24
  v4  FIELD 4  SUBTRACT 10 POWER 3 DROP <= 1
END     {data}
and the corresponding new syntax is
DATA
  v1  FIELD 1  DROPIF v1 < 0
  v2  FIELD 2  = (v2 + 10)*2
  v3  FIELD 3  KEEPIF v3 >= 24
  v4  FIELD 4  = (v4 - 10)^3  DROPIF v4 <= 1
END     {data}
```

Chapter 2
Installing and running *mle*

The *mle* interpreter is a small, self-contained program that can be run from the command line of the operating system. This chapter describes how to install *mle* in both the DOS environment and the Windows environment. A brief tutorial is given on how to run *mle*, and how to edit program files using a text editor. Additionally, the editor *emle* is described. All command line options are described.

Installing mle

Under Windows, *mle* is installed using a built-in installer. This will install the interpreter along with a rudimentary editor that can be used to edit and run *mle* programs. If you prefer, you can install everything by hand under Windows as well (this is especially helpful if you want to run *mle* from the DOS command line.

The current releases of *mle* can be found on the web at http://faculty.washington.edu/~djholman/mle. For the purposes of this manual we will assume that the current release is 2.1.16.

Unix

Find the current release of *mle*. For a Linux ELF binary, the current release might be called: `mle-2.1.15.linux.i386.tar.Z`. Experienced Unix users will recognize this as a compressed tar file. Here are the steps for installation:

- Copy the file to a subdirectory (say, ~/mle).
- Uncompress the archive with the command `uncompress`: `mle-2.1.11.linux.i386.tar.Z`
- Extract everything from the archive with the command `tar –xvf mle-2.1.11.linux.i386.tar`
- Make sure you have permission to execute the program. Type: `chmod u+x mle`
- The directory now contains the executable (`mle`), example programs, etc. At this point you can run programs from within the directory. You can add the directory to your `PATH` so that you can execute the program from anywhere.

Alternatively, you can move the executable program to a directory in your path. For example: `mv mle ~/bin`

Windows

Find the current release of the *mle* setup and installation program. The current release might be called: `mle_2_1_15_setup.exe`. Note that there are versions with and without the *mle* documentation. The versions should be apparent from the file names. Here are the steps for installation:

- The easiest way to install *mle* is to "open" the setup program via a web browser. Windows will, in effect, execute the install the package. Alternatively, you can download the setup program to any directory, and then run the program (from a DOS window or using the Start→ Run… command).

- The setup program will walk you through a number of steps for installation. If you are not an administrator or power-user on the computer, you will want to change the location where the program is installed from the default of `C:\Program Files\mle` to some other location like `C:\Documents and Settings\<username>\mle`

- Once the installation is complete, you can optionally modify your `PATH` variable so that *mle* can be run from any directory on the command line. The `PATH` variable can be changed in most versions of Windows via Start→Settings→Control Panel→System→Advanced→Environment Variables.

Editing a program

Writing an *mle* program requires that you edit the text of the program, and then "submit" it to the *mle* interpreter. The next step is to view the output of the program. Depending on the results, you will then edit the program again and submit it again. Almost any text editor can be used to edit a program. Additionally, the Windows version of *mle* comes with a simple text editor that is tailored to editing and running programs. This section first describes some text editors available in DOS and Unix that can be used for editing programs. Then the mle editor is briefly described.

Under Unix, there are a number of *de facto* standard editors that are used for programming. The *vi* editor, in particular, is available on almost every installation. Other commonly used text editors on Unix systems are *Pico* and *EMACS*. Before you can develop *mle* programs, you will need to know one of these editors.

Under DOS or Windows, there are a number of editors available (besides the one that comes with *mle*). A standard editor available in all later versions of DOS is called *EDIT*. Alternatives that come as part of Windows are *NOTEPAD* and *WordPad*. Even word processing programs (like MS-Word) can be used, although you must be certain to save the programs as *text files*.

emle

A rudimentary editor is now available with Windows versions of *mle*. This section of the manual briefly describes the editor and its functions.

The editor can be started from the Start→ Program menu. A window pops up that looks like the this:

Alternatively, the editor can be opened from a DOS command line. To do so, the `emle.exe` command must be in your path or current directory. The command `emle myfile.mle` will open the editor and load (or create) the file myfile.mle

The text being edited is displayed in the black area of the screen (although the color can be changed). The top of the screen shows the current menu. The bottom of the screen shows status information. The first '*' means that the current file has been changed. The line number and column number come next. The "Insert" or "OvrWrt" indicates the mode the editor is in. Finally the filename is given if a file is opened for editing.

Editor commands can be accessed through the keyboard (there is currently no mouse support). Keystrokes work as expected— that is, the arrow keys navigate around the text, <PgUp> and <PgDn> keys scroll up and down through the text, etc. Additionally, menu items (which are listed at the top of the screen) are accessed using the <Alt> key along with the highlighted character.

Menus

This section shows and describes the menu commands available in *emle.*

File menu

From the main menu, `<Alt>F` brings up the File menu. The File menu provides a number of commonly used file-related operations. The menu contains these elements:

Open	`<Alt>O` provides a menu for opening up a file. The arrow keys can be used to move through files and directories. Note that the special file "`..`" is used to change to the previous directory.
Save	Saves the current file.
saveAs	Prompts for a new name and then saves the current work as that name.
Close	Closes the current file.
eXit	Exits the program.
Backups	Toggles whether or not back-ups are made while saving files.
Dos	Escapes to a DOS session.

Edit menu

From the main menu, `<Alt>E` brings up the Edit menu. The Edit menu provides some special editing functions. The menu contains these elements.

Del_line	Deletes the current line.
Flipcase	Flips the case of all characters from the cursor to the end of the current line.
Lowercase	Changes characters to lower case to the end of the current line.
Uppercase	Changes characters to upper case to the end of the current line.
Ctrl_key	After selecting this, a control key can be entered into the text.
Quit	Quits this menu.

Block menu

From the main menu, `<Alt>B>` brings up the Block menu. This menu provides editing functions for selecting, moving and performing other functions on blocks of text. The menu contains these elements.

markBegin	Marks the beginning of a block.
markEnd	Marks the end of the block.
Goto	Goes to the currently marked block.
Copy	Copies the current block.
Delete	Deletes the current block.
Move	Moves the current block.
cLear	Removes the current block.
Write	Writes the current block to a file.
Quit	Quits this menu.

Search menu

From the main menu, `<Alt>S` brings up the Search menu. This menu provides text searching and replacement functions. The menu contains these elements.

Find	Searches for a string of text.
Find (Next)	Searches for the next occurrence of the text.
Find (Opts)	Searches for text after setting the search options.
Replace	Searches and replaces text.
Replace (neXt)	Searches and replaces text again.
Replace (oPts)	Searches and replaces text after setting some options.
Goto_line	Goes to the specified line number
Quit	Exits the menu.

Mle menu

From the main menu, `<Alt>M` brings up the Mle menu. This menu provides some several mle-related special functions. The menu contains these elements.

Parse	Submits the current file to *mle* with the parse option (-p). This, in effect, checks for syntax errors.
Run	Submits the current file to *mle*, so that the program is run.
Expression	Prompts the user for an expression to evaluate via *mle*.
template (Insert)	Inserts a code template at the current location.
template (Options)	Sets options (intent level, case for code, case for comments) for the templates.
Quit	Exits the menu.

Window menu

From the main menu, `<Alt>W` brings up the Window menu. This menu provides some several mle-related special functions. The menu contains these elements.

Backcolor	Switches through the background color for the text.
Forecolor	Switches the foreground color of the text.
Wordwrap	Toggles word-wrap
Setmargins	Sets the left and right margins.
Ruler	Toggels a ruler display (Off, Top, Bottom).
reDraw	Redraws the current screen.
Quit	Exits the menu.

Help menu

From the main menu, `<Alt>H` brings up the Help menu. This menu provides for several types of help information. The menu contains these elements.

Editor_keys	Displays the current mapping between editor commands and the keyboard.
Key_map	Displays the current mapping of key to editor commands.
Mle_help	Submits the current word (the word the cursor is currently sitting on) to *mle* with the help option (-h) option. Any mle help messages that match the keyword exactly will be displayed.
mle_Search	Submits the current word to *mle* with the help option (-H) option. Any mle help messages that match any part of the keyword will be displayed.
About	Shows information about the editor.
Quit	Exits the menu.

Default settings

The editor preserves a number of settings from one editing session to the next: foreground color, background color, insert status, word wrap status, right and left margins, ruler setting, *mle* indent setting, *mle* keyword case setting, *mle* comment case setting, back-up setting, search “from top” flag, search “ignore case” flag.

The information for these settings is stored in the file `emle.cfg` which resides in the same directory as `emle.exe`.

The configuration file can also save a series of user-defined commands that are executed whenever the editor is started. To add commands to the file, use the `Alt_F9` command, which prompts for additional commands before saving the configuration file.

Default command mapping

The default mapping between editor commands and the keyboard is described in this section. Notice that a command can have more than one key assigned to it. The default keyboard mapping can be changed by saving the current map (`Shift_F9` by default), and editing the resulting file. The editor will then read the keyboard map by default. The keymap is stored in the file `emle.kbm` which resides in the same directory as `emle.exe`.

Cursor control commands

RtArr ..... Go to next character
LtArr ..... Go to previous character
Ctrl_PgUp ..... Go to beginning of file
Ctrl_PgDn ..... Go to end of file
End..... Go to end of line
Home..... Go to beginning of line
DnArr ..... Go to next line
UpArr ..... Go to previous line
PgDn ..... Go down one page
PgUp ..... Go up one page
Ctrl_I..... Go to next tab
Shift_Tab..... Go to previous tab
Ctrl_Home..... Move window up
Ctrl_End ..... Move window down
Ctrl_RtArr ..... Skip ahead one word
Ctrl_LtArr ..... Skip back one word

Insert and delete commands

Delete..... Delete character (del)
Ctrl_H ..... Delete character (backspace)
Ctrl_J, Ctrl_M ..... Break line at current position
Insert ..... Toggle insert/overwrite
Ctrl_Y ..... Delete line
Ctrl_B..... Delete to beginning of line
Ctrl_E..... Delete to end of line
Ctrl_N ..... Insert new line
Ctrl_R..... Delete word

File commands

<not assigned>..... Close file. Save if necessary
<not assigned>..... Close file without saving
<not assigned>..... Save and close file
Ctrl_O ..... Open. Save current file if necessary
<not assigned>..... Open without saving current file
<not assigned>..... Save current and open
Alt_X ..... Quit. Save if necessary
Ctrl_K ..... Quit without saving

Shift_F3..... Save and quit
<not assigned>..... Save as
<not assigned>..... Save
<not assigned>..... Save file
Alt_F3 ..... Set whether backup files are made

Block commands

Shift_F4, Alt_-..... Mark beginning of block
Alt_P ..... Copy block
Alt_Q ..... Delete block
Ctrl_F4, Alt_= ..... Mark end of block
Alt_O ..... Go to block
Alt_C..... Clear block marks
Alt_V, Alt_F4..... Move block
Alt_T..... Write block to a file

Page formatting commands

Ctrl_F5 ..... Set background color
Shift_F5..... Set foreground color
Shift_F8..... Set margins
F5..... Redraw the screen
Alt_K ..... Toggle ruler display
F8..... Toggle word wrap

Help commands

F1..... Displays editor commands
Alt_F1 ..... Displays keys mapped to commands
Ctrl_F1..... Give help on an mle keyword
Shift_F1..... Match and give help on a keyword
<not assigned>..... Program information

Execution commands

F9..... Open up OS window
Shift_F2..... Parse in mle
F2..... Run in mle
Alt_F2 ..... Run an mle expression

Search commands

F6..... Find text
Shift_F6..... Find next occurrence
Ctrl_F6..... Find with options
F7..... Find and replace
Shift_F7..... Find and replace next occurrence
Ctrl_F7..... Find and replace options
Alt_G ..... Goto line

Other commands

Ctrl_T, F10..... Insert an mle template
Shift_F10..... Change mle template options
Ctrl_F..... Change case to end of line
Ctrl_L..... Change to lower case to EOL
Ctrl_U ..... Change to upper case to EOL

Alt_A ..... Enter ASCII code
Ctrl_V ..... Accept <Ctrl> key
Shift_F9..... Writes startup key map file: emle.kbm
Ctrl_F9..... Reads key map file: emle.kbm
Alt_F9..... Saves configuration information to the file: emle.cfg
Alt_F8..... Shows internal information (used for debugging).
Alt_F5..... Turns debugging on

Menu commands

<not assigned>..... Main menu
Alt_F, F3..... File menu
Alt_E..... Edit menu
Alt_B, F4..... Block menu
Alt_S..... Search menu
Alt_M..... mle menu
Alt_W..... Window menu
Alt_H ..... Help menu

Default keyboard mapping

The default keyboard map is described in this section. The default keyboard mapping can be changed by saving the current map (Shift_F9 by default), and editing the resulting file.

Ctrl_A ..... unmapped.....
Ctrl_B..... linedelBOL.....Delete to beginning of line
Ctrl_C..... unmapped.....
Ctrl_D ..... unmapped.....
Ctrl_E..... linedelEOL .....Delete to end of line
Ctrl_F..... flipcase.....Change case to end of line
Ctrl_G ..... unmapped.....
Ctrl_H ..... chardelback .....Delete character (backspace)
Ctrl_I..... tabnext.....Go to next tab
Ctrl_J..... enter .....Break line at current position
Ctrl_K ..... quitnosave .....Quit without saving
Ctrl_L..... tolower .....Change to lower case to EOL
Ctrl_M..... enter .....Break line at current position
Ctrl_N ..... lineins.....Insert new line
Ctrl_O ..... open .....Open. Save current file if necessary
Ctrl_P..... unmapped.....
Ctrl_Q ..... unmapped.....
Ctrl_R..... worddel .....Delete word
Ctrl_S..... unmapped.....
Ctrl_T..... mletempl .....Insert an mle template
Ctrl_U ..... toupper .....Change to upper case to EOL
Ctrl_V ..... ctrl.....Accept <Ctrl> key
Ctrl_W..... unmapped.....
Ctrl_X ..... unmapped.....
Ctrl_Y ..... linedel .....Delete line
Ctrl_Z..... unmapped.....
Ctrl_[..... unmapped.....
Ctrl_\..... unmapped.....
Ctrl_]..... unmapped.....

Ctrl_^ ..... unmapped.....
Ctrl__ ..... unmapped.....
Shift_Tab..... tabprev .....Go to previous tab
Alt_Q ..... blockdel.....Delete block
Alt_W..... windowmenu .....Window menu
Alt_E..... editmenu.....Edit menu
Alt_R..... unmapped.....
Alt_T..... blockwrite .....Write block to a file
Alt_Y ..... unmapped.....
Alt_U ..... unmapped.....
Alt_I..... unmapped.....
Alt_O ..... blockgoto.....Go to block
Alt_P..... blockcopy.....Copy block
Alt_A ..... ascii.....Enter ASCII code
Alt_S..... searchmenu.....Search menu
Alt_D ..... unmapped.....
Alt_F..... filemenu .....File menu
Alt_G ..... gotoline .....Goto line
Alt_H ..... helpmenu.....Help menu
Alt_J..... unmapped.....
Alt_K ..... rulertoggle.....Toggle ruler display
Alt_L..... unmapped.....
Alt_Z..... unmapped.....
Alt_X ..... quit.....Quit. Save if necessary
Alt_C..... clearmarks .....Clear block marks
Alt_V ..... blockmove.....Move block
Alt_B..... blockmenu.....Block menu
Alt_N ..... unmapped.....
Alt_M..... mlemenu.....mle menu
F1..... helpedit .....Displays editor commands
F2..... mlerun.....Run in mle
F3..... filemenu .....File menu
F4..... blockmenu.....Block menu
F5..... redraw .....Redraw the screen
F6..... find.....Find text
F7..... replace.....Find and replace
F8..... wordwraptoggle.....Toggle word wrap
F9..... exec.....Open up OS window
F10..... mletempl .....Insert an mle template
Home..... linebegin.....Go to beginning of line
UpArr..... lineprev .....Go to previous line
PgUp ..... pageup.....Go up one page
LtArr ..... charprev .....Go to previous character
RtArr..... charnext.....Go to next character
End..... lineend.....Go to end of line
DnArr..... linenext .....Go to next line
PgDn ..... pagedown .....Go down one page
Insert ..... inserttoggle.....Toggle insert/overwrite
Delete..... chardel.....Delete character (del)
Shift_F1..... helpmlesearch.....Match and give help on a keyword
Shift_F2..... mleparse.....Parse in mle

Shift_F3..... quitsave .....Save and quit
Shift_F4..... blockbegin.....Mark beginning of block
Shift_F5..... colorforeset .....Set foreground color
Shift_F6..... findnext .....Find next occurrence
Shift_F7..... replacenext .....Find and replace next occurrence
Shift_F8..... marginset.....Set margins
Shift_F9..... writekeymapfile.....Writes startup key map file
Shift_F10..... mletmplopts.....Change mle template options
Ctrl_F1..... helpmle .....Give help on an mle keyword
Ctrl_F2..... unmapped.....
Ctrl_F3..... unmapped.....
Ctrl_F4..... blockend.....Mark end of block
Ctrl_F5..... colorbackset .....Set background color
Ctrl_F6..... findopts .....Find with options
Ctrl_F7..... replaceopts .....Find and replace options
Ctrl_F8..... unmapped.....
Ctrl_F9..... readkeymapfile.....Reads key map file
Ctrl_F10..... unmapped.....
Alt_F1..... helpkeyboard.....Displays keys mapped to commands
Alt_F2..... mleexpr .....Run an mle expression
Alt_F3..... makebackup .....Set whether backup files are made
Alt_F4..... blockmove.....Move block
Alt_F5..... debug .....Turns debugging on
Alt_F6..... unmapped.....
Alt_F7..... unmapped.....
Alt_F8..... debugscreen.....Shows internal information
Alt_F9..... configsave .....Saves configuration information
Alt_F10 ..... unmapped.....
Ctrl_PrtSc..... unmapped.....
Ctrl_LtArr ..... wordprev .....Skip back one word
Ctrl_RtArr ..... wordnext .....Skip ahead one word
Ctrl_End..... windowdown.....Move window down
Ctrl_PgDn ..... fileend .....Go to end of file
Ctrl_Home..... windowup.....Move window up
Alt_1 ..... unmapped.....
Alt_2 ..... unmapped.....
Alt_3 ..... unmapped.....
Alt_4 ..... unmapped.....
Alt_5 ..... unmapped.....
Alt_6 ..... unmapped.....

Running a program

mle programs are usually run by typing `mle` followed by any command-line options, followed by the name of the program file on the DOS or Unix command line. The *mle* interpreter will then read in and parse the entire program file, and the program statements will be executed.

If *mle* encounters an error in the program, an error message is printed and further execution terminates. Warning messages are printed from *mle* without terminating the run.

The following sections provide more details on how to run *mle* from the command line.

Specifying the Program File and Command Line Options

There are several methods for specifying the program file. Typically, the program file is specified on the command line. Here are some examples of how the `mle` command is used to run a program file called `test.mle`:

```
c:\test> mle test.mle                  Runs mle on the file analysis.mle.
c:\test> mle -v test.mle               Runs mle, verbose option is set.
c:\test> mle -p test.mle               Parses test.mle, reports syntax errors.
C:\test> mle                           mle will request the input file name.
mle Program file to run? test.mle
```

The last example shows that if a program file name is not given on the command line, you will be prompted for the program file name.

The middle two examples show command line options (`-v` and `-p`) being specified. Command line options are used to change the behavior of mle, and are discussed below. If you type an erroneous command line option, or the file is not recognized by *mle* the following synopsis is given:

```
c:\test> mle -z analysis.mle             There is no -z option.
Error: Incorrect number of parameters

Usage: mle [-v] [-p] [-i] [-dd] [-de] [-di] [-dl] [-dp] [-ds] [-dx] [mlefile]
  -v  Iteration histories and other messages are written to the screen
  -p  Only parses the mle file
  -i  Runs mle interactively
  -dd Turns on data debugging
  -de Echos characters while parsing
  -di Turns on integration debugging
  -dl Turns on likelihood debugging
  -dp Turns on parser debugging
  -ds Turns on symbol table debugging
  -dx Turns on debugging during execution
  mlefile is the name of the file with the program

Usage: mle -h [name1 name2 . . . .]
  help for PDFs, functions, symbols, parameter transforms
  -h matches words exactly, -H searches within words

Usage: mle -pn n1 n2 . . . .
  parses n's and returns values and type
```

Table 1 gives a list of valid command line options. A useful command line option is `-p` (parse only) which tell *mle* to parse the program (without running it) and report any errors in the grammar. The statements within the program are not executed. Another very useful option is the `-v` (verbose) option, which tells *mle* to provide periodic status reports while solving a likelihood. Among other things, the status report prints out the likelihood and parameter values at each iteration.

Help Options

mle predefines a large number of functions, variables, constants, and reserved words. The `-h` (help) option provides short summaries of *mle* language parts, PDFs, and concepts. Typing **`mle -h`** yields

```
Type mle -h <keyword> to match keywords exactly.
Type mle -H <keyword> to match partial keywords.

 mle -h MLE gives a program outline.
 mle -h PROCEDURES lists procedures.
 mle -h PDFS lists PDF types.
 mle -h FORMS lists parameter forms.
 mle -h HAZARD gives an example of a hazard specification.
 mle -h SYMBOLS lists pre-defined variables.
 mle -h NUMBERS lists number formats.
 mle -h FUNCTIONS lists simple functions,
Help is available for the following types of functions/expressions:
IDENTIFIER     FUNCTION       ARRAY          DATA           DATAARRAY
DERIVATIVE     FINDMIN        FINDZERO       FUNCTION       IF
INTEGRATE      LEVEL          LEVELDELTA     PARAM          PDF
PHAZARD        PPDF           POSTASSIGN     PREASSIGN      PRODUCT
QUANTILE       QDF            SUMMATION

Help is available for the following statements:
ASSIGNMENT  BEGIN  BREAK  CONTINUE   CURVE  DATA       EXIT   FOR
FUNCTION    IF     MODEL  MULTIPLOT  PLOT   PROCEDURE  REPEAT WHILE
This option is particularly helpful for providing a short summary of intrinsic
parameters for predefined PDFs.  For example, typing  mle -h weibull  yields:
WEIBULL Distribution
4 continuous variables: t(open), t(close), t(left trunc), t(right trunc)
Exact failure when t(open)=t(close)
Range:   t: (Time)  0 <= t < +oo
2 intrinsic parameters:
  a: (Scale)  0 < a < +oo
  b: (Shape)  0 < b < +oo
a is the characteristic life ~= 63.2th % in units of a
f(t) = S(t)h(t);  S(t) = exp[-(t/a)^b];  h(t) = [b*t^(b-1)]/(a^b)
mean = a*Gamma[1+1/b]; var = (a^2)*Gamma[1+2/b]-{Gamma[1+2/b]}^2
mode = a(1-1/b)^(1/b) for b>1; mode = 0 for b<=1; median = a*log(2)^0.5
   Gamma(x) is the gamma function
Covariate effects may be modeled on the hazard
```

Table 1. Command line options.

Option	Description
`-v`	Sets `VERBOSE` to `TRUE` so that an iteration history and other information is printed to standard output while solving a likelihood model.
–h –h <*name*>	Provides help information about PDFs, functions, variables, constants, reserved words, and parameter transformations. When <*name*> is replaced by a PDF name, a transformation name, a function, or a predefined variable, a brief help message is given. If <*name*> is not a known topic, a list of topics is printed.
–H <*name*>	Provides help information like `-h`, but matches anything that contains the string <*name*>. If <*name*> is not given, all help messages are given.
`-i`	Runs *mle* interactively. Commands are typed directly in from the keyboard. Using interactive mode is helpful for using *mle* as a probability calculator. Interactive mode is discussed later in this chapter.
`-p`	The program file is parsed for errors and not run. Sets the internal variable `PARSE` = `TRUE`.
-I <path>	Specifies a file system path to include while searching for include files (see command `INCLUDE`).
-b	Batch mode. Turns off keyboard monitoring (for interactive debugging) while executing models.
-t	Tells *mle* to watch for a termination file while solving a model, and if it is found, terminates solving the model at the end of the next iteration.
-Sr	Tells *mle* to read in values from the "start-file" to initialize start values for a `MODEL` statement. The start-file is automatically created by the `-Sw` option.
-Sw	Tells *mle* to write a "start-file" following each iteration during a `MODEL` statement. The values are read and used as "updated" start values when the `-Sr` option is used.
-S	A special flag equivalent to `-Sr -Sw -t -v`
-af	A flag used by the editor *emle* to interact with *mle*.
–pn # ...	*mle* supports various number formats (dates, times, Roman, etc.). This command line option takes a list of numbers, parses them, and reports the results.
-vx	Prints out a version number string.
–dd	Turns on data debugging, where details are printed as each observation is read from the data file and converted into a data set. Sets `DEBUG_DATA` = `TRUE`.
–de	Echos each character in the program file as it is being read. Sets `DEBUG_ECHO` = `TRUE`.
–di	Turns on debugging for the integration routines, so that a report for each integration call is written to the standard output. Sets `DEBUG_INT` = `TRUE`.
–dl	Turns on likelihood debugging, so that parameter estimates and an individual likelihood is written to standard output for every likelihood evaluation. Sets `DEBUG_LIK` = `TRUE`.
–dp	Turns on debugging while reading and parsing the program file. Sets `DEBUG_PARSE` = `TRUE`.
–ds	Turns on debugging for the symbol table routines, so that information is printed to standard output whenever variables and symbols are created or destroyed. Sets `DEBUG_SYM` = `TRUE`.
–dx	Turns on debugging while running (executing) the program file, so that a message is written to the screen just prior to executing each statement. Sets the internal variable `DEBUG_EXEC` = `TRUE`.
–d #	Sets the internal variable `DEBUG` to the value set by #. When # is greater than zero, debugging messages are printed. The nature and type of messages changes, and the output is used for program development. A value of 0 turns off debugging.

which shows that there are two intrinsic parameters. Note that equations are given for the probability density, survival function, or hazard function. At least one of these is given for other PDFs as well. Here is another example: `mle -h pi`

```
Symbol: PI{REAL Const Static} = 3.14159265359
And, a third example: mle -h besseli
Function BESSELI(x1, x2)
 returns the modified Bessel fcn I (integer order x1) of real x2
```

The `-h` option provides summaries for a few topics. For example, `mle -h FUNCTIONS`, will list all of the intrinsic simple functions, and `mle -h SYMBOLS` which lists all variables in the symbol table. Typing `mle -h functions | more` is a useful way to examine all *mle* intrinsic functions because the `more` program will stop the display after each page of output is listed.

The `-H <name>` option is similar to the `-h` option except that any function, variable, constant, or reserve word that includes `<name>` as some part of the reserve word is printed. The `-H` option is particular useful when you cannot recall the exact name for some keyword. Thus, `mle -H integra` lists all keywords with the string "integra":

```
INTEGRATE v (expr1, expr2) expr3 END
INTEGRATE v (expr1, expr2, expr4) expr3 END
 v is the variable of integration.
 expr1 is evaluated for the lower limit of integration.
 expr2 is evaluated for the upper limit of integration.
 expr3 is the integrand, and may reference v.
 expr4 is an optional convergence criterion

 INTEGRATE_METHOD = I_TRAP_CLOSED uses closed trapezoidal integration
 INTEGRATE_METHOD = I_TRAP_OPEN uses open trapezoidal integration
 INTEGRATE_METHOD = I_SIMPSON uses open simpson integration
 INTEGRATE_METHOD = I_AQUAD (default) uses adaptive quadrature integration
 INTEGRATE_N is the number of iterations (default: 100)
 INTEGRATE_TOL is the convergence criterion (default:  1.0E-0006)

INTEGRATE_METHOD{INTEGER} = 3
INTEGRATE_N{INTEGER} = 100
INTEGRATE_TOL{REAL} = 0.00000100000
```

Debugging Options

A number of command line options assist in debugging models, data files, program options, numerical methods, and the *mle* program interpreter itself (see Table 1). The `-dx` option provides a way of tracing the execution of each statement in turn. The `-dl` option is useful for examining likelihoods every time a complete likelihood is computed. More advanced debugging options assume some familiarity with the internal workings of parsers, symbol tables, and an advanced understanding of likelihood estimation. The `-di` option offers help with debugging problems of numerical integration in *mle*.

The debugging and help options send output to the screen (or standard output device). The standard DOS and Unix redirection symbols ">" and "|" can be used to redirect the output to other devices. For example, the command `mle -d 25 test.mle > test.dbg` will create a (possibly large) file called test.dbg. The output file specified within the test.mle program will not be affected.

Other Options

testing number formats

mle supports many formats for numbers. Each number begins with a numeral, but can contain additional symbols to specify different meanings. A full discussion of the number formats is given in the data chapter. You can test the way in which *mle* reads numbers by using the `-pn` option. The command line `mle -pn 8x3017 22'16" 12k` returns

```
"8x3017" is the integer 1551
"22'16"" is the real 0.0064771107796
"12k" is the real 12000.000000000
```

A list of all number formats is given with `mle -h numbers`

Start-file options

The `-Sr` and `-Sw` options work together to read and write temporary results to a file, called a start-file, while a `MODEL` statement is executing. When the `-Sw` option is used, the current parameter estimates are written at each iteration. The `-Sr` option will read the start-file and replace the `START=` parameter values with the start-file values.

The purpose for using these options is to preserve intermediate results for models that take a long time to solve. For example, if a program will take weeks or months to solve, using these options can prevent the loss of work in the event the computer crashes.

Batch options

"Batch" refers to running programs in an unattended mode. Typically, batch mode is used when a user (or another program) starts running a program and then logs out. *mle* provides a few options that assist in running in a batch mode.

The `-b` option turns off keyboard monitoring (for interactive debugging) while executing models. Normally, a user can interrupt *mle* while solving a model, and the interactive debugger can be used. However this can potentially lead to difficulties because the keyboard must be monitored. While running in a batch mode, the `-b` option turns off this monitoring and slightly speeds up execution.

The termination file option `-t` tells *mle* to watch for a termination file while solving a model. The term file is given the same name as the program file name, but with a `.trm` file extension replacing the `.mle`. If the file is found, *mle* terminates solving the model at the end of the next iteration.

interactive mode

mle can be run interactively using the `-i` command line option. When run interactively, commands are typed directly into the command line. This option is particularly useful when *mle* is used as a "calculator", which is described in the last section of this manual. Of course, a full program can be written directly from the keyboard using this option.

Calculator Mode

mle can act like a calculator. In this mode, instead of a program filled with assignment statement, data statements, and model statements, a series of expressions are given to *mle*. The expressions are evaluated and the result is printed. This can be done either interactively (using the `-i` command line option) or by reading in a program file.

This "calculator" mode is assumed when the first keyword of a program is not `MLE`. *mle* will then execute all subsequent commands as expressions to be interpreted. Here is an example

```
c:\>mle -i
sin(pi * 3)This is the user-defined expression
2.168404E-0019     And this is what was returned

PDF normal(2, 3) 1, 2 end Compute the area under normal pdf from 2 to 3, μ=1, σ=2
0.1498822726114    resulting area

INTEGRATE z (2, 3) PDF NORMAL(z) 1, 2 end end    Expressions can be nested. Integrate
for 2 to 3 a normal pdf with μ=1, σ=2
0.1498822847945    This should be close to the previous result

gamma(3.8) Evaluates the gamma function
4.6941742051124
summation i (1, 10) 1/i^2 end     Sum from 1 to 10, 1/i2
1.5497677311665

end Ends and returns to DOS
```

In version 2 of *mle*, when using calculator mode interactively, there will always be a delay of one expression before the results is returned. This is because an expression can continue indefinitely. For example, the expression "`SIN(2*pi)`" followed by a carriage return does not complete the expression because the next line may be "`+ 1/2`". A new expression is needed to denote the end of the old expression. Thus, typing "`1 pi 2`" followed by a carriage return will result in two complete expressions (returning `1` and `3.1415926535898`). The third expression is not yet complete.

Note that if you begin *mle* with the options `-i -v` and begin typing expressions, the verbose result will show the entire expression in functional form (i.e. as a series of functions). For example

```
c:\>mle -i -v
sin(pi^2/4 + 1)                                          This is the user-defined
expression
returns
SIN(ADD(DIVIDE(POWER( PI ,  2),  4),  1)) ->  -0.320074806512
```

Chapter 3
Creating data sets

As a first step in parameter estimation, a *data set* must be read in or created. This chapter discusses aspects of creating a data set, including

- How to read a data set into *mle*
- How to set up a data file
- How to transform variables
- How to drop unwanted observations
- The number formats recognized by *mle*

Reading data from a file

Data sets are read into *mle* from an input file. They consist of at least one, and usually many, *observations*. Each observation is a collection of one or more *variables*. The *mle* `DATA` statement defines how observations are to be read from a file. The data statement also has mechanisms for doing transformations to the data as they are being read. In the current implementation of *mle* the transformations and other data manipulations provided by the data statement are adequate for most tasks, but are not particularly powerful. Other programs (spreadsheets or database managers, for example) can be used for complicated data transformations, and the resulting data set can be then used by *mle*.

Naming the data file

Data sets are created by a `DATA` statement. The data statement typically works by reading observations from a data file. This file must be named and opened with a call to the `DATAFILE()` procedure. The call to `DATAFILE()` is usually defined near the top of the program, before the `DATA` statement, as in the example in Chapter 1. The data statement begins with the word `DATA` and is terminated by a matching `END`. So, if the name of the data file is `MYDATA.DAT`, you include the statement `DATAFILE("MYDATA.DAT")` prior to the `DATA` statement. Full path names are permissible: you might call the `DATAFILE` procedure as `DATAFILE("C:\STATS\MLE\BONES\DATAFILE.DAT")`.

The DATA statement

The DATA...END statement reads in the data file. Within the DATA...END is a sequence of one or more variable names. Here is a simple DATA statement that creates three variables.

```
DATAFILE("test.dat")
DATA
  first_time      FIELD 3
  missing_data    FIELD 4
  last_time       FIELD 1
END
```

This example shows three components for defining each variable, the variable name, the key word FIELD and a field number.

Variable name: Variables names begin with a letter and can then contain any combination of letters, numbers, the underscore, and period characters. A variable name may be up to 255 characters long and all characters are significant. Examples of valid variable names are: LAST_ALIVE, VARIABLE_14 , A_REALLY_LONG_VARIABLE_NAME, and A. Variable names are not case sensitive so the variable abc is the same as ABC and aBc.

In the current version of *mle*, all variables created in the DATA...END statement are defined to be type *real*. This is so even if the number format suggests that the variable should be type integer. Integer values read from the data file are simply converted to real number values. Text strings can exist within a text file, but must not be assigned to a variable.

mle pre-defines many built in constants and variables, so you should avoid variable names that exist for some other purpose such as an *mle* constant (a list of all variables appears in a later chapter). Likewise, *mle* uses the period as an internal delimiter for some purposes. Conflicts might arise if your variable names contain a period; you are free to use periods, but an underscore might be a better choice.

Field: The word FIELD refers to which column within an input file a variable is found in. In the hammes.dat file used in Chapter 1, four fields (or columns) existed in the input file. The field specifier must be a positive integer constant.

A number of other elements can be added to a variable definition as well. These are defined below, but the grammar used for specifying each variable is:

```
 <variable name>  [FIELD x [LINE y]] [= <expr>] [DROPIF <expr> | KEEPIF <expr> ...]
```

Line: Sometimes observations take up multiple lines in the data file. An example might be times to first birth for a married couple in which female characteristics appear on the first line and the male characteristics occur on the second line. When the LINE keyword is used, e.g. LINE 2, *mle* keeps track of the maximum number of lines specified this way. Then, *all* observations are assumed to have the maximum number of lines. If observations are each on one line, the statement LINE 1 may be dropped—one line per observation is assumed. The line specifier must be a positive integer constant.

The remaining specification provides ways of transforming variables and dropping (or keeping) observations. The next several sections discuss transformations and gives additional examples of declaring variables in the DATA section.

Dropping or keeping observations

A series of statements to drop (or keep) individual observations from the input file can be specified as the last items in a variable declaration within the DATA statement. Here are some example of this:

```
DATAFILE("test.dat")
my_drop_value = 100
DATA
  first_time      FIELD 3  DROPIF first_time <= 0
  missing_data    FIELD 4  DROPIF missing_data <> 1
  last_time       FIELD 1  KEEPIF last_time > 0
                           DROPIF (last_time == INFINITY) OR (first_time < last_time)
  alt_missing     FIELD 5  KEEPIF alt_missing == missing_data
END
```

The DROPIF keyword specifies that a condition will be tested; if the condition is true, then the entire observation is dropped. The first DROPIF statement here specifies that the entire observation is to be dropped if first_time is less then or equal to zero. The KEEPIF keyword is like DROPIF except that the observation will be kept if the condition is true, and dropped otherwise. The grammar is KEEPIF <*bexpr*> and DROPIF <*bexpr*>, where <*bexpr*> is a boolean expression. A boolean expression is one that evaluates to true or false. Typically, boolean expressions use relational operators (>, >=, <, <=, ==, <>) and boolean operators (NOT, AND, OR, XOR). Functions that return boolean values can be used as well.

Multiple KEEPIF and DROPIF statements can be used for a single variable. As *mle* reads in variables, each condition is tested in sequence, until the end of the tests are reached or the observation deemed dropped (that is, boolean short-circuiting will be used to drop variables at the first opportunity). The third example is a test that keeps the observation if last_time is greater then zero; the second test will examine if the value is equal to INFINITY (a built-in constant) or less than first_time, and drop the observation if either condition is true. Then, if the variable is to be dropped, the *entire* observation is dropped. Note that the value of other variables in the current observation may be used in a DROPIF and KEEPIF statement.

Observation frequency

Each observation in a data file (which typically occurs on a single line) is usually a single observation. Sometimes it is convenient to place multiple identical observations on a single line along with a count of how many observations are represented. The names FREQUENCY or FREQ have a special meaning when defined as variables in a DATA statement. They are taken as the frequency (or count) for each observation. (If both variable names are used, FREQUENCY is taken as the frequency variable). For example:

```
DATAFILE("test.dat")
DATA
  frequency       FIELD 1 DROPIF frequency <= 0
  start_time      FIELD 2
  last_time       FIELD 3
END
```

will take the first field in "test.dat" as the frequency for each observation. The maximizer will automatically use the frequency variable as a count of repeated observations.

Transformations of data

A number of simple data transformations can be made within *mle*. The transformations are done while the data are being read from the input file. Examples of transformations are:

```
DATA
  event_time   FIELD 5 = (event_time - 1900)*365.25  DROPIF event_time < 0
  direction    FIELD 6 = COS(direction)
  winglength   FIELD 8 = LN(winglength/2.25)
  estage               = 3.7 + winglength*12.76 + winglength^2 * 1.14
END
```

Transformations begin with '=' which is followed by an expression. Expressions are discussed in great detail in the reference manual. Basically, expressions in *mle* are similar or identical to expressions found in other computer languages and spreadsheets.

In the first variable declaration of the example, `event_time` is read in from the input file. That initial value of `event_time` is then used in the transformation, and a new value of event_time is computed as `(event_time - 1900)*365.25`. This result is assigned back to `event_time`. Following that, the `DROPIF` statement will conditionally decide whether or not the observation is to be dropped.

Variables are read in the same order in which they are defined. This is true even if they are read over several lines. Once a variable is defined, its value can be used in later transformations. Then, when reading in the data file, *mle* will take the value of that variable for the current observation for use in the later transformation. An example might be:

```
DATA
  subject_id   FIELD 1  DROPIF subject_id =1022 DROPIF subject_id = 3308
  births       FIELD 6  DROPIF births = -1
  miscarriages FIELD 8  DROPIF miscarriages = -1
  abortions    FIELD 9  DROPIF abortions = -1
  pregnancies  = births + miscarriages + abortions  KEEPIF pregnancies > 0
END
```

This data statement will read `subject_id`, then `births`, then `miscarriages` and then `abortions`. These variables will then be added together and assigned to the variable `pregnancies`. An observation will be dropped if any of `births`, `miscarriages`, or `abortions` are negative one (in this case, the "missing" code), or if two particular `subject_ids` are found, or if `pregnancies = 0`.

Creating dummy variables

Dummy variables (sometimes called indicator variables) are variables that take on the values 0 and 1 to denote two different states for an observation. A typical example is a dummy variable for an individual's sex, taking a 0 for females and a 1 for males. Frequently dummy variables are used to simplify a more complex continuous or ordinal variable. Maternal age, for example, might be measured as a continuous variable, but the characteristics of interest are teen mothers, mothers from 20 to 35, and mothers over age 35. Two dummy variables can be created from the continuous measure of age. The reference age group can be defined as mothers from 20 to 35. One dummy variable is created that takes on the value 1 for mothers under 20 and 0 otherwise. And the second dummy variable takes on a value of 1 for mothers over 35, and a 0 otherwise.

Dummy variables are easy to create within the `DATA` statement. Suppose you are measuring the length of some study animal. You want to create four dummy variables for the length range short [0 to 30 mm)[5], medium [30 to 40 mm) long [40 to 50 mm) and very long [50+ mm):

[5] The [xxx, yyy) notation defines an interval that includes exact number xxx and up to, but not including yyy.

```
DATA
  length       FIELD 5 DROPIF length <= 0
  is_short     = IF length < 30 THEN 1 ELSE 0
  is_medium    = IF (length >= 30) AND (length < 40) THEN 1 ELSE 0
  is_long      = IF (length >= 40) AND (length < 50) THEN 1 ELSE 0
  is_verylong  = IF length >= 50 THEN 1 ELSE 0
END
```

Skipping initial lines in the data file

Data files may have initial descriptive lines at the top that must be skipped. The INPUT_SKIP variable controls how many lines to skip in a data file. For example, if the first four lines must be skipped, the line

```
INPUT_SKIP = 4
```

should appear *before* the DATA statement. It will direct *mle* to discard the first four lines of the data file. The default value is zero so that no lines are skipped.

Delimiters in the data file

Data files consist of a series of text elements separated by one or more *delimiters*. One or more delimiters must appear between each record within a data file. The delimiters define the fields within each line in which variables reside. By default, the characters space, tab, and comma are treated as delimiters. You can redefine the delimiters by changing the variable DELIMITERS before the DATA statement. If, for example, you wanted the colon and semicolon character as the only valid delimiters, you would add the line:

```
DELIMITERS = ":;"
```

Creating observations without a file

Sometimes it is useful to *create* observations, rather than reading observations from a file. For example, you can simulate data sets using the random number generator in *mle*. To create variables, simply set the variable CREATE_OBS to some positive number, prior to the DATA statement. That number of observations will be created. Here is an example

```
CREATE_OBS = 10         {create 10 observations}
SEED(8936)              {set the random number generator seed}
DATA
  var1   = QUANTILE WEIBULL(RAND) 3.2, 2.5 END  {draw variates from a Weibull(3.2,2.5) pdf}
  var2   = IRAND(100, 200)                      {draw discrete variates from a uniform}
  var3   = sin(pi*RAND)                         {sine-transformed variates}
END
```

that yields the following data set:

```
var1          var2  var3
2.6679777032  157.0  0.9809586099
3.7136215828  117.0  0.2439682743
3.8714564727  173.0  0.7307000229
4.6521659697  139.0  0.8642639946
2.5649275178  197.0  0.8824737096
0.6017912164  136.0  0.0966561712
2.6553390371  136.0  0.3989167160
0.7412253145  198.0  0.7812333882
2.7631538913  185.0  0.3651667470
4.0772026291  193.0  0.4812826931
```

Printing observations and statistics

Some other variables can be used to fine-tune the DATA statement.

The variable PRINT_DATA_STATS, when set to TRUE, prints summary statistics for each variable, including the mean, variance, standard deviation, minimum and maximum. The default is TRUE, so this report can be suppressed with PRINT_DATA_STATS = FALSE.

When PRINT_OBS is set to TRUE, each observation is printed to the output file. The report is printed *after* all transformations have been done. The default value is FALSE, so you must have the statement PRINT_OBS = TRUE to print the observations.

The variable PRINT_COUNTS, when set to TRUE, prints out how many lines were read from the input file, how many observations were kept, and how many observations were dropped. The default value is TRUE, so these reports can be suppressed with PRINT_COUNTS = FALSE.

The PRINT_BASIC variable, when TRUE directs that the title, parameter file name, input file name, and the count of variables to be read from the input file are printed. The PRINT_FIELDS variable, when TRUE, prints out the name of each variable and the field it is read in from the input file.

An example of creating and reading a data file

Data file are read as ordinary ASCII text files, which means they can be created with any text editor. Word processors can be used to create files as well, but the results must be saved as ASCII text file. Nearly all word processors provide an ASCII text option. An example of a typical data file can be seen in Chapter 1, but here we will examine a more complicated data file and write the *mle* program to read and process the file.

The current version of *mle* creates variables of type real, and attempts to read real numbers from each field for which a variable is defined. Even so, any delimited text can appear in fields that are not assigned to variables. Consider how we would create a DATA statement to read the numeric values for the following file:

```
Last   First,MI     Age   Amount     More   Rate  Time
Smith  James,A      42     12000     TRUE   18%    4.2
Jones  David,J      38      8000     FALSE  12%    3.1
Connor Mary         50     11000     TRUE   19%    2.1
```

First of all, notice that the first line of the file is a comment. Clearly, we do not want ***mle*** to treat this line as an observation, so we can discard the line by setting INPUT_SKIP=1. From there, the data file has one line per observation, with each variable corresponding to one column (meaning that we will not need to use the LINE specification here; Some data files place each observation across multiple lines, so that the LINE option in the DATA statement must be used).

This sample data file consists of seven fields delimited by space characters. Since the space character is one of the default delimiters, we do need to change the DELIMITERS variable to recognize the space as such. But, since we have commas embedded in the text that should not to be taken as a delimiter, we must redefine DELIMITERS to exclude the comma and include the space (and the tab character, if necessary). The numeric values appear in fields 3, 4, 6, and 7.

We do not need to do anything with fields 1, 2, and 5. Let suppose that we want to convert Time from years into months. Here is the complete *mle* code to read and process this file (but no analyses are specified):

```
MLE
  DATAFILE("THEDATA.DAT")
  PRINT_OBS = TRUE     {print out each observation}
  INPUT_SKIP = 1       {get rid of the header line}
  DELIMITERS = " "     {spaces only--treat commas as text}
  DATA
    age       FIELD 3
    amount    FIELD 4  DROPIF amount <= 0
    rate      FIELD 6    {% is a legal number suffix in mle}
    time      FIELD 7 = time*12
  END
END
```

Running *mle* on this file produces the output to the screen (or standard output) since no `OUTFILE` procedure was called. Here are the results:

Table 2. Standard metric/SI suffixes (Taylor 1996) and IEC suffixes for integer and real numbers.

Suffix	Name	Conversion	Suffix	Name	Conversion
da	Deka	$\times 10$	d	deci	$\times 10^{-1}$
h	Hector	$\times 10^{2}$	c, %	centi, percent	$\times 10^{-2}$
k	Kilo	$\times 10^{3}$	m	milli	$\times 10^{-3}$
M	Mega	$\times 10^{6}$	μ, u	micro	$\times 10^{-6}$
G	Giga	$\times 10^{9}$	n	nano	$\times 10^{-9}$
T	Tera	$\times 10^{12}$	p	pico	$\times 10^{-12}$
P	Peta	$\times 10^{15}$	f	femto	$\times 10^{-15}$
E	Exa	$\times 10^{18}$	a	atto	$\times 10^{-18}$
Z	Zeta	$\times 10^{21}$	z	zepto	$\times 10^{-21}$
Y	Yotta	$\times 10^{24}$	y	yocto	$\times 10^{-24}$
Ki	Kibi	$\times 2^{10}$			
Mi	Mebi	$\times 2^{20}$			
Gi	Gibi	$\times 2^{30}$			
Ti	Tebi	$\times 2^{40}$			
Pi	Pebi	$\times 2^{50}$			
Ei	Exbi	$\times 2^{60}$			

```
3 lines read from file THEDATA.DAT
3 Observations kept and 0 observations dropped.

NAME          age      amount        rate        time
    1  42.0000000  12000.0000  0.18000000  50.4000000
    2  38.0000000  8000.00000  0.12000000  37.2000000
    3  50.0000000  11000.0000  0.19000000  25.2000000

MEAN   43.3333333  10333.3333  0.16333333  37.6000000
VAR    37.3333333  4333333.33  0.00143333  158.880000
STDEV  6.11010093  2081.66600  0.03785939  12.6047610
MIN    38.0000000  8000.00000  0.12000000  25.2000000
MAX    50.0000000  12000.0000  0.19000000  50.4000000
```

Accessing observations

Variables created by the DATA statement are treated somewhat differently than are other variables. The value of a particular variable changes depending on a counter that keeps track of the *current observation*. The value of a variable for the current observation is accessed by specifying the variable name. What determines the current observation? Within MODEL statements, the current observation is usually set by the DATA function. Internally, the DATA function loops through all observations and sums the individual likelihood computed for each observation. The LEVEL and LEVELDELTA functions work in similar ways.

Here are more specific details on how the individual observations are accessed. Consider the variables read in the example above. When the DATA function is specified with a model, a variable called D_IDX is initialized to the value of 1. When D_IDX is 1, any reference to the DATA variables returns the value of the first observation. Thus, the variable age yields the value 42. As each likelihood (within the DATA *function*) is computed, the value of D_IDX is incremented up to the last observation.

The total number of observations read by DATA statement is accessed by the variable N_OBS. This variable is assigned the count of lines of observations read in (assuming one line per observation) and kept (i.e. not dropped). However, this variable is incorrect if a single line represents more than one observation. For example, if the FREQUENCY variable is defined and some observations have frequencies other than one, the N_OBS will no longer represent the correct number of observations. Another variable, TOTAL_OBS, is the sum over all FREQUENCY observations, and can be used as a count of the total number of observations.

Internally, variables are stored as special array variables. Whenever a data variable name is specified, the value of D_IDX is used as the index into the array. All observations are easily accessed outside of the DATA, LEVEL, or LEVELDELTA functions by directly manipulating D_IDX. Here is an example that builds on the previous example. The following code, which is placed after the DATA statement, counts and prints the number of observations under and over the age of 40:

```
lessthan40 = 0
greaterthan40 = 0
FOR D_IDX = 1 TO N_OBS DO
  IF age >= 40 THEN
    greaterthan40 = greaterthan40 + 1
  ELSE
    lessthan40 = lessthan40 + 1
  END {if}
END  {for}
WRITELN(lessthan40, " < 40 and ", greaterthan40, " >= 40")
```

Number formats

The *mle* language primarily works with numbers. With this in mind, a wide variety of number formats, including some automatic conversions, are supported. The standard formats for real and integer numbers are recognized, so that "`3.14159`", "`-12.14`" and "`0.001`" are read as would be expected. Real numbers must have a digit both before and after the decimal point, so ".23" is not valid but "`0.23`" is. Real numbers can be specified in scientific notation so that "`2.1E-23`", "`0.3E12`", "`-1e4`", "`12345e-67`" are valid numbers.

Table 3. Standard number formats.

Format	Examples	Conversion	Result
D	1, 200		integer
d.d, d.	3.1415, 3.		real
ds, -ds, d.ds, -d.ds,	14%, 23.7M, 45.7da, 2n, 2.418E	Metric / other suffix (Table 2)	real
*d*E*d*, *d*E-*d*, *d.d*E*d*, *d.d*E-*d*, *d.*E*d*, *d.*E-*d*	3e23, 511E-10, 31.416e-1, 7.0E-10, 12.e-6, 1.45E-3, 1.0E0	Standard exponential format. $xEy \Rightarrow x \times 10^y$	real
0R*v*	0RXLVII, 0rMXVI, 0rmdclxvi	Roman numerals to integer	integer
*d*X*y*	2x1001 (binary), 8X3270 (octal), 16xA4CC (hex), 32x3vq4h (base 32).	Converts *y* from base *d* (from 2 to 36) into integer.	integer
d:*d*:*d*, *d*:*d*:*d.d*, *d*:*d*, *d*:*d.d*	10:42, 14:55:32, 10:40:23.4, 16:53.2	24-hour time into hours. Hours must be 0-24.	real
d:*d*:*d*AM, *d*:*d*:*d*PM, *d*:*d*:*d.d*AM, *d*:*d*:*d.d*PM, *d*:*d*PM, *d*:*d*AM, *d*:*d.d*AM, *d*:*d.d*PM	10:42AM, 2:55:32pm, 10:40:23.4am	12-hour time with AM and PM suffixes into hours. Hours must be 0-12.	real
*d*H*d*'*d*", *d*H*d*'*d.d*", *d*H*d*', *d*H*d.d*", *d*H*d.d*"	230h16'32", 14H32'6", 100h22', 30H32.2', 0h12', 0H12'3"	Degree/hour minute, second format. Converted to real angle/time.	real
d`*d*'*d*", *d*`*d*'*d.d*", *d*`*d*', *d*`*d.d*", -*d*`*d*'*d*", *d*`, *d.d*`, *d*°*d*'*d*", *d*°*d*'*d.d*", *d*°*d*', *d*°*d.d*", *d*°, *d.d*°	230`16'32", 14`32'6", 100`22', 30`32.2', 14`, 230°16'32", 14°32'6", 270°10'0", 30°18.2', 3.4°	Degree, minute, second format, converted to radians.	real
d'*d*", *d*'*d.d*", *d*', *d.d*', *d*", *d.d*"	12'32", 166'12.9", 19', 14.7', 12", 607.3"	Minute-second and second format, converted to radians.	real
d_d/*d*	12_5/16, 3_2/3, 0_1/7	Fraction notation.	real
*d*D*d*M*d*Y	16d12m1944y, 1D6M1800Y	Date converted to Julian day	integer
*d*M*d*D*d*Y	12m16d1944y, 6M1D1800Y	Date converted to Julian day	integer
*d*Y*d*M*d*D	1944y12m16d, 1800Y6M1D	Date converted to Julian day	integer
Dmmmy	14Dec1999, 30jun1961, 1MAY1944	Date converted to Julian day	integer

d is a strings of one or more positive digits; *s* is a one or two character case-sensitive metric or percent suffix (see Table 2), *v* is a string of one or more Roman numeral digits {IVXLCDM}, *y* is a string of one or more characters, *mmm* is a 3-character English month name. E.g. jan, Feb, MAR, etc. The degree character (°) is available on some hardware platforms as ASCII code 230. On many Intel platforms, holding down the <ALT> key and typing 230 on the numeric keypad gives the degree character.

The Greek letter micro (µ) is available on some hardware platforms as ASCII code 248. On many Intel platforms, holding down the <ALT> key and typing 248 on the numeric keypad gives this character.

Less common formats include numbers with metric and percent suffixes, numbers interpreted as times, numbers in an angle notation (one format that converts degrees to radians), numbers in bases from 2 to 36, Roman numerals ("why?" you ask. Why not!), numbers in fraction notation, and several date formats. These formats are supported in data files as well as numeric constants within an *mle* program. Table 3 is a comprehensive list of formats recognized by *mle* , and Table 2 is a list of suffixes permissible on standard integer and real format numbers.

Chapter 4
Building Likelihood Models

The MODEL statement is at the heart of parameter estimation. It specifies the likelihood, defines parameters, and specifies which parameters are to be estimated. A complete understanding of how models are built in mle requires an understanding of the structure of the MODEL statement, an understanding of parameters and how they are specified, an understanding of how expressions are specified and are built into likelihoods, and an understanding of the specification for running models.

This chapter discusses the MODEL statement. It is assumed that you understand the basics of expressions and data types for the mle language. The reference manual and Chapter 1 provides much of the necessary background on expressions. This chapter covers several aspects of expressions that are primarily used for building typical likelihood models in mle: the PARAM function, the PDF function, the DATA function, and LEVEL functions.

Structure of the MODEL Statement

The basic structure of the `MODEL` statement looks like this:

```
MODEL
  <expression>
RUN           [THEN … END]
  <runlist>
END
```

The single <*expression*> in the `MODEL` statement *defines the likelihood* that is to be maximized. Technical details about writing expressions are given in the Reference manual; some details are provided here as well.

The optional `THEN…END` clause gives you a way to do something after each model is solved. For example, you could insert code to transform the parameters from one form into another, plot distributions, or write results to another file. Most legal statements can come between the `THEN` and `END` (except `DATA…END` and `MODEL…END` statements).

The <*runlist*> is a series of one or more commands that specify which of the parameters are to be changed in maximizing the likelihood. The commands are `FULL`, `REDUCE`, or `WITH`.

A simple example

Here is an example of a simple model for finding the two parameters of a normal distribution from a series of interval-censored observations. Suppose there are *N* interval-censored observations. The interval in which events occur fall between

the times t_{open} and t_{close}. The goal is to estimate the parameters μ and σ of the normal distribution (we will use `mu` and `sigma` as parameter names).

The likelihood needed for this problem looks like this:

$$L = \prod_{i=1}^{N} \left[S(t_{open_i} \mid \mu, \sigma) - S(t_{close_i} \mid \mu, \sigma) \right]$$

where $S(t)$ is the survival function for a normal distribution. The *mle* program for this likelihood looks like this:

```
{1}  MODEL
{2}    DATA
{3}      PDF NORMAL(topen, tclose)
{4}        PARAM  mu     LOW = 5   HIGH = 14  START = 8   END
{5}        PARAM  sigma  LOW = 0.1 HIGH = 5   START = 1.2 END
{6}      END  {pdf}
{7}    END  {data}
{8}  RUN
{9}    FULL
{10} END
```

Everything beginning with the `DATA` function on line 2 to the `END` on line 7 is a single expression that defines the likelihood. The `DATA` function corresponds to the product in the likelihood. It loops through all data and evaluates the expression nested within it for each observation.

The expression `PDF NORMAL(topen, tclose)…END` defines the area under a normal distribution in the interval [topen, tclose). Finally, the `PARAM` functions tell *mle* that `mu` and `sigma` are the parameters in the model that are to be changed in pursuit of maximizing the likelihood. Values for the parameters `mu` and `sigma` will be tried until those that maximize this likelihood are found.

The word `FULL` between `RUN` and `END` tells *mle* that all parameters defined in the likelihood—in this case `mu` and `sigma`—are to be manipulated in order to maximize the likelihood. Alternatively, the `REDUCE` or `WITH` keywords can be used in place of `FULL`.

Another example

The expression that defines the likelihood within a model statement can become much more complicated than the first example. Consider the following likelihood:

$$L = \prod_{i=1}^{N} \left\{ p\left[S(t_{open_i} \mid \mu_1, \sigma_1) - S(t_{close_i} \mid \mu_1, \sigma_1) \right] + (1-p)\left[S(t_{open_i} \mid \mu_2, \sigma_2) - S(t_{close_i} \mid \mu_2, \sigma_2) \right] \right\}.$$

This is the likelihood for a mixture model, in which observations are drawn from two distributions (that is, two different sets of parameters for the same distribution), and mixed at some fraction *p*. This type of model arises when one cannot tell which of the two distributions observations are drawn from. An example might be a collection of people heights with no information on the sex of each individual. Even without such information, the proportion of each sex can be treated as a latent variable, and sex-specific parameters can be estimated along with the proportion.

This more complicated likelihood can be coded as follows:

```
MODEL     {mixture of two normal distributions}
  DATA
    MIX(
      PARAM   p  LOW = 0  HIGH = 1  START = 0.5 END
    ,
      PDF NORMAL(topen, tclose)
        PARAM  mu1     LOW = 5   HIGH = 14  START = 8 END
        PARAM  sigma1  LOW = 0.1 HIGH = 5   START = 1.2 END
      END  {PDF}
    ,
      PDF NORMAL(topen, tclose)
        PARAM  mu2     LOW = 0   HIGH = 6  START = 2 END
        PARAM  sigma2  LOW = 0.01 HIGH = 5   START = 1.2 END
      END  {PDF}
    )      {mix}
  END {data}
RUN
  FULL
END      {model}
```

Here, again, the <*expression*> begins with the `DATA` function and ends with a matching `END` just before the `RUN`. Within the `DATA` function, the `MIX` function is immediately called, and the `MIX` function contains three arguments separated by commas. Each of these three arguments contains an expression. Here, we see one parameter `p` (a mixing proportion) and two function calls: `PDF...END`. Within each `PDF...END`, two parameters are defined.

The model contains a total of five parameters. The `FULL` keyword specifies that all parameters will be estimated.

Runlist

Parameters that are defined with the `PARAM…END` function can be *free parameters*, and therefore estimated as part of maximizing the likelihood. Alternatively, they can be constrained for the purpose of hypothesis testing or otherwise modifying the model. Parameters may be held constant, or fixed to the value of another parameter. These are called *fixed parameters*, and an estimate will not be found for them when the likelihood is maximized. The <*runlist*> in *mle* provides the mechanism to specify a series of one or more models containing different combinations of free and fixed parameters.

For example, in the mixture model likelihood above, we may have reason to believe that the proportion parameter (`p`) ought to be 0.5. Perhaps this is because of the nature of the system being modeled. We could first fit our collection of *t* values to the model with parameter `p` free, and secondly fit it with `p` held constant to 0.5. Statistical criteria (a likelihood ratio test, Akaike's Information Criterion, or a Walt test) can then be used to determine whether `p` deviates from the value 0.5.

The run list defines which parameters are free and allows the user to test reduced models. The run list begins with the word `RUN` and ends with a matching `END`. Between the `RUN` and the `END` comes a list that specifies how the model is to be run. Each model can be run with a different combination of free and fixed parameters. Generically, a runlist looks like this:

```
RUN
  FULL                  [THEN … END]
  REDUCE  <reducelist>  [THEN … END]
  WITH  <withlist>      [THEN … END]
  ...
END
```

FULL

When FULL is specified, all model parameters defined with the PARAM…END function are taken to be free parameters and estimated. Only one FULL is usually needed for a model.

REDUCE

The REDUCE keyword provides a mechanism to constrain some parameters of the model. The REDUCE keyword is followed by a list of constraints. All parameters of a model will be considered free except those constrained in the <*reducelist*>. Parameters may be constrained to other parameters, to constants or to variables. More than one REDUCE keyword may occur in a single run list.

The <*reducelist*> is a set of one or more constraints that look like assignment statements. Parameters so constrained will not be estimated. Consider the following likelihood:

$$L = \prod_{i=1}^{N} \left[f(t_i \mid \mu e^{sex_i \times \beta_{sex}}, \sigma) \right].$$

This likelihood estimates the effect of the variable *sex* on the mean of a distribution. Suppose $f(t)$ is a normal distribution. This likelihood would be written as

```
largeeffect = -1.9

MODEL
  DATA
    PDF NORMAL(topen, tclose)
      PARAM mean low=5 HIGH=500 START=100 FORM=LOGLIN
        COVAR sex  PARAM b_sex LOW=-5 HIGH=5 START=0 END
      END {param}
      PARAM stdev LOW=0.001 HIGH=25 START=10 END
    END  {pdf normal}
  END  {data}
RUN
  FULL   {Runs the model with no constraints}
  REDUCE  b_sex = 0                {One constraint}
  REDUCE  mean = 100  b_sex = 0    {Constrains 2 parameters}
  REDUCE  b_sex = largeeffect      {Fixes sex to another param or variable}
END
```

Notice that there are four versions of the model that will be estimated. The first case (FULL) estimates all three parameters (mean, b_sex, and stdev). The second case constrains the parameter b_sex to 0 (no effect), so that only two parameters are estimated. The third case constrains the parameter mean 4 and b_sex to 0, so that only one parameter is estimated. The forth REDUCE constrains b_sex to the value of a variable.

WITH

The WITH keyword provides a mechanism to include certain parameters in a model. The WITH differs from the FULL and REDUCE keywords because a single WITH command can generate more than one model. The WITH keyword is followed by a list of parameters to always include in each model. Additionally, a list of parameters can be specified that will be used to create a series of models. More than one WITH keyword may occur in a single run list.

The <*withlist*> is a list of parameters. Parameters are listed in one of two ways. Parameters listed outside of parentheses are included in every model. Parameters listed in within parentheses are included in some models, but not others—essentially, all permutations of models are generated from parameters listed in parentheses.

Here is an example. Suppose the likelihood of interest specifies a logistic regression model with three covariates:

$$L = \prod_{i=1}^{N} B\left[t, \frac{1}{1+\exp\left(\beta_0 + \beta_1 x_{1i} + \beta_2 x_{2i} + \beta_3 x_{3i}\right)} \right].$$

$B(t, p)$ is a Bernoulli trial with parameter p; the function returns p whenever t is 1 (success) and returns $1 - p$ when t is 0 (failure). This likelihood has four parameters. β_0 defines the baseline probability of success. β_1 to β_3 are the effects of covariate x_1 to x_3 on the baseline probability, respectively.

A natural way of estimating this model is try every permutation of covariates, and take the most parsimonious of the models. Here is a likelihood that will do just that.

```
MODEL
  DATA
    PDF BERNOULLITRIAL(success)
       PARAM b_0 LOW = -500 HIGH = 500 FORM = LOGISTIC
         COVAR x1 PARAM b_1 LOW = -10 HIGH = 10 START = 0 END
         COVAR x2 PARAM b_2 LOW = -10 HIGH = 10 START = 0 END
         COVAR x3 PARAM b_3 LOW = -10 HIGH = 10 START = 0 END
       END  {param}
    END {pdf}
  END  {data}
RUN
  WITH b_0 (b_1 b_2 b_3)
END  {model}
```

The single `WITH` keyword creates a total of eight models. All of the models include the parameter `b_0`. And, all models will be created from the list `(b_1 b_2 b_3)`. Here is the equivalent list of models that will be estimated from this single `WITH` statement.

```
MODEL
  ...
RUN
  WITH b_0 b_1 b_2 b_3
  WITH b_0 b_1 b_2
  WITH b_0 b_1 b_3
  WITH b_0 b_2 b_3
  WITH b_0 b_1
  WITH b_0 b_2
  WITH b_0 b_3
  WITH b_0
END  {model}
```

The use of parameters within parentheses in the <*withlist*> raises the issue of the number of models that will be created. Since each parameter has two states (included and not included), there are 2^K models formed, where K is the number of parameters given in parentheses. The practical use of `WITH` in this way depends on how quickly a single model solves. With eight parameters, there are 256 models estimated. At 10 parameters, the number is 1024, and 15 parameters yields 32768 models.

THEN…END

Each of the keywords `FULL`, `REDUCE`, and `WITH` can be followed by an optional `THEN…END` clause gives you a way to do something a particular model is solved (or set of models for `WITH`). For example, you could insert code to transform the parameters from one form into another, plot distributions, or write results to another file. Most legal statements can come between the `THEN` and `END` (except `DATA…END` and `MODEL…END` statements).

Bayesian model averaging

The WITH keyword can generate many models from a single line of text. Ideally, the uncertainty of estimating multiple models can be taken into account. *mle* supports Bayesian model selection and Bayesian model averaging. Accessible introductions to these topics can be found in Burnham and Anderson (1998) and Raftery (1995). The following show how to enable Bayesian model selection and the types of model selection are supported:

```
AIC_SELECT = TRUE     {selects via Akaike's information criterion (AIC)}
AICC_SELECT = TRUE    {selects via sample-size corrected AIC}
BIC_SELECT = TRUE     {selects via Bayesian information criterion (BIC)}
```

When any of these three variables are set to TRUE, Bayesian model averaging will be conducted according to the criterion. Bayesian model averaging uses certain assumptions to find relative probabilities that each of the models is the true model or the best fitting model. A final set of parameters (estimated according to the best overall model) is computed, and a second set of standard errors are computed that is an average over all models, weighted by the probability of each model. The standard errors contain a component of variability from model-selection uncertainty and a component for uncertainty of the parameter estimates. See Burnham and Anderson (1998:325).

Results

The output report from a *mle* MODEL statement consists of a number of smaller reports. Most reports can be enabled or disabled by modifying variables. Some examples are: parameter estimate reports, the variance-covariance matrix, a list of the individual likelihoods for each observation, and tables of distributions, Bayesian model averaging reports, etc. This section describes the output options and how to direct the output to a file.

Defining the output file

mle defines a special file that is used for the results of DATA and MODEL statements. The OUTFILE is used to define where the results will be sent (otherwise they are sent to the screen). A number of variables control the format of the output. Typically, an program used to estimate a likelihood model contains a line like the following near the top of the program:

```
OUTFILE("analysis.out")     {writes to the file analysis.out}
```

As an alternative to specifying the file name explicitly, the function DEFAULTOUTNAME can be called. This function will use the name of the program to automatically generate an output file name. Suppose you run the command `mle myprog.mle`. The statement

```
OUTFILE(DEFAULTOUTNAME)
```

Will create a file called `myprog.out` for the output.

Standard Error Report

A report with estimated standard errors is printed when PRINT_SE = TRUE. The parameters will be written with an estimate of standard errors. By default standard errors are written to the output file. Whenever standard errors are reported, a variance-covariance matrix will be estimated. If the matrix is singular (which can happen for a number of reasons), the standard errors are $+\infty$.

When the variable PRINT_SHORT = TRUE, the report format is modified so that all parameters estimates are printed on one line.

Variance-covariance Matrix

The estimated variance-covariance matrix is printed by setting `PRINT_VCV = TRUE`. The number of elements of the matrix printed on a single line is normally 5, but can be changed by modifying the value of `VCV_WIDTH`.

The asymptotic variance-covariances of maximum likelihood estimates are found by inverting the local Fisher's information matrix *I* for the *n* parameters:

$$I = \begin{bmatrix} E\left(\frac{-\partial^2 l}{\partial \theta_1^2}\right) & \cdots & E\left(\frac{-\partial^2 l}{\partial \theta_1 \theta_n}\right) \\ \vdots & \ddots & \vdots \\ E\left(\frac{-\partial^2 l}{\partial \theta_n \theta_1}\right) & \cdots & E\left(\frac{-\partial^2 l}{\partial \theta_n^2}\right) \end{bmatrix}$$

The expectations are, ideally, taken at the true parameter values. In practice, we have parameter estimates, not the true values. Hence, numerical estimates of the information matrix, $\hat{I}$, are found by plugging in parameter estimates, $\hat{\theta}$. An estimated variance-covariance matrix is then estimated as $\hat{\mathbf{V}} = \hat{\mathbf{I}}^{-1}$.

mle uses two different estimates for the variance-covariance matrix. Either one or both methods may be used by setting `INFO_METHOD1` or `INFO_METHOD2` to `TRUE` or `FALSE`. The default method (`INFO_METHOD1=TRUE`) computes the variance and covariance matrix by inverting Nelson's (1983) approximation to the Fisher's information matrix. The *x*th, *y*th element of that matrix is computed as $\hat{\mathrm{E}}_{xy} = \prod_i \left(\partial L_i / \partial x\right)\left(\partial L_i / \partial y\right)$, using the standard perturbation method for approximating the partial derivative. Appropriate sizes for Δx and Δy are iteratively computed for each parameter. *mle* initially uses a Δx (and Δy) of `DX_START` and then iteratively finds a Δx that changes the loglikelihood by at least `DX_TOOSMALL` but no more than `DX_TOOBIG`. Up to `DX_MAXITS` such iterations are permitted. The default values are almost always suitable. The one serious limitation of this method is that it does not work well for hierarchical likelihoods.

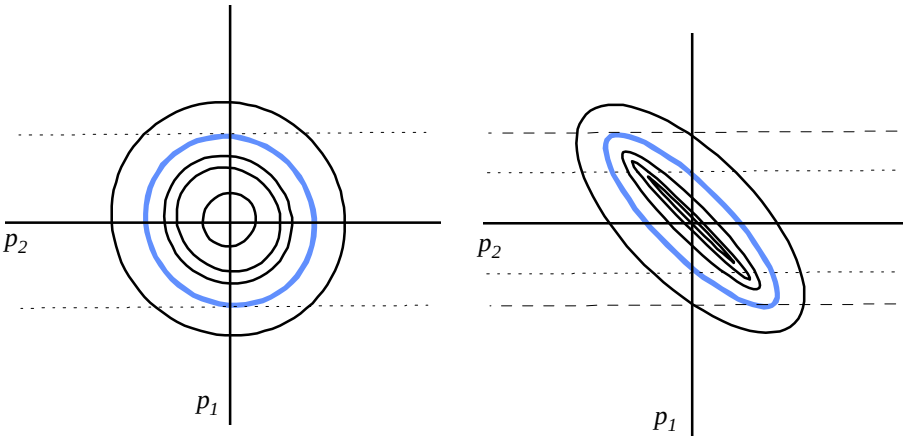
The second estimate of the variance-covariance matrix is computed by estimating the second partial derivative by numeric perturbation. This method does not truly compute an expectation, and is sometimes inaccurate—you can compare the two methods by setting both `INFO_METHOD1=TRUE` and `INFO_METHOD2=TRUE`. Nevertheless, when hierarchical likelihoods are being computed, this method will produce better estimates.

Confidence Interval Report

An approximate confidence region for each parameter can be estimated by *mle*. The report is printed when `PRINT_CI = TRUE`. When the variable `PRINT_SHORT = TRUE`, the report format is modified so that all parameters estimates are printed on one line.

The confidence interval is defined as the extent of upper and lower perturbations away from the estimates that change the loglikelihood by a specified amount. For example, approximate 95% confidence intervals are formed when the change in the loglikelihood in each direction is 5.0239. This value corresponds to an expected probability of 0.025 on each tail of the chi-squared distribution with one degree of freedom. Over both directions, the total interval can be considered a 95% confidence interval for the parameter.

The interpretation of the one-dimensional confidence region must be done with caution, as the method assumes that parameters are uncorrelated. Figure 4 shows what happens when parameters are correlated (which is quite common). Panel a. shows the contour of the loglikelihood surface when parameter 1 is changed over the p_1 axis, and parameter 2 is changed over the p_2 axis. The bold ellipsis represents the desired confidence level (say, 95%). The dotted lines show the confidence limits when p_1 is perturbed along the axis to each side of the estimate; this occurs where the bold ellipse intersects the p_1 axis. Panel *b*. shows what happens when parameters are correlated. Now, the dotted lines still show the 95% confidence limits when p_1 is perturbed from the estimate and p_2 is held constant at its maximum. The dashed lines show the true confidence region defined as the greatest extend of the 95% confidence ellipse over the space of p_1 and p_2. It is easy to see that the one-dimensional confidence interval will always underrepresented the true interval p_1 and p_2 are correlated.



a. b.

Figure 4 The log likelihood contour over the space of parameters p_1 and p_2. The bold ellipse represents the target change in likelihood that defines the upper and lower bounds of the confidence interval. Panel a: uncorrelated parameters, where the one dimensional change in likelihood is identical to the change over both parameters. Panel b: correlated parameters where the change in likelihood (dotted lines) is less than the change in likelihood over both parameters (dashed lines).

Given the limitation of these confidence intervals, why use them? There are several cases where they are helpful:

- When a single parameter is being estimated.
- In some models where parameters are statistically independent, like while estimating the location and scale parameters of a normal distribution.

There are circumstances when the variance-covariance matrix is singular. For example, this happens when one or more parameters are collinear and don't independently contribute information to a likelihood. Under these circumstances, the confidence intervals are helpful for identifying poorly identified parameters so that the model can be modified to eliminate collinear parameters.

The confidence intervals are found iteratively in one dimension at a time. For each of the limit pairs, *mle* first evaluates the likelihood at the extremes `LOW + CI_LIMIT_DELTA` and `HIGH + CI_LIMIT_DELTA`. Convergence occurs when the difference between the likelihood at the parameter estimate and the confidence limit estimate is equal to `CI_CHISQ`, down to an absolute error of ±`CI_CONVERGE`. The maximum number of iterations for each of the limits is `CI_MAXITS`.

Report with no standard error or confidence intervals

At times, it is desirable to print parameter values without standard errors or confidence intervals. This can be done by including the assignment `PRINT_PARAMS = TRUE`. This will print out an additional report with parameter estimates. Additionally, `PRINT_SE` and `PRINT_CI` can be set to `FALSE` so that neither confidence intervals nor the variance-covariance matrix are computed.

When the variable `PRINT_SHORT = TRUE`, the report format is modified so that all parameters estimates are printed on one line.

Printing Distributions

The values of all survival function, the probability density function and the hazard function can be tabulated for each PDF function in the likelihood. To do so, set `PRINT_DISTS = TRUE`. All distributions that are in the model will be tabulated. The tabulation starts at value `DIST_T_START`, ends at the value `DIST_T_END`, and is tabulated for `DIST_T_N` equally spaced points. The mean values of data variables (e.g. covariates) are used when computing the distributions.

For example, to print the SDF, PDF, and hazard function at 101 points from 0 to 100 use the following code:

```
PRINT_DISTS   = TRUE     {print out distributions}
DIST_T_START  = 0        {lowest value to print}
DIST_T_END    = 100      {highest value to print}
DIST_T_N      = 101      {number of points to print}
```

Other Printing Options

The `MIN_SIGNIFICANT` variable controls the minimum number of significant digits in each numeric field of the confidence interval and standard error reports. More significant digits are displayed if there is room. If the number of leading zeros becomes too large, that number will be printed in scientific notation (e.g. 1.2343E-56).

The variable `PRINT_INFO`, when `TRUE`, directs *mle* to print basic information about the model, including the method being used, the maximum number of iterations, the maximum number of function evaluations, and the criterion for normal convergence.

The `PRINT_FREE_PARAMS` variables, when `TRUE`, directs *mle* to print a list of all free parameters and the attributes of those parameters.

The variable `PRINT_LLIKS` controls printing of the individual likelihoods in a model. When set to `TRUE`, the likelihood and frequency for each observation will be printed to the output file.

Variables created by models

mle creates variables in order to access the results from previous runs (either within or outside of the `MODEL` statement). Each `MODEL` statement is numbered (beginning with 1) in the order in which they are found in the program. Furthermore, each run of the model, defined by the `FULL` or `REDUCE` statement, is numbered beginning with 1 for each `MODEL`. The following variables are created:

```
<param>.<m>.<r>
<param>.LOW.<m>.<r>
<param>.HIGH.<m>.<r>
<param>.START.<m>.<r>
<param>.UCI.<m>.<r>
<param>.LCI.<m>.<r>
<param>.SE.<m>.<r>
LOGLIKELIHOOD.<m>.<r>
FREE_PARAMS.<m>.<r>
DELTA_LL.<m>.<r>
ITERATIONS.<m>.<r>
EVALS.<m>.<r>
VCV_EVALS.<m>.<r>
CI_EVALS.<m>.<r>
INVERTFLAG.<m>.<r>
CONVERGENCE.<m>.<r>
VCV.<m>.<r>
```

where <*m*> is the model number and <*r*> is the run number for the model, and <*param*> is the name for a free parameter in the model. Each `VCV.<m>.<r>` is an *n*×*n* matrix where *n* is the number of free parameters, which is available in `FREE_PARAMS.<m>.<r>`. The variable `INVERTFLAG.<m>.<r>` is a boolean variable that specifies whether or not the variance-covariance matrix was inverted without error.

Each `CONVERGENCE.<m>.<r>` variable has an integer value that takes on a value given in Table 4.

Table 4. Meaning of the `CONVERGENCE` *variable.*

Value	Meaning
0	Not done
1	Stopped after maximum function evaluations
2	Stopped after maximum number of iterations
3	Converged normally
4	Trouble converging in one dimension
5	Starting value is not within min and max bounds
6	Starting temperature is not positive
7	Did not converge

Building MODEL statements

Expressions are used in many ways within *mle*, so that you should become thoroughly acquainted with expressions before attempting to develop *mle* programs. The likelihood within a `MODEL` statement is a single (sometimes complicated) expression. Expressions are used to define limits of integration, summations, and products, they can be used to define `START`, `HIGH`, `LOW`, and `TEST` values for parameters, and many other things. This section briefly discusses expressions and functions, and then provides some details on functions of special interest when building likelihood models. The reference manual should be consulted for summaries of expressions and descriptions of all functions defined in *mle* .

At the simplest level, an expression in *mle* can be a numerical constant or a variable name. More complex expressions consist of algebraic operators (*,^,+, etc.) and function calls each with zero or more arguments. Most functions in *mle* are simple functions with a fixed number of arguments, for example: `PERMUTATIONS(x, y)`, `ARCSIN(x)`, `ABS(x)`, `MIX(p, x, y)`.

A second class of functions are more complex, and have a more complicated syntax. These functions begin with a keyword, and end with an `END`. Examples of some of these functions are the `PARAM...END` function, `DATA...END` function (not to be confused with the `DATA END` *statement* described in a previous chapter), the `PDF...END` function, the `INTEGRATE a (b, c)...END` function, and the `IF THEN...ELSE...END` function.

Suppose you want to integrate $\sin(x^2 + 2x)$ from $-\sqrt{\pi}$ to $\sqrt{\pi}$. Here is an example of how that could be coded: `INTEGRATE x (-SQRT(PI), SQRT(PI)) SIN(x^2 + 2*x) END`. (The function evaluates to ≈ -1.525). Here it is with comments:

```
INTEGRATE x  (      {x is the variable of integration}
  -SQRT(PI),        {This is the lower limit of integration}
   SQRT(PI)         {This is the upper limit of integration}
             )      {Close of the argument list}
    SIN(x^2 + 2*x)  {The function to be integrated}
END                 {End of the integrate function}
```

Any of the predefined probability density functions can be used as part of an expression. For example, the area under a normal distribution with μ=10 and σ=3, between 8 and 12, could be calculated by

```
PDF NORMAL(8, 12) 10, 3 END
```

The DATA function

The `DATA...END` function provides a mechanism to "feed" observations to the likelihood. This function specifies that observations are to be "fed" to the likelihood one at a time, corresponding to the product ($\prod$) over all observations shown in likelihoods (or the Σ shown in loglikelihoods). The `DATA` function loops through all observations that were previously read in by the `DATA` statement. In other words, the `DATA...END` function returns the *total logloglikelihood* or *total likelihood*, given a series of *observations* and an expression for an *individual likelihood* or *individual loglikelihood*. The general form for the `DATA` function is:

```
DATA <optional_form>
  <expression>
END
```

where optional_form is one of

- `FORM = SUMLL` — This takes the log of each individual likelihood and sums the loglikelihoods over the data. A likelihood (rather than a loglikelihood) is specified for <*expression*>. This is the default value if no <*formtype*> is specified.

- `FORM = SUM` or `FORM = SUMMATION` — Sums loglikelihoods over the data without first taking the log. This is used when a loglikelihood is specified rather than a likelihood for <*expression*>.

- `FORM = PROD` or `FORM = PRODUCT` — Takes the product of likelihoods over the data and does not take the log of the likelihood. This is used when a likelihood (rather than a loglikelihood) is specified for <*expression*> and some function appears outside the data function that takes the log.

Here are three models that yield the same overall likelihood function, but uses different forms for the `DATA` function:

```
MODEL
  DATA  FORM = SUMLL        {the default form}
    PDF NORMAL(topen tclose)
      PARAM mu     LOW = 10     HIGH = 100 START = 30 END
      PARAM sigma  LOW = 0.0001 HIGH = 10  START = 1  END
    END  {pdf}
  END {data}
RUN
  FULL
END  {model}
MODEL
  DATA  FORM = SUM         {The loglikelihood is specified}
    LN(PDF NORMAL(topen tclose)
         PARAM mu     LOW = 10     HIGH = 100 START = 30 END
         PARAM sigma  LOW = 0.0001 HIGH = 10  START = 1  END
       END  {pdf}
    )
  END {data}
RUN
  FULL
END  {model}
MODEL
  LN(
    DATA  FORM = PRODUCT         {The likelihood is specified}
      PDF NORMAL(topen tclose)
        PARAM mu     LOW = 10     HIGH = 100 START = 30 END
        PARAM sigma  LOW = 0.0001 HIGH = 10  START = 1  END
      END  {pdf}
    END {data}
  )
RUN
  FULL
END  {model}
```

In theory, these three models will yield identical results. In practice, results may differ slightly because of round-off errors. This will be most noticeable in the last model, because the product of very small numbers will lead to smaller and smaller numbers before the log is taken of the entire likelihood. There are several reasons for providing these three ways of specifying how the data is used within the likelihood:

Some likelihoods are much easier to write as a loglikelihood.

- Some likelihoods require things like taking an expectation outside of the individual likelihoods, where the integration is done outside of the data function.

- Some multilevel or hierarchical likelihoods require this type of control over the likelihood.

There are two functions that are closely related to the `DATA` function: the `LEVEL` function and the `LEVELDELTA` funciton. These two functions provides a mechanism by which multilevel or hierarchical models can be constructed.

The PARAM function

mle has a general method for defining all parameters to be used in a likelihood model.[6] The `PARAM` function defines a parameter and its characteristics. The function should only be used within a `MODEL` statement. When models are "solved", *free parameters* are estimated by iteratively plugging new values in for those parameters until the values that maximize the likelihood are found. In other words, free parameters are values that are to be estimated by *mle* —they are the unknowns in likelihood models. When the `MODEL` statement is run, *mle* will estimate the value of

[6] The word *parameter* is used in a very specific way, as defined in Chapter 1. Parameters are the quantities to be estimated in a likelihood model

that parameter, unless the parameter is constrained to some fixed value in the REDUCE part of the model statement.

In the simplest case, parameters are specified as

```
PARAM  <p> HIGH = <expr> LOW = <expr> START = <expr> TEST = <expr> FORM = <formspec> END
```

where <*p*> is the name chosen for the parameter. The keywords HIGH, LOW, START, and TEST specify characteristics for the parameter. HIGH and LOW specifies the minimum and maximum value allowed for the parameter. *mle* will not exceed these values while trying to maximize the likelihood. START tells the maximizer what value to start with. TEST denotes the value against which to test the parameter for significance. By default, TEST is zero. It is used for a Wald test as the parameter is being written to the output file. Additionally, this is the value that the parameter is constrained to when left out by the WITH command.

Setting Parameter Information

Five characteristics may be set for each parameter. They are: 1) the highest possible value that can be tried for the parameter, 2) the lowest possible value that can be tried for the parameter, 3) an initial value for the parameter, 4) a test value against which the parameter will be tested when standard errors are computed, and 5) a form for the parameter that defines simple algebraic transformations and the mathematical from for incorporating covariates. The following model statement defines all five characteristics for the parameters of a beta distribution:

```
MODEL
  DATA
    PDF BETA(p)
      PARAM  a  LOW = 0.5  HIGH = 10  START = 1  TEST = 1  FORM = NUMBER  END
      PARAM  b  LOW = 0.5  HIGH = 10  START = 1  TEST = 1  FORM = NUMBER  END
    END {pdf}
  END {data}
RUN
  FULL
END {model}
```

The two parameters of the beta distribution are limited to the range 0.5 to 10, whereas, mathematically, they are only restricted to positive values. The TEST = 1 specifies that the parameter will be tested against one instead of the default value of zero, after standard errors for the parameters are found. The START value of one simply gives *mle* a starting place that falls within the LOW and HIGH values.

Use care when setting the HIGH and LOW limits. Most importantly, limits must be constrained to valid ranges for the intrinsic parameters. Thus, for the MIX mixing proportion parameter (the first of the three parameters) then, HIGH = 1 and LOW = 0, should be defined as is appropriate for a probability—unless some FORM like FORM = LOGISTIC is used to constrain the resulting parameter to between 0 and 1 for estimates from -∞ to ∞. Sometimes it is useful to impose narrower limits, perhaps to avoid getting hung-up at a local maximum or to solve the model more quickly. Be careful, though. Limits that are too narrow may exclude the global maximum—after all, the best parameter estimates for a set of data are presumably unknown. Excessively narrow limits may cause problems when numerical derivatives for the variance-covariance matrix are computed, as well. Also, likelihood confidence intervals will bump up and stop at the limits you set.

The TEST = xxx part of a PARAM function provides a value against which the parameter will be tested (in some reports). In a sense, the TEST value is a null hypothesis value (h_0). The test performed is $t = (\hat{p} - h_o) / SE(\hat{p})$, where $\hat{p}$ is the maximum likelihood parameter estimate and

$SE(\hat{p})$ is the standard error for the parameter estimate. The Wald test is provided for convenience only. *mle* does not make use of the test in any way.

Modeling Covariate Effects

The PARAM function allows covariate effects (and their associated parameters) to be modeled within the parameter statement. This is done as follows:

```
PARAM  x HIGH = <expr> LOW = <expr> START = <expr> TEST = <expr>  FORM = <formspec>
  COVAR <expr>  PARAM  z .HIGH = ... END
  COVAR <expr>  PARAM  z .HIGH = ... END
  ...
END  {param}
```

With covariates, the <*expr*> following COVAR is a covariate effect. Typically this is a variable like age, sex, income, etc. The effect of the covariate is multiplied by the value of the PARAM function that follows. The way in which covariates and parameters are modeled is discussed in more detail below.

Here is an example of a likelihood hand-coded for an exponential PDF for exact failure times. PARAMs and built-in simple functions, and algebraic expressions are all shown in this likelihood:

```
MODEL
  DATA
    PARAM lambda LOW = 0 HIGH = 1 START = 0.23 END * EXP(-lambda * t)
  END
RUN
  FULL
END
```

Notice that lambda is first defined as a parameter, and thereafter is used as an ordinary variable. As *mle* iteratively seeks a solution, new values of lambda will be tried. As the likelihood itself is being computed, the PARAM function will simply return the current estimate of lambda.

An alternative way to code this example is to define the parameter first and assign it to another variable:

```
MODEL
  PREASSIGN
    lam = PARAM lambda LOW = 0 HIGH = 1 START = 0.23 END
    DATA
      lam*EXP(-lam*t)
    END  {data}
  END  {preassign}
RUN
  FULL
END {model}
```

The PREASSIGN function is described in another chapter.

In the next example, five parameters are defined, two each for the two PDF functions and one parameter that was added for the first argument to the MIX function call.

Typically, parameters are defined for the intrinsic parameters of a PDF function. For example, the normal PDF has two intrinsic parameters μ and σ. The first parameter specified in the parameter list will be treated as μ. The second will be treated as σ. How can you know the proper order for parameters? Generally location parameters appear first (and are usually denoted *a* in this manual), scale parameters are second and shape parameters are third. You can get a quick synopsis of each type of PDF by using the -h option from the command line, e.g.: `mle -h SHIFTWEIBULL`

Parameters are also used to model effects of covariates on other parameters. Here is an example in which two parameters, used in place of some fixed values of μ and σ for a normal distribution, are defined with two covariate parameters, each:

```
PDF NORMAL(topen tclose)
  PARAM mean  LOW = 100  HIGH = 400  START = 270  TEST = 0  FORM = LOGLIN
    COVAR  sex    PARAM b_sex_mu     LOW = -2  HIGH = 2  START = 0 END
    COVAR  weight PARAM b_weight_mu  LOW = -2  HIGH = 2  START = 0 END
  END
  PARAM stdev     LOW = 0.1  HIGH = 100 START = 20  FORM = LOGLIN
    COVAR  sex    PARAM b_sex_sig     LOW = -2  HIGH = 2  START = 0 END
    COVAR  weight PARAM b_weight_sig  LOW = -2  HIGH = 2  START = 0 END
  END
END
```

In this example, the first parameter of the normal distribution (μ) has two covariates and their corresponding parameters modeled on it. The exact specification of how covariates and their parameters are modeled depend on the `FORM` of the intrinsic parameter. In the example, the `FORM = LOGLIN` specifies that a log-linear specification is to be used. The log-linear specification is $\mu_i = \mu' \exp(\mathbf{x_i} b)$, where μ' is the estimated intrinsic parameter (`mean` in this case). Thus, for the *i*th observation, the μ parameter of the normal distribution will be constructed as: $\mu_i = \texttt{mean} \times \exp(\texttt{sex}_i \times \texttt{b\_sex} + \texttt{weight}_i \times \texttt{b\_weight})$. The second parameter, `stdev`, has the same two covariates modeled on it, but the parameter names are (and must be) different from the parameters modeled on `mean`.

For some forms, the parameter itself is transformed. For example, when a parameter is a probability (as it is for the `MIX` function in above) the parameter can be defined as:

```
PARAM p  LOW = -999  HIGH = 999  START = 0  FORM = LOGISTIC END
```

The logistic transformation permits the parameter `p` to take on any value from negative infinity to infinity, but the resulting value passed used by the likelihood will be constrained to the range (0, 1). In other words, *mle* will estimate a parameter over the range –999 to 999, but before that parameter is used in computation, it will undergo a logistic transformation as $p = 1/[1 + \exp(p')]$, so that the value of *p* will be a probability. *mle* currently provides a limited number of specifications for how parameters and covariates are modeled (see the Reference Manual). Even so, this mechanism for modeling covariates on any parameter is extremely general and provides the basis for building unique and highly mechanistic (Box et al. 1978) or etiologic (Wood 1994) models.

The PDF functions

One of the most frequently used functions in the `MODEL` statement is the `PDF` function. The purpose of the `PDF` function is to specify the component of a pre-defined probability density or distribution functions. Although the name is `PDF`, the `PDF` function can return the probability density function, areas under the PDF curve including the cumulative and survival density functions, and the hazard function. In addition, the `PDF` function can return areas or densities that are left and right truncated. The structure of the `PDF` function call is:

```
PDF <PDF name> ( <time variable1>, <time variable2>, ... )
  <intrinsic parameter 1>,
  <intrinsic parameter 2>,
  ...
  <optional HAZARD>
END
```

The *name* following `PDF` is the name of the built-in distribution. *mle* predefines over 60 density functions, including most well-known ones like the normal, lognormal, weibull, gamma, beta, and exponential distributions. A complete summary of built-in distribution is given in a later chapter.

Time variable list is a list of the time arguments passed to the PDF. Most univariate PDFs can take from one to four 'time' arguments.[7] In fact, these four times describe a single observation in such a way as to incorporate a number of defects in the observation process, including right censoring, left truncation, right truncation, cross-sectional observations. A description of how the four arguments combine to specify a probability are given in the section that follows. Note that the time arguments can be any expression, so that time shifts and transformations can be incorporated in this list.

Intrinsic parameter list provides specifications for the PDF's intrinsic parameters. The order that the intrinsic parameters are specified is important; it corresponds to how the PDF is defined within *mle*.. The PDFs chapter lists the order for intrinsic parameters; alternatively, the command line `mle -h` can be used to determine the proper argument order. Note that any expression can be used for an intrinsic parameter. That is, you do not need to use a `PARAM` function for the intrinsic parameters, although this is the most common use. Here is an example in which the location parameter is fixed to a constant for a shifted lognormal distribution:

```
PDF SHIFTLOGNORMAL ( tooth_eruption_age )
  9,  {shift the time back to conception}
  PARAM location LOW = 1 HIGH = 4 START = 2.5 END,
  PARAM scale LOW = 0.0001 HIGH = 3 START = 0.9 END
END
```

PDF Time Arguments

Most PDFs can have as few as one and as many as four time arguments specified. They are: t_u, the last observation time before an event; t_e, the first observed time after the event; t_a, the left truncation time for the observation or the PDF; and t_w, the right truncation time for the observation or the PDF. Understanding how these four times act on the `PDF` statement is critical to creating the desired and proper likelihood.

[7] These are called *time* variables in the context of survival analysis; however, they may represent other measurements (length, dose, height, etc.).

Table 5. Likelihoods returned by **PDF** *for one, two, three, and four time variables under different conditions. The Log Normal distribution is used as an example.*

Example	When	Class	Resulting Likelihood
LNNORMAL(t_e)	1 arg.	Exact failure at t_e	$L = f(t_e)$
LNNORMAL(t_u, t_e)	t_u=t_e	Exact failure at t_u=t_e	$L = f(t_u) = f(t_e)$
LNNORMAL(t_u, t_e)	t_e=oo $t_e < t_u$	Right censored or cross-sectional non-responder at t_u	$L = \int_{t_u}^{\infty} f(z)dz = S(t_u)$
LNNORMAL(t_u, t_e)	t_u = 0	Cross-sectional responder at t_e	$L = \int_{0}^{t_e} f(z)dz = F(t_u)$
LNNORMAL(t_u, t_e)	$t_u \neq t_e$	Interval censored over the interval (t_u, t_e). Includes, as a limiting case cross-sectional responder and right-censored.	$L = \int_{t_u}^{t_e} f(z)dz = S(t_u) - S(t_e)$
LNNORMAL(t_u, t_e, t_a)	$t_u = t_e$	Left-truncated exact failure	$L = \frac{f(t_u)}{\int_{t_\alpha}^{\infty} f(z)dz} = \frac{f(t_u)}{S(t_\alpha)}$
LNNORMAL(t_u, t_e, t_a)	$t_u \neq t_e$	Left-truncated, interval censored failure	$L = \frac{S(t_u) - S(t_e)}{\int_{t_\alpha}^{\infty} f(z)dz} = \frac{S(t_u) - S(t_e)}{S(t_\alpha)}$
LNNORMAL(t_u, t_e, t_a, t_w)	$t_u = t_e$	Left- and right-truncated, exact failure	$L = \frac{f(t_e)}{\int_{t_\alpha}^{t_\omega} f(z)dz} = \frac{f(t_e)}{S(t_\alpha) - S(t_\omega)}$
LNNORMAL(t_u, t_e, t_a, t_w)	$t_u < t_e$ $t_\alpha \leq t_u$ $t_\omega \geq t_e$	Left- and right-truncated, interval censored failure	$L = \frac{S(t_u) - S(t_e)}{\int_{t_\alpha}^{t_\omega} f(z)dz} = \frac{S(t_u) - S(t_e)}{S(t_\alpha) - S(t_\omega)}$
LNNORMAL(t_u, t_e, t_a)	t_u=t_e=t_α	Hazard	$L == \frac{f(t_u)}{S(t_u)} = h(t_u)$
LNNORMAL(t_u, t_e, t_a, t_w)	t_u=t_e=t_α	Right-truncated hazard	$L == \frac{f(t_u)}{S(t_u) - S(t_\omega)} = h(t_u)$

PDFs contribute to likelihoods in a number of ways. In survival analysis, for example, the likelihood for an exact failure time is given by the value of the PDF at the exact point of failure. For a right censored observation, the likelihood is given by summing up (integrating) all possible PDF values from the last observation time until the maximum possible time. The likelihood for a cross-sectional "responder" is the integral from zero to the time of first observation. Table 5 lists the likelihoods that result from the four time variables for different conditions. For example, when t_u=t_e or when only one time variable is specified, *mle* returns the density at t_u. This is the desired likelihood for an exact failure. Likelihoods for right and interval censored observations, with and without left and right truncation are given in Table 5.

The Hazard Parameter

For most parametric distributions (like the normal or lognormal distributions) the hazard function does not take on a simple or closed form. For this reason, most studies have modeled the covariates as acting on the failure time for these distributions. Nevertheless, there is no inherent reason why hazards models cannot be constructed using distributions without a closed form for the hazards functions. Most of the PDFs included in *mle* provide a general mechanism for covariates to be modeled as affecting the hazard of failure, rather than (or in addition to) affecting intrinsic parameters. Here is an example:

```
PDF NORMAL(topen tclose)
  PARAM mean   LOW = 100  HIGH = 400  START = 270  TEST = 0  FORM = LOGLIN END,
  PARAM stdev  LOW = 0.1  HIGH = 100 START = 20 END,
  HAZARD COVAR  sex     PARAM b_sex     LOW = -2  HIGH = 2  START = 0 END
         COVAR  weight  PARAM b_weight  LOW = -2  HIGH = 2  START = 0 END
END
```

The covariates `sex` and `weight` are modeled to effect on the hazard of failure. Parameters `b_sex` and `b_weight` provide estimates of the effect.

The `HAZARD` statement always provides a proportional hazards specification modeled directly on the hazard of the PDF. Usually, the specification is loglinear, so that the hazard for the *i*th observation including the covariate effects defined as $h_i(t_i|\mathbf{x}_i\mathrm{b}) = h(t_i)\exp(\mathbf{x}_i\mathrm{b})$, where $h(t)$ is the baseline hazard for the specified PDF, and $\mathbf{x}_i\mathrm{b}$ is a vector of covariates $\boldsymbol{x_i}$ and parameters b, so that $\mathbf{x}_i\mathrm{b} = x_{i1}\beta_1 + x_{i2}\beta_2 + x_{i3}\beta_3 \ldots$. Then, the survival function becomes $S_i(t_i|\mathbf{x}_i\mathrm{b}) = S(t_i)^{\exp(\mathbf{x}\mathrm{b})}$, and the probability density function becomes $f_i(t_i|\mathbf{x}_i\mathrm{b}) = f(t_i)S(t_i)^{\exp(\mathbf{x}\mathrm{b})-1}\exp(\mathbf{x}_i\mathrm{b})$.

This particular hazards model specification is commonly used. By exponentiating the $\mathbf{x}_i\mathrm{b}$ array, the covariate effects will never cause the hazard to go negative (hazards are *never* negative).

A multiplicative form for the proportional hazards specification can also be specified by setting the constant `EXP_HAZARD = FALSE` (it is `TRUE` by default). Then, the model is $h_i(t_i|\mathbf{x}_i\mathrm{b}) = h(t_i)\mathbf{x}_i\mathrm{b}$, $S(t_i|\mathbf{x}_i\mathrm{b}) = S(t_i)^{\mathbf{x}\mathrm{b}}$, and $f(t_i|\mathbf{x}_i\mathrm{b}) = f(t_i)S(t_i)^{\mathbf{x}\mathrm{b}-1}\mathbf{x}_i\mathrm{b}$. You must insure that $\mathbf{x}_i\mathrm{b}$ never goes negative.

The LEVEL function

The `LEVEL` function provides a mechanism by which multilevel or hierarchical models can be constructed. The syntax of the `LEVEL` function is

```
LEVEL <boolean expression> THEN <optional_form>
  <expression>
END
```

The effect of the `LEVEL` function is to test the <*boolean expression*> for each observaton and, while the condition is true, form the sum of loglikelihoods out of the observations. The <*optional_form*> provides alternative ways of tallying the likelihoods, and is specified as it is for the `DATA` function, save for one difference:The default form is `.FORM = PRODUCT`.

The best way to understand the effect of the `LEVEL` command is by an example. Consider the likelihood

$$L = \prod_{i=1}^{N} \int_{\alpha}^{\omega} g(z) \left[\prod_{j=1}^{n_i} f(t_{i,j} \mid \theta, z) \right] dz .$$

This is a standard model for which a distribution of clustering (or heterogeneity), $g(z)$, is estimated along with the model's other parameters (q). There are two levels that make up this model. Let us call the outer level, denoted by the outer product, the *subject* level—that is, we have N individual subjects and this outer product is taken over all subjects. For each of N

subjects, there are multiple repeated observatons taken. For the *i*th subject, we have n_i repeated observations. The inner level formed by the innermost product is the likelihood formed by n_i repeated observations of the *i*th subject.

The rationale for this type of model is that the repeated observations for individuals violate the condition that the likelihoods for each observation are independent. To fix this problem, we can compute an expected likelihood for each individual's observations. The integral computes the expected likelihood for each subject. Here is a concrete example

Say we have data in which levels are denoted by the number 1 or 2 as in

```
1  Tom Smith
2  23.4   26.8 . . .
2  19.2   22.9 . . .
2  26.8   -1   . . .
1  Steven Jones
2  19.5   23.7 . . .
2  26.8   -1   . . .
1  Martin Johnson
2  0      44.1 . . .
2  19.9   22.7 . . .
2  19.9   -1   . . .
...
```

where the observations beginning with a 2 correspond to the individual at the preceding 1, so that Tom Smith has three observations beginning 23.4, 19.2, and 26.8. If we were to treat all observations, within and among individuals, as independent, we could simply drop all of the level 1 lines, and form a likelihood as the product of all observations. But, if we want to treat observations within individuals as correlated (non-independent), the we can integrate over a distribution of common effects as shown in the likelihood above. Usually, we will estimate one or more parameters for the distribution $g(z)$, in addition to q.

If we assume that $g(z)$ and $f(t)$ are normal distributions, the likelihood in *mle* would be specified as

```
MLE
  DATAFILE("example.dat")
  OUTFILE("example.out")

  DATA
    lev FIELD 1
    topen FIELD 2
    tclose FIELD 3
  END

  MODEL
    DATA
      LEVEL lev = 2 THEN
        INTEGRATE z (-12, 12)
          PDF NORMAL (z)
            0, PARAM sigmaz LOW = 0.0001  HIGH = 3 START = 0.2 END
          END {pdf}
         *
          PDF NORMAL(topen tclose)
            PARAM mu LOW = 10 HIGH = 100 START = 30 END
            PARAM sigma  LOW = 0.0001 HIGH = 10 START = 1 END
            HAZARD COVAR z 1
          END  {pdf}
        END {integrate}
      END {level}
    END {data}
  RUN
    FULL
  END  {model}
END  {mle program}
```

The LEVEL statement advances through all of the individual level observations and computes the product of the likelihoods for each individual. The DATA statement only "sees" observations that begin with a 1, because the LEVEL statement "consumes" all of the observations that begin with a 2. The LEVEL statement returns a likelihood, which is the product of likelihoods taken within each subject; the DATA statement takes those likelihoods, one per subject, takes the natural log of each, and sums them over all subject.

The LEVELDELTA function

The LEVELDELTA function is very similar to the LEVEL function. LEVELDELTA provides a mechanism by which multilevel or hierarchical models can be constructed. The syntax of the LEVELDELTA function is

```
LEVELDELTA <expression> THEN <optional_form>
  <expression>
END
```

The effect of the LEVELDELTA function is to evaluate *<expression>* for each observation and, while the expression does not change, form a product of likelihoods out of the observations. The *<optional_form>* is specified as it is for the DATA function, but with one difference: the default form is .FORM = PRODUCT.

The only real difference between the LEVELDELTA and the LEVEL function is how each function decides when to "exit" the current level. The LEVELDELTA function simply looks for a change in the value of *<expression>* whereas LEVEL evaluates a boolean function *<bexpr>* for each observation and terminates when the expression evaluates to FALSE. In the example given under the LEVEL function, the only change necessary to use the LEVELDELTA function is replace the LEVEL line with

```
LEVELDELTA lev THEN
```

Here is an example program uses the LEVELDELTA function. The program estimates the change in oxygen consumption ($\Delta V0_2$) in individuals undergoing repeated exercise tests, using a variety of predictor variables like the increase in heart rate over the resting state. Since there are repeated measures on individuals, a distribution of individual effects is estimated along with other parameters. The likelihood is

$$L = \prod_{i=1}^{N} \int_{-\infty}^{\infty} g_z(z \mid 0, \sigma_z) \prod_{k=1}^{m_i} f_v(v_{ik} \mid \mu + \mathbf{x}_{ik}^{'}\mathbf{ß} + z, \sigma) dz$$

Where $g_z(z)$ is the distribution of individual effects, with a mean of zero and a variance of σ_z^2, $f_v(v)$ is the distribution of $\Delta V0_2$ values with parameters b, μ, and σ.

```
MLE
  { -- does a linear regression w/ repeated measures model}

  DATAFILE("example.dat")
  OUTFILE(DEFAULTOUTNAME)

  DATA
    subject      FIELD 1    {subject ID}
    sex          FIELD 2    {individual's sex 0=female, 1=male}
    age          FIELD 3    {individual's age}
    weight       FIELD 4    {individual's weight}
    height       FIELD 5    {individual's height}
    armcirc      FIELD 6    {mid-upper arm circumference}
    skinfold     FIELD 7    {individual's skinfold measurement}
    deltahr      FIELD 8    {heart rate adjusted for baseline rate}
    deltav02     FIELD 9    {volume of 02 used during exercise adjusted for baseline}
  END  {data}

  MODEL
    PREASSIGN
      BEGIN
        sigz = PARAM sigmaz LOW = 0.001 HIGH = 50 START = 1 END
        upperlim = 6*sigz
        lowlim = -upperlim
      END,
      DATA
        INTEGRATE z (lowlim, upperlim)
          PDF NORMAL(z) 0, sigz END *
          LEVELDELTA subject THEN
            PDF NORMAL(deltav02)
              PARAM b0 LOW = -200  HIGH = 50  START=0  FORM=ADD
                COVAR sex      PARAM  bsex      LOW=-10  HIGH=50 START=0 END
                COVAR age      PARAM  bage      LOW=-10  HIGH=50 START=0 END
                COVAR weight   PARAM  bweight   LOW=-10  HIGH=10 START=0 END
                COVAR height   PARAM  bheight   LOW=-10  HIGH=10 START=0 END
                COVAR armcirc  PARAM  barmcirc  LOW=-10  HIGH=10 START=0 END
                COVAR skinfold PARAM  bskinfold LOW=-10  HIGH=10 START=0 END
                COVAR deltahr  PARAM  bdeltahr  LOW=-10  HIGH=10 START=0 END
                COVAR z 1
              END {param b0}
              PARAM sigma LOW = 0.00001 HIGH = 50 START=5 END
            END {pdf normal}
          END {leveldelta}
        END {integrate}
      END {data}
    END  {preassign}
  RUN
    WITH sigmaz b0 sigma (bsex bage bweight bheight barmcirc bskinfold bdeltahr)
  END {model}
END  {mle}
```

Setting the maximization method

mle has four methods for maximizing the likelihood function. Each of the methods has strengths and weaknesses for different types of functions. Understanding some of the details of each method is useful for deciding which to use for any given application. The following sections describe each of the maximizers and points out strengths and weaknesses of each. The behavior of some methods can be modified considerably by the user.

The maximization method is selected by setting the variable `METHOD`. For example, `METHOD = ANNEALING` will use the simulated annealing method. The default method is `DIRECT`.

The overall goal of function maximization is to find the set of parameters that maximize a function. A simple analogy is to imagine that you are looking at a topographic map that codes altitude by color. You want to find the longitude and latitude coordinates (the "parameters") that will put you at the highest point on the map. By looking over the map, you may be able to

quickly ascertain a mountain peak or some other maximum. In order to do this, however, you effectively scanned hundreds of thousands of points on the map until finding those places where the colors suggest the highest altitude. With a little more work, the highest peak is easily resolved. Visual evaluation of maximum elevation is easy and takes almost no time because the map shows the elevations evaluated at hundreds of thousands of points on the map, and our eyes can quickly scan those points. That is, each "function" evaluation was inexpensive—we merely had to look at a point to know its value. Now imagine that the map surface is covered by a piece of paper. You can only expose a tiny hole in the map in order to read the color at that point (that is, to evaluate the function at that point). Furthermore, each hole takes a long time to cut, perhaps minutes or hours. Then the question becomes this: how do we find the maximum elevation of the map in the shortest possible time? The map analogy will be used to understand how different computer algorithms finds the maximum of a likelihood surface.

Many different function maximization methods have been developed at least since Isaac Newton developed methods out of the calculus. Nevertheless, no single method has emerged as superior for all types of problems. In general, function maximization is easiest to do when information is available for the derivative of the function. A traditional way of finding maximum likelihood parameters for simple functions is to symbolically find the derivatives of the function with respect to each free parameter. Each partial derivative is set to zero. This set of equations is collectively called the likelihood equations. Since the derivatives are defined as the slope of the function, it follows that any place where all the partial derivatives go to zero must be a minimum or a maximum of the function. If practical, the likelihood equations are "solved"; that is, the sets of parameter values are analytically found that simultaneously yields zero for each of the partial derivatives. The maximum likelihood estimates for a parameter is found from a particular series of observations by simply applying that equation on the set of observations. Unfortunately, this method is difficult and non-general and, therefore, not practical for general-purpose maximization as found in *mle*. Advances in computer-assisted symbolic mathematics (packages like Maple and Mathematica) may eventually prove this method feasible for many users, but the need for specialized mathematical knowledge and skills still limits this method. A general method must work for most types of likelihood functions, whether or not analytical derivatives are easy (or even possible) to find.

Another class of fast maximizers estimates derivatives numerically. These methods are not robust for complex surfaces with many local maxima. From some starting point, they tend to rush up to the top of the nearest local maximum. A given function may have one or many points where the derivatives goes to zero, so this method may not find the global maximum. Numerical derivatives have limitations resulting, in part, from the inaccuracy of real number representation in computers, so that a number of derivative-free methods have been developed. One clever method solves a two dimensional maximization problem by trying to enclose the maximum within a triangle. The triangle grows and shrinks based only on information from the three points of the triangle at a given step. A rather unsophisticated method alternates between maximizing the function first by longitude, using as many evaluations as needed to find the maximum longitude for a given latitude, and then does the same for latitude. By repeating this many times, a maximum (usually the global maximum) is found. Needless to say, this method can be very slow. Finally, a newer method has been developed that mimics natures own maximization method. The method can be slow, but seems to be as robust at finding the global maximum as any iterative method.

Conjugate gradient method

The conjugate gradient method searches through parameter space for combinations of parameters where the slope of the likelihood function goes to zero. Now, the computer numerically computes a slope (or gradient) using the equation $m_i = [f(x_i + \Delta x_i) - f(x_i]/\Delta x_i$, for parameters **x** and

small values $\Delta\mathbf{x}$. This procedure uses the slopes (m_i) to figure out the next set of **x** under the idea that the slope will decrease as the maximum is approached (unless the surface is flat).

The conjugate-gradient method used in *mle* was developed by Powell (1964), Brent (1973), and further developed by Press et al. (1989). For problems of more then two free parameters, the conjugate gradient method is usually much faster than the direct method. Caution must be exercised when using this method. At times a local maximum is latched onto by the solver and the rest of the parameter space is excluded. Furthermore, some conditions can cause the maximizer to leap to another part of the surface, where a local minimum might be reached. For example, when maximizing a likelihood function that includes numerical integration, the tolerance in the integrator must be several orders of magnitude smaller than that of the solver, or else the error in integration can lead the solver astray.

Two forms of the conjugate gradient method are available, `METHOD=CGRADIENT1` and `METHOD=CGRADIENT2`.

Simplex

The simplex method is a derivative-free maximization method described by Nelder and Mead (1965) and popularized by Press et al. (1989). The method is set with `METHOD=SIMPLEX`.

Direct Method

A simple method for finding a maximum is to consider only one dimension at a time. So, for our map, we would find the highest latitude for a given longitude by examining points along a line of longitude. We could use the method of bisection or even better ways to find the maximum along that line of longitude in the fewest number of evaluations (i.e. fewest holes). Once we have settled on a latitude, we can find the longitude of highest elevation along that latitude. We next go back and find a new latitude for the new longitude, etc. This is known as the direct method (Nelson 1983), and works well for some functions over a small number of dimensions. In fact, the method is usually more robust at finding a global maximum than the simplex or congugate gradient methods. Furthermore, it is easy to constrain the algorithm so that new parameter values never overstep the user-defined (or mathematically defined) limits—that is, it respects the boundaries of our map. Unfortunately, the number of function evaluations goes up as an exponent of the number of dimensions in the problem. When the number of parameters gets large, the solution is very slow in coming. Furthermore, some functions that have the maximum along a long narrow ridge at a 45° angle to the lines of longitude and latitude require a large number of tiny movements before reaching the maximum.

The direct method and is set by `METHOD=DIRECT`. It uses the `HIGH =` value and `LOW =` values to constrain all parameters (as discussed below). The `START =` values define the initial starting parameters.

The direct method uses Brent's (1973; see also Press et al. 1989) parabolic interpolation to find the maximum along a single direction (i.e. for a single parameter holding all other parameters constant). The maximizer uses the `HIGH =` value and `LOW =` value to define the extreme bounds of the problem. The `START =` value is the first "guess" at the maximum. A parabola is then fit through the set of three points, and the maximum is analytically computed. This procedure is repeated with the three points enclosing the maximum until the maximum in that dimension is found to some prespecified tolerance. There are three ways you can modify the Brent maximizer. First, the maximum number of iterations in a single dimension can be set with `BRENT_ITS =` value, which is sufficient for almost every function. The next modification is to change the value of `BRENT_MAGIC` to some other number. This number defines the interpolation point between two

points of a parabola—the so-called golden mean of ancient Greece. With such a heritage, there is little reason to change it. Finally, the value `BRENT_ZERO` is an arbitrary tiny number used in place of zero for the difference of two equal function evaluations.

Simulated Annealing Method

The simulated annealing method is an exciting and relatively new idea in maximization. It was first proposed by Kirkpatrick et al. (1983) for combinatorial problems. The algorithm was further developed for functions of continuous variables by Corana et al. (1987) and refined by Goffe et al. (1994); both papers lucidity describe how the method works.

As a metal is heated to its melting point, it loses its crystalline organization. Then as it again cools, the crystalline pattern reemerges. When cooled slowly, a process called *annealing*, small crystals of metal rearrange themselves and join other crystals with maximum orderliness (or minimum energy). This occurs as random movements of atoms and groups of atoms eventually fall into an alignments that minimize gaps. Once these structured alignments arise, they form a larger crystal and are subsequently less likely to fall out of alignment. As the temperature drops and the atoms move around less, large overall changes in structure become less probable. When absolute zero is reached, the structure becomes fixed (at room temperature, solid metals continue to anneal very slowly). Rapid cooling of the metal, called *quenching* in metallurgy because the metal is thrust into cool water or pickle, does not provide sufficient time for crystals to move about and organize. Thus, numerous vacancies and dislocations exist among many small crystals, and orderliness is minimal. Maximizing the crystalline order (or minimizing vacancies and dislocations) is done by cooling the metal very slowly and providing ample opportunity for the random crystal movements to fortuitously align themselves into more ordered structures.

The simulated annealing method attempts to mimic the physical process of annealing. An initial "temperature" is set, and a cooling rate is specified. New parameters are randomly chosen over a large range of the parameter space. As the temperature cools, smaller and smaller ranges of the parameter space are explored. Additionally, the maximizer will not always travel up hill. At any given temperature, a certain fraction of downhill moves will be taken so that local maxima will not trap the maximizer.

The advantage of simulated annealing over other methods is that it is very good at finding the global maximum, even in the presence of highly multimodal likelihood surfaces. The user can fine tune the behavior of the algorithm so that functions with complex topography can be searched more thoroughly for the maximum. Another advantage of simulated annealing is that it does not require computation of derivatives. In fact, simulated annealing can find the maximum of discontinuous functions and those otherwise without first derivatives. Finally, the simulated annealing algorithm is extremely simple and intuitive. The disadvantages of simulated annealing are that it usually takes from one to several orders of magnitude more function evaluations than do other methods and the user must have an understanding of the algorithm to set up initial parameters that lend themselves to efficient estimation. Sometimes it is worth experimenting to find the best combinations of input parameters to the simulated annealing algorithm so as to minimize the total number of function evaluations.

Simulated annealing begins at some user-defined temperature (T) and a user-defined rate of cooling (r). At the end of one cycle of annealing, the temperature is reduced as $T = T \times r$, and a new cycle of annealing is performed. Typically the temperature will be 1 for simple function to 100,000 for difficult functions, and it is cooled every cycle by $r = 0.85$. When the algorithm begins, the starting point is evaluated and becomes the best value, so far. Each iteration will then search the likelihood surface in a partially random way and always keep track of the best point so far. A single cycle of annealing (i.e. one iteration) consists of the following. First, a cycle of random movements is started. N_{rand} random steps are taken over one direction at a time. The

maximum width of the random step for parameter i is controlled by the step length variable v_i. For our map example, this would correspond to evaluating N_{rand} randomly picked points along a line of longitude or latitude. Initially we would use the entire height and with of the map for the maximum step length. As each point is evaluated, we keep track of the overall best maximum. Any time we find a point higher than our current maximum, we move to that point and consider it our new starting point. But, if a lower point is found we *might* accept that point according to the Metropolis criterion (Metropolis et al. 1953) by which the point is accepted with probability $\exp(-\Delta l/T)$, where Δl is the difference between the current starting point and the downhill point we have just evaluated. In other words, we draw a uniform random number on [0, 1), and accept the move if that number is less than a negative exponential survival function of Δl, with parameter $1/T$. This criterion means that at high temperatures we will frequently accept downhill moves with large changes in the loglikelihood, but as temperature drops, downhill moves will only occur at small changes in the loglikelihood. After completing the N_{rand} movements and evaluations, we now adjust the maximum steplength vector $\boldsymbol{v}$. The reduction or increase in steplength is done according to the proportion of accepted and rejected movements by an algorithm described in detail below. In short, the maximum step length is reduced or increased so that we can expect to accept about one half of all moves in the next cycle of random steps. Following this adjustment, a new cycle of random steps is initiated until a total of N_{adj} of these adjustments have been completed. Thus, after $N_{rand} \times N_{adj}$ function evaluations, a single iteration completes, and a new iteration is begun until convergence, the maximum number of iterations is reached, or the maximum number of function evaluations is reached.

The simulated annealing method is set by `METHOD=ANNEALING`. The method does use the `HIGH =` value and `LOW =` values to constrain all parameters (as discussed below). The `START =` values define the initial starting parameters. A number of other variables should be set with this method. Since the simulated annealing method uses random numbers, the user must set a random seed, by calling the procedure `SEED()` with a positive integer. The starting temperature is set with `SA_TEMPERATURE`. The default value is 1000.0, which is too high for all but extremely wild functions. It is difficult to know what a good starting temperature is for a function, but values under 100 empirically seem to work for all but the most topographically complicated likelihood functions. When a likelihood is to be solved multiple times on similar data sets, like when running on bootstrapped data sets, it is worth exploring a couple of different temperatures and monitoring the progress of the annealing by using the verbose (`-v`) option. In fact, watching the entire annealing process is useful for developing and understanding of the algorithm. The variable `SA_COOLING` controls the cooling rate, and is 0.85 by default. Too high a value will slow down cooling and may lead to unnecessary evaluations, whereas too low a value may resulting in (simulated) quenching. The number of steps of random parameter perturbation is set using `SA_STEPS`. The number of step length adjustments taken every iteration is controlled by `SA_ADJ_CYCLES`. Finally, the size of each step adjustment can be controlled by `SA_STEPLENGTH_ADJ`, but the default value of 2.0 usually works well.

The simulated annealing algorithm uses a different criterion for convergence than do the other solvers. An array of the best likelihoods of size `SA_EPS_NUMBER` (default is 4) is created and updated every iteration. Convergence is considered achieved when the likelihood for the current iteration differs from all `SA_EPS_NUMBER` likelihoods by the value of `EPSILON`.

Several other variables can be used for fine tuning of the simulated annealing algorithm, but there is rarely a need to mess with them. `SA_STEPLENGTH` is the initial step length for all parameters. Empirically, the starting step length value has little effect on the outcome of the maximizer. `SA_ALT_ADJUSTMENT` uses an alternative formula for adjusting the step length. `SA_ADJ_LOWERBOUND` defines a "null" area for which step length is not adjusted. If the proportion of accepted moves is greater than `SA_ADJ_LOWERBOUND` and is less than 1 – `SA_ADJ_LOWERBOUND`, the current steplength will continue to be used. See Corana et al. (1987) for more details.

Stopping Criteria

There are three ways to terminate finding the solution of a model. The first way is to minimize the change in the log-likelihood to below some specified minimum value. You can specify this by setting, for example, `EPSILON=1E-8`. When the absolute difference between the log-likelihoods of the previous iteration and the current iteration falls below this value, the problem will be considered to have converged normally.

The second way of controlling the stopping criteria is by specifying the maximum number of iterations permissible. For example, setting `MAXITER=1000`, would stop searching for the maximum after 1,000 iterations, regardless of the change in the likelihood. Note that a single iteration is that over all dimensions.

The third stopping criterion is by specifying the maximum number of function evaluations permissible. You can specify, for example, `MAXEVALS=10000`, which would stop searching for the maximum likelihood after 10,000 evaluations of the likelihood.

Looping Through Methods

mle provides a mechanism to specify that different methods be used to solve the same likelihood. For example, you can set

```
METHOD1=DIRECT
MAXITER1=10
METHOD2=CGRADIENT1
MAXITER2=500
```

to begin the problem with the direct method and then switch to a conjugate gradient solver for the next 500 iterations. The variables `METHOD`, `MAXEVALS`, `MAXITER`, and `EPSILON` can have a digit appended in this way. When the variable `METHOD_LOOP` is set to true, *mle* will loop back to the first method and continue the solver sequence again until one of the methods converges normally.

The Interactive Debugger

mle incorporates an interactive debugger that provides some degree of control while models are being solved. Entries in the symbol table can be viewed and changed, so that convergence can be forced early or postponed, output variables can be changed, and the values of various debugging options can be set and reset.

The debugger is called by typing <CTRL> C on most systems. The <BREAK> key also works on some systems. After *mle* gets to some reasonable stopping point—usually the end of an iteration—control will be passed to the user. The debugger responds with

Exit: immediately exits the program.

Resume: resumes running *mle* from where it left off.

One step: continue from where it left off for one more iteration and then reenters the interactive debugger.

Pick a symbol: selects a symbol to display. The value of the symbol is displayed between debugger commands, for this and all subsequent calls to the debugger.

Change the value of a symbol: If no symbol is selected, the user will be prompted for a symbol to change and then a value to change it to. If a symbol is selected (with ***Pick***), then that symbol will be changed.

Search for symbols: Prompts the user for search text, and then searches the symbol table for symbol names that match any part of the search text. The name, types, and value of matching symbols are displayed.

Chapter 5
Plots and graphs

The PLOT command is used to create plots and charts in *mle*. This chapter discusses the command, and gives some examples of creating graphs.

mle does not directly generate graphs. Instead, it writes graphing programs in the *Gnuplot* plotting language. The graphs can be printed using one of the many device drivers included in *Gnuplot*. Additionally, graphs can be imported into a number of text processing languages like TEX or *MSWord*, or manipulated in graphics editing programs.

Here is a list of the plotting capabilities offered by *mle*:

- Two-dimensional data plots of data points, parametric functions, bar charts, histograms, graphs with error bars for *x*, *y* or both.
- Three-dimensional plots including surfaces and contour plots.
- Multiple curves or surfaces can be drawn on a single plot.
- A simple mechanism to specify a grid of multiple plots on a single page.
- Data points and fitted curves
- Up to two *x* and two *y* axes on a single (two-dimensional) graph.
- Cartesian or polar coordinates in two dimensions. Rectangular, spherical, or cylindrical coordinates in three dimensions.
- Simple generation of estimated distributions with error bars.
- One- and two-dimensional likelihood profiles

Creating Plots

There are four steps used for creating graphs in *mle*.

- Define the plot file using the PLOTFILE(<*name*>) procedure in a program.

- Define one or more plots using the `PLOT . . . END` statement in a program. Usually the statements within `PLOT . . . END` will include one or more `CURVE . . . END` statements that draw the curve on the current plot.

- Run the *mle* program. The plot file and its data files will be created as a *Gnuplot* program. At this point you have the option to edit the plot as a *Gnuplot* program.

- Run the *Gnuplot* program on the plot file to create, display, or print the graph. In some cases, this forth step can be done from within the *mle* program using the `FINISHPLOT` procedure.

Defining the Plot File

The first step in creating a graphic is to define a plot file using the `PLOTFILE( <name> )` procedure. *mle* writes a *Gnuplot* program to the plot file (*Gnuplot* is discussed in a later section). The name of the plot file also determines the name of data files created for use by the plot file.

Suppose we wish to create a plot called `sincos.plt`. The statement `PLOTFILE("sincos.plt")` will create a plot file by that name. Information will be written to this file that defines the plot. The information comes from six places:

- The `PLOTFILE()` procedure writes an initialization string to the plot file. The string is stored in the variable `GNUPLOTINIT`. For example, in DOS-based operating systems, this variable is initially set to `"set terminal windows; reset; set data style lines; set autoscale; set nokey"`. These *Gnuplot* statements specify that the terminal is *Windows*, plot parameters will be reset, lines will be plotted by default, *Gnuplot* will figure out a good scale to use, and a graph key will not be generated. You can change this initialization string by assigning a new string to the `PLOTINIT` variable. Alternatively, you can keep this string as is and add new program lines using the `WRITEPLOTLN()` statement (discussed next).

- The `WRITEPLOTLN()` and `WRITEPLOT()` procedures provide a simple way of writing *Gnuplot* statements directly to the plot file. These statements must be used *after* the `PLOTFILE()` statement. For example, if you want to add a title to the plot, the statement `WRITEPLOTLN("set title 'Sin and Cos functions'")`. You can insert any *Gnuplot* statement into the plot file this way. The difference between `WRITEPLOTLN()` and `WRITEPLOT()` is that the former adds a newline after writing, whereas the latter does not.

- The `MULTIPLOT(<x>, <y>) . . . END` statement can be used to create *x* by *y* grids of *x*×*y* plots on a single page. The statement writes commands to the plot file, and an initialization string taken from the variable `MULTIPLOTINIT`.

- The `PLOT . . . END` statement initiates a single plot, graph, or chart. It will write an initialization string to the plot file taken from the variable `PLOTINIT`.

- The `CURVE . . . END` statement writes a single curve to the current plot. This is the statement that writes the *Gnuplot* `plot` and `splot` statements to the plot file. Each `CURVE` statement also creates a data set used by the plot file.

The name of a plot file should usually end in the file extension `".plt"`, because this extension is used by *mle* and *Gnuplot*.

mle can select a plot file name based on the name of the program file by using the DEFAULTPLOTNAME function. The statement PLOTFILE(DEFAULTPLOTNAME) will create a plot name that matches the name of the program file, but with the ".plt" extension replacing the ".mle" extension.

The plot file will accumulate graphics instructions from the *mle* MULTIPLOT, WRITEPLOTLN, PLOT, and CURVE commands until a new plot file is opened or the *mle* program terminates. The plot file is then processed through *Gnuplot* to display or print the plots.

The Plot Statement

The PLOT...END statement initiates a single graph or chart. The statement does not do the plotting itself, instead each CURVE...END statement executed within the PLOT...END statement will add a single curve to the plot.

The format of the statement is

```
PLOT [(<string_expr>. . .)]
  <statements>
END
```

When a PLOT statement is executed, a few statements may be written to the plot file. Then, the *<statements>* are executed. All CURVE statements executed before the END is reached will result in one curve being added to the current plot.

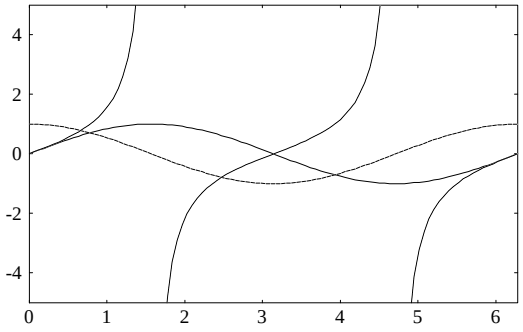
The optional series of string expressions (enclosed within parentheses) can immediately following the PLOT statement. These strings will be written to the plot file. The purpose of these strings is to provide additional information to the *Gnuplot* program, such as titles, ranges, and borders. They are simply written verbatim to the plot file. In fact, plots can be written in the *Gnuplot* language with these strings. Here is an example:

```
MLE
  PLOTFILE("gploteg.plt")
  PLOT ( "plot [0:2*pi][-5:5] sin(x), cos(x), tan(x)" ) END
END
```

The resulting *Gnuplot* file is:

```
set terminal windows; reset; set data style lines; set autoscale; set nokey

plot [0:2*pi][-5:5] sin(x), cos(x), tan(x)
```

And, here is the resulting plot.



The PLOT statement writes the PLOTINIT string to the plot file. You can assign a string to the PLOTINIT variable, and it will be written for each PLOT.

The Curve Statement

The CURVE...END statement does the bulk of the work in creating plots. Each CURVE statement generally creates a single curve or surface. For simplicity, the curve statement will be discussed separately for two-dimensional and three-dimensional plots.

Two-dimensional Plots

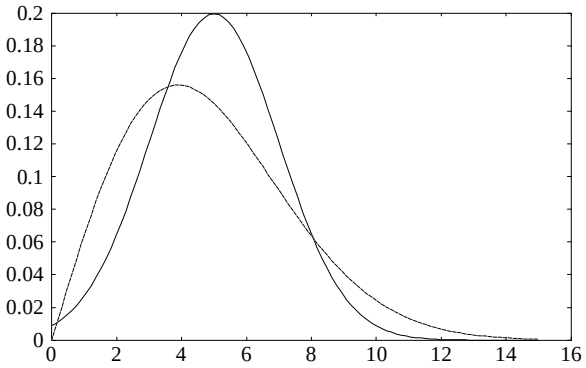
The idea of the curve statement is to generate a series of points for a function. For simple curves two points must be defined: an *x* value and its corresponding *y* value. There are two forms for the CURVE statement (for producing two-dimensional plots). One form generates a series of REAL *x* values for use in computing *y* values. The second form generates an INTEGER series of points. The REAL version looks like this:

```
CURVE
  [KEY <keystring> | WITH <withstring> | AXES <axesstring> . . . ]
  <x_var> ( <x_min>  <x_max> [ <x_points> ] )
    <x_expr> <y_expr> [ <expr> . . .] [ <strings> . . .]
END
```

The KEY, WITH, and AXES will be discussed later. This form of the CURVE statement creates a series of *x* points. It begins with the point <*x_min*> and ends with the point <*x_max*>; <*x_points*> points will be generated in total. Each point will be assigned to <*x_var*> in turn. The value of <*x_var*> will be used at each point to compute <*x_expr*> and <*y_expr*> (and perhaps other expressions as well). If the expression for <*x_points*> is missing, the value stored in PLOTPOINTS will be used instead (which is initially 100).

Here is an example that draws two curves on a plot:

```
MLE
  PLOTFILE(DEFAULTPLOTNAME)
  PLOT
    CURVE z ( 0, 15, 100 ) z, PDF NORMAL(z)  5, 2   END   END
    CURVE z ( 0, 15, 100 ) z, PDF WEIBULL(z) 5.5, 2 END   END
  END  {plot}
END
```



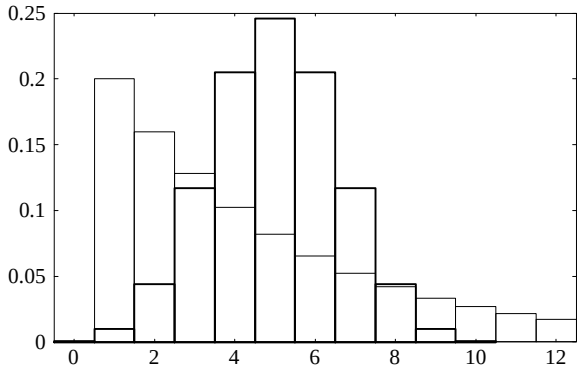
The second form for the two-dimensional curve statement generates a series of INTEGER *x* values for use in computing *y* values. It looks like this:

```
CURVE
  [KEY <keystring> | WITH <withstring> | AXES <axesstring> . . . ]
  <x_var> = <x_min> TO <x_max>
    <x_expr> <y_expr> [ <expr> . . .]  [ <strings> . . .]
END
```

This form of the CURVE statement creates a series of INTEGER *x* points. It begins with <*x_var*> set to <*x_min*> and ends with the point <*x_max*>. The value of <*x_var*> will be incremented by 1 for

each point and will be used to compute <*x_expr*> and <*y_expr*> (and perhaps other expressions as well). Here is an example that draws two curves on a plot:

```
MLE
  PLOTFILE(DEFAULTPLOTNAME)
  PLOT ("set data style boxes", "set xrange [-0.5:12.5]")
    CURVE i = 0 TO 10   i, PDF BINOMIAL(i)  0.5, 10  END   END
    CURVE i = 1 TO 12   i, PDF GEOMETRIC(i) 0.2      END   END
  END  {plot}
END
```



Each `CURVE...END` statement defines a single graph as a series of *x* and *y* points. The *x* and *y* values (and perhaps some values used for error bars and other things) are written to a data file. These data files (one per `CURVE...END` statement) are read by *Gnuplot* when creating the graphs.

KEY

There are three optional keywords that can be used in the `CURVE...END` statement. The first is `KEY`, followed by a string expression. This sets up a title for the plot key.

AXES

The `AXES` keyword defines the axis to which a curve will be plotted. A single string expression follows `AXES`. Valid values for this string are "`x1y1`", "`x2y1`", "`x1y2`", and "`x2y2`".

WITH

The `WITH` keyword defines the style of curve to be plotted, along with any options for that style. A single string expression follows `WITH`. The string begins with one of the *Gnuplot* plot styles, and is followed by options for that style. *mle* checks the first word of this string and makes sure there are enough `PLOT` expressions for the desired graph type. The information is also used to put together the *Gnuplot* `plot` or `splot` command. Valid values for the first word of this string are:

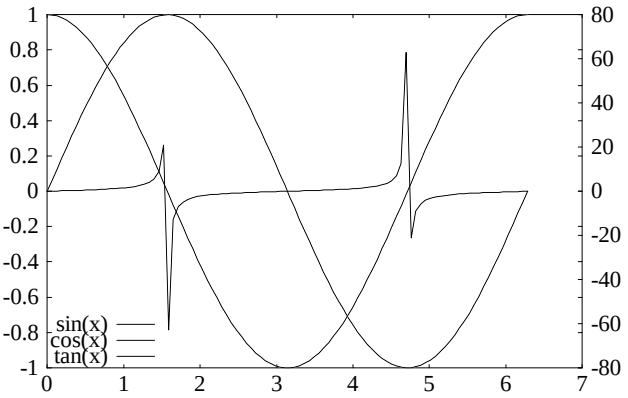
WITH style string	Number of expressions
"boxerrorbars"	4 to 6 CURVE expressions (2d only)
"boxes"	2 CURVE expressions (2d only)
"boxxyerrorbars"	4 to 7 CURVE expressions (2d only)
"candlesticks"	7 CURVE expressions (2d only)
"dots"	2 (2d) or 3 (3d) CURVE expressions
"errorbars"	3 to 4 CURVE expressions (2d only)
"financebars"	7 CURVE expressions (2d only)
"fsteps"	2 CURVE expressions (2d only)
"histeps"	2 CURVE expressions (2d only)
"impulses"	2 (2d) or 3 (3d) CURVE expressions

"lines"	2 (2d) or 3 (3d) CURVE expressions
"linespoints"	2 (2d) or 3 (3d) CURVE expressions
"points"	2 (2d) or 3 (3d) CURVE expressions
"steps"	2 CURVE expressions (2d only)
"vector"	4 (2d) or 5 (3d) CURVE expressions
"xerrorbars"	3 to 4 CURVE expressions (2d only)
"xyerrorbars"	4 to 6 CURVE expressions (2d only)
"yerrorbars"	3 to 4 CURVE expressions (2d only)

Options can follow each plot style in the `WITH` string. The options are `linetype <number>`, `linesize <number>`, `linewith <number>`, `pointtype <number>` and `pointsize <number>` (the options can be abbreviated `lt`, `ls`, `lw`, `pt`, `ps` respectively). The *Gnuplot* manual discusses these options in more detail.

Here is example of a simple plot that makes use of some of the `CURVE` options:

```
MLE
  PLOTFILE(DEFAULTPLOTNAME)
  PLOT("set key bottom left; set y2tics")
    CURVE   KEY "sin(x)" AXES "x1y1" WITH "lines linetype 3"
      x (0, 2*PI, 100)
        x, SIN(x)
    END
    CURVE   KEY "cos(x)" AXES "x1y1" WITH "lines linetype 3"
      x (0, 2*PI, 100)
        x, COS(x)
    END
    CURVE   KEY "tan(x)" AXES "x1y2" WITH "lines linetype 2"
      x (0, 2*PI, 100)
        x, TAN(x)
    END
  END  {plot}
END  {mle}
```



ERRORBARS

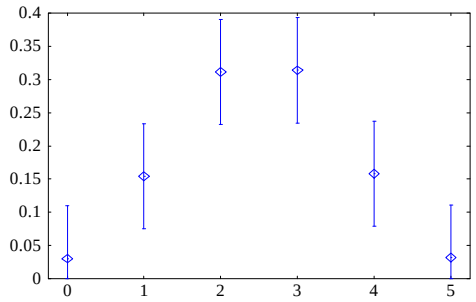
Additional expressions within `CURVE...END` define things like error bars. *Gnuplot* provides two standards for error bars. If only one additional (error bar) expression exist, that value is taken as a delta value to add and subtract from the *y* value. If two error bar expressions exist, the values are taken as the minimum and maximum (respectively) values for the error bars.

Here is an example of plotting error bars for a binomial experiment involving 40 observations:

```
MLE
  { -- Plots the probabilities of observing x boys in a families of exactly 5 children.}
  n = 5       {bernoulli trials -- for families of size 5}
  p = 0.502   {probability of a male child per trial}

  { -- Also plots the standard errors for each outcome assuming that}
  fam = 40  {a sample of fam families are observed}

  PLOTFILE(DEFAULTPLOTNAME)
  PLOT("set yrange [0:]; set xrange [-0.25:" + REAL2STR(n + 0.25, 6, 2) + "]")
    CURVE WITH "errorbars"
      x = 0 TO n
        x                              {x-axis value}
        PDF BINOMIAL(x) p, n END       {y-axis value}
        SQRT(p*(1 - p)/fam)            {errorbar delta}
    END  {curve}
  END  {plot}
END  {mle}
```

The *Gnuplot* file and graph resulting from this program looks like this

```
set terminal windows; reset; set data style lines; set autoscale; set nokey

set yrange [0:]; set xrange [-0.25:5.2500]
plot  "eg5.001" using 1:2:3 notitle with errorbars \
```



Other strings

A series of one or more string expressions can follow the numeric expressions in the `CURVE...END`. These strings will be appended to the *Gnuplot* plot statement so that plot options or other functions can be plotted. The statements will be written to the plot file. The typical purpose is to re-plot curves in a different style.

Suppose we want to plot the normal distribution with μ=0 and σ=5 over the range -10 to 10, and also show an 21-point histogram superimposed on the continuous curve. The *mle* code to do this is:

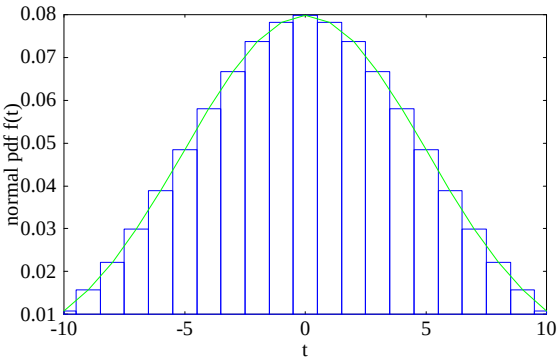
```
MLE
  PLOTFILE(DEFAULTPLOTNAME)    { open a plot file}

  PLOT("set ylabel 'normal pdf f(t)'; set xlabel 't' ")
    CURVE WITH "boxes"
      x (-10 10 21)
        x                          { the x value}
        PDF NORMAL(x) 0, 5 END     { the function to plot}
        ", '' with lines"
     END  {do}
  END  { plot}
END  {mle}
```

The plot file, written in the *Gnuplot* graphics language looks like this:

```
set terminal windows; reset; set data style lines; set autoscale; set nokey

set ylabel 'normal pdf f(t)'; set xlabel 't'
plot  "eg6.001" using 1:2 notitle with boxes \
 , '' with lines
```

The first line was written when the PLOTFILE() statement was executed. The next line is blank, because the PLOTINIT variable, written to the file when PLOT was executed, is empty. The next line came directly from the string argument list for the PLOT statement. The line beginning with plot was generated by the CURVE statement. Notice that the *Gnuplot* continuation character \ comes at the end of the line. This means that the next line (taken from optional string expression in the CURVE statement) is a continuation of the plot statement. That line, beginning with a comma, tells *Gnuplot* to re-plot the same data file using lines.

The name eg6.001 is the data file containing the plot points. These file is written by *mle*, and read by *Gnuplot*. Here is the result of running *Gnuplot* on this plot file:



Three-dimensional Plots

Three-dimensional plots follow the same syntax as do two-dimensional plots, except that both an <*x_var*> and a <*y_var*> must be defined in the CURVE statement along with their ranges. Here is the formal definition for one form:

```
CURVE
   [KEY <keystring> | WITH <withstring> | AXES <axesstring> . . . ]
   <x_var>  ( <x_min>  <x_max> [ <x_points> ] )
   BY <y_var> (<y_min>  <y_max> [ <y_points> ] )
        <x_expr>, <y_expr>, <z_expr> [ <expr> ... ]
        [<string>. . .]
  END
Note that there is now a variable for both x and y.  The specification for each variable is separated
by the keyword BY.  If the value of <x_points> or <y_points> is missing, it will be taken from the
variable PLOTPOINTS (which is initially 100).
```

Alternatively, the INTEGER from of the CURVE statement can be used:

```
CURVE
   [KEY <keystring> | WITH <withstring> | AXES <axesstring> . . . ]
   <x_var> = <x_min> TO <x_max>
   BY <y_var> = <y_min> TO <y_max>
        <x_expr>, <y_expr>, <z_expr> [ <expr> ... ]
        [<string>. . .]
  END
```

Additionally, the REAL and INTEGER forms can be combined:

```
CURVE
   [KEY <keystring> | WITH <withstring> | AXES <axesstring> . . . ]
   <x_var> = <x_min> TO <x_max>
   BY <y_var> (<y_min>  <y_max> [ <y_points> ] )
        <x_expr>, <y_expr>, <z_expr> [ <expr> ... ]
        [<string>. . .]
  END
```

or

```
CURVE
   [KEY <keystring> | WITH <withstring> | AXES <axesstring> . . . ]
   <x_var>  ( <x_min>  <x_max> [ <x_points> ] )
   BY <y_var> = <y_min> TO <y_max>
        <x_expr>, <y_expr>, <z_expr> [ <expr> ... ]
        [<string>. . .]
  END
```

Gnuplot does not support error bars or boxes for three-dimensional plots. Thus, there are three required numeric expression (<*x_expr*>, <*y_expr*>, <*z_expr*>) following the <*y_var*> definition (although additional numeric expressions can be written to the data file for other uses). These three required expressions gives the *x*, *y*, and *z* values to be plotted for each combination of *x_var* and *y_var*.

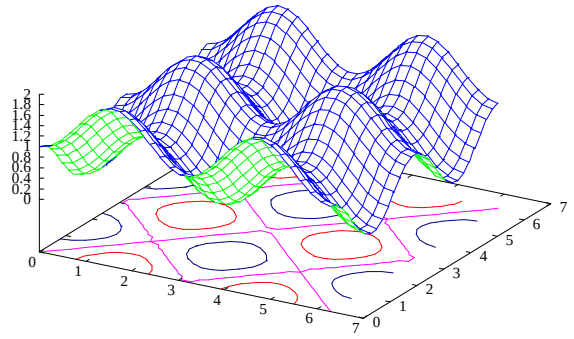
Here is an example of a simple three-dimensional plot. Suppose we want to plot the function `SIN(x)^2 + COS(y)^2` over the range 0 to 2π with 30 points in each dimension. The *mle* code to do this is:

```
MLE
  PLOTFILE(DEFAULTPLOTNAME)                  { open plot file}

  PLOT("set contour base; set hidden3d"      { plot a surface plot and a contour plot}
       "set view 50")                        { change the perspective a bit}
    CURVE x (0, 2*PI, 30) BY y (0, 2*PI, 30)  { define the ranges }
      x,  y,  SIN(x)^2 + COS(y)^2              { the function to plot}
    END  {curve}
  END  {plot}
END  {mle}
```

The resulting *Gnuplot* file is:

```
set terminal windows; reset; set data style lines; set autoscale; set nokey

set contour base; set hidden3d
set view 50
splot "eg7.001" using 1:2:3 notitle \
```

The file `eg7.001` contains the points generated by ***mle***. Here is the resulting plot.



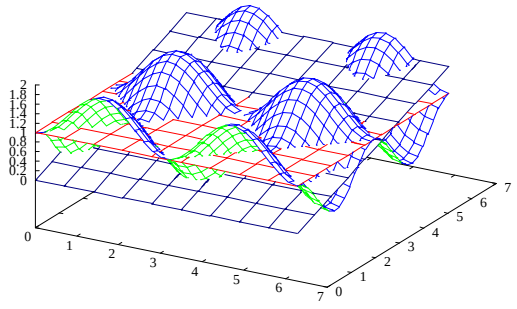
Three-dimensional plots can include multiple curves. For example, to the previous curve, we can add to the graph, a plane through $z = 1$, and another plane through $z = y/4$.

```
MLE
  PLOTFILE(DEFAULTPLOTNAME)                    { open plot file}
  PLOT("set nocontour"                         { no contours}
       "set hidden3d"                          { hide lines}
       "set view 50")                          { change the perspective a bit}
    CURVE x (0, 2*PI, 30) BY y (0, 2*PI, 30)  { curve 1}
      x,  y,  SIN(x)^2 + COS(y)^2
    END  {curve}
    CURVE x (0, 2*PI, 10) BY y (0, 2*PI, 10)  {curve 2}
      x,  y,  1
    END  {curve}
    CURVE x (0, 2*PI, 10) BY y (0, 2*PI, 10)  {curve 3}
      x,  y,  y/4
    END  {curve}
  END  {plot}
END  {mle}
```

The resulting *Gnuplot* file is:

```
set terminal windows; reset; set data

set nocontour
set hidden3d
set view 50
splot "eg8.001" using 1:2:3 notitle \
    , "eg8.002" using 1:2:3 notitle \
    , "eg8.003" using 1:2:3 notitle \
```

Notice that there were three plot data files created: one for each surface. The resulting graph looks like this



Multiple plots

Multiple plots can be placed on a single page with the `MULTIPLOT...END` statement. The form of the statement is:

```
MULTIPLOT( <xplots> <yplots> )
  <statements>
END
```

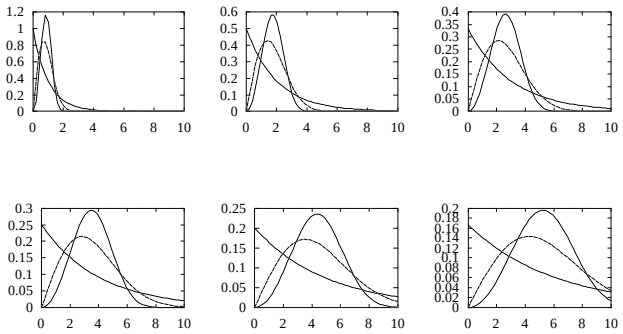
The two arguments determine the number of plots that are placed across the page (<*xplots*>) and vertically down the page (<*yplots*>). In this way, <*xplots*> by <*yplots*> pages of plots are generated. Once a page is filled, a new page is automatically generated.

The <*statements*> are any valid *mle* statements, including `PLOT...END` statements (typically two or more `PLOT` statements are executed). The `PLOT...END` statements may be executed within a user-defined procedure call.

The `PLOTFILE()` procedure must be called *before* the `MULTIPLOT` statement.

Here is an example. The following program shows a series of Weibull distributions.

```
MLE
  PLOTFILE(DEFAULTPLOTNAME)
  nx = 3
  ny = 2
  MULTIPLOT(nx, ny)
    totp = nx*ny
    FOR mu = 1 to totp DO
      PLOT
        FOR sig = 1 TO 3 DO
          CURVE t (0, 10, 50) t, PDF WEIBULL(t) mu, sig END  END
        END  {for sig}
      END  {plot}
    END  {for mu}
  END  {multiplot}
END  {mle}
```



The `MULTIPLOT` statement makes use of a `multiplot` routine available in *Gnuplot*. The *Gnuplot* statement does not work correctly for all terminal types. In particular, the *x* axis labels an plot titles do not always print correctly for the right-most plots. Also, plots with *x* axis labels and plot titles are sometimes scaled to an overly small size.

mle attempts to scale the multi-plots so that none of the figures overlap, and so that the aspect ratio is unchanged. You can affect the scaling size from within *mle* by changing the variables `MPLOTYSCALE` and `MPLOTXSCALE` (both begin as 1.0). These variables control the relative degree of shrinkage or expansion beyond that required to fit a plot in its rectangle.

Working with Gnuplot

What is Gnuplot?

Gnuplot is a function and data plotting program that is designed to work on a large range of computer systems. The program has many graphing capabilities, including the ability to plot directly from files. *mle* makes use of a relatively small subset of the *Gnuplot* capabilities to generate graphs. In fact, *mle* simply writes a *Gnuplot* program and creates data sets, *Gnuplot* does the rest.

The authors of *Gnuplot* provide for free distribution of the software, including the source code. Over the years, many individuals have contributed to writing the program, but the main authors are Thomas Williams, Colin Kelley, Russell Lang, Dave Kotz, John Campbell, Gershon Elber, and Alexander Woo.

How to Obtain Gnuplot

```
mle requires Gnuplot version 3.7 (or later).
```

Gnuplot and its documentation can be downloaded from many ftp and web sites. *Gnuplot* can be downloaded and compiled on your computer system. For some platforms (particularly *DOS* and *Windows*) executable packages are commonly available. Here are some ways of obtaining *Gnuplot*

The official ftp distribution site for the *Gnuplot* source is ftp.dartmouth.edu. The file is called /pub/gnuplot/gnuplot.3.7.tar.Z.

Most comp.sources.misc archive sites distribute *Gnuplot*.

Executable versions of *Gnuplot* for MS-DOS and MS-Windows are available from oak.oakland.edu [141.210.10.117] as pub/msdos/plot/gpt37*.zip; garbo.uwasa.fi (Europe) [128.214.87.1] as /pc/plot/gpt37*.zip and archie.au (Australia) [139.130.4.6] as micros/pc/oak/plot/gpt37*.zip. The files are: gpt37doc.zip, gpt37exe.zip, gpt37src.zip and gpt37win.zip.

- OS/2 2.x binaries are at ftp-os2.nmsu.edu [128.123.35.151], in /os2/2.x/unix/gnu/gplt37.zip.

- There are many other web-sources are available. Give the name "Gnuplot" to any major search engine to find a location near you.

- Most sites that distribute software under the Free Software Foundation GNU Public License also distribute *Gnuplot*.[8]

- Many Linux distributions contain *Gnuplot* as a package.

Basics of Gnuplot

Full documentation for *Gnuplot* is available for free with the program. Here are a few notes on the language.

- *Gnuplot* can be used interactively or in a batch mode. For example, you can read in a file created by *mle* into the *Windows* version of *Gnuplot*, and then modify the plot interactively.

- The *Gnuplot* language usually takes one statement per line. Multiple statements on one line by are formed by separating the commands by a semicolon(;). Also, a single statement can be spread across multiple lines by using the backslash (\) character as the last character on a line. The pound sign (#) is used as a comment delimiter.

- The *Gnuplot* language is case sensitive. Lower case is used for functions and key words. Also, algebraic operators follow the syntax of *c*. So, `!=` in *Gnuplot* is equivalent to `<>` in *mle*, and `%` in *Gnuplot* is equivalent to `mod` in *mle*. Exponentiation in *Gnuplot* uses the operator `**`.

- Many options in *Gnuplot* are set with the `set` command. Here are some examples: `set terminal hpljii; set key on; set title "fun with graphics"; set logscale xy; set size 0.5 0.5; set xlabel "time (hours)-4 "; set ylabel "density"`. There are many set options available in *Gnuplot*. These are usually inserted into the plot file using *mle*'s `WRITEPLOTLN()` statement or in the initial string list in the `PLOT` statement.

Setting the Output Device

Gnuplot is relatively device independent. That is, it can work across a number of computer platforms, and write to different types of graphics devices. In order to plot or display a graph on a particular device, you must specify a "terminal" type. *Gnuplot* can then generate graphics for that specific device.

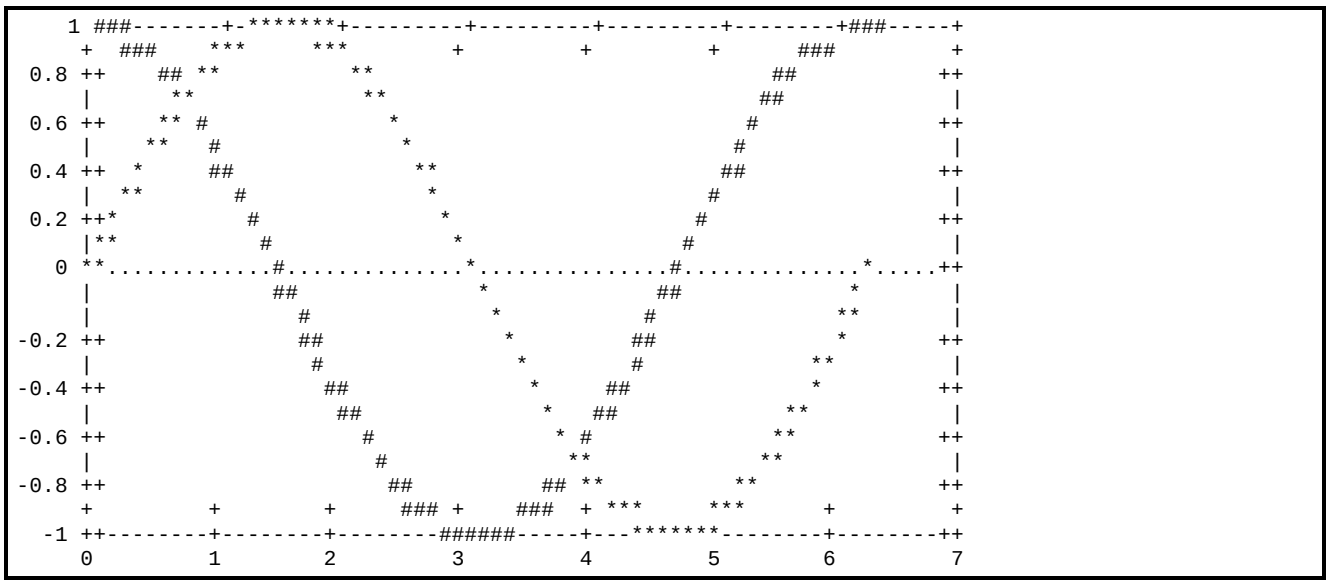
As an example, in previous graphs in this chapter, the device was set to *Windows* (the graphs were copied and pasted into this document). The terminal *Gnuplot* statement

```
set terminal windows
```

is in all of these programs. You can set the terminal to another device. One type of device defined by *Gnuplot* is a dumb terminal, specified by `set terminal dumb`. You can the graphics device to a dumb terminal in two ways. First, you can editing the *Gnuplot* program (i.e. the program that ends in .plt) and add this statement before the `plot` command (and after any other `set terminal` statement). Alternatively, you can insert the command `WRITEPLOTLN("set terminal dumb")` in the *mle* program after the `PLOTFILE()` statement.

The following example shows the result of plotting the previous sine and cosine example with the terminal set to dumb.

[8] Even so, *Gnuplot* is not distributed under the same license. In fact, it is a coincidence that *GNU* appears in *Gnuplot* and is the name adopted by the Free Software Foundation. See the *Gnuplot* manual for details.



Some terminal types allow device-specific options to be included after the name of the terminal. For example, `set terminal dumb 80 60` would set the size of the previous plot to 80 characters across by 60 characters high. Information on specific device options is available in the *Gnuplot* manual. Here is a synopsis of some commonly used terminal devices:

- `set terminal dumb <xsize> <ysize>` for "dumb" terminals and printers. (see the previous example).
- `set terminal epson` for printing bit mapped graphics to an Epson printer
- `set terminal gpic` for generating TEX output for use with the gpic/groff package from the Free Software Foundation.
- `set terminal hpljii <resolution>` for printing to an Hewlett Packard LaserJet II printer. The `<resolution>` is `75`, `100`, `150`, or `300`.
- `set terminal hpdj <resolution>` for printing to an Hewlett Packard Deskjet printer. The `<resolution>` is `75`, `100`, `150`, or `300`.
- `set terminal latex <font> <size>` for generating TEX output for use with LaTeX and EMTeX.
- `set terminal pcl5 <mode> <font> <size>` for printing to an Hewlett Packard HGPL-2 printer or plotter.
- `set terminal postscript` for printing to a postscript printer or device. There are a number of mode, color, and font options for this device.
- `set terminal table` for printing a table of values as an ASCII text file instead of a graph.
- `set terminal windows <color> "<fontname>" <size>` for displaying in windows

The FINISHPLOT procedure

The procedure `FINISHPLOT` provides a way to execute *Gnuplot* from within the *mle* program itself. The procedure takes a single boolean argument. Here is what the procedure does:

- If the argument is `TRUE`, a "`pause -1`" statement will be written to the plotfile. This will cause the graph to be displayed until you either press a key or click on a dialog box. If the argument is `FALSE`, the pause statement is not written to the plotfile.

- The plotfile is closed. No more curves can be written to this file.

- The *Gnuplot* program is executed with plotfile as its argument. This will cause the plot to be written to whatever terminal is defined. For example, if the command `set terminal windows` (Windows) or `set terminal x11` (Unix) is specified in the plotfile, the graph will be displayed on the screen. Other drivers will cause the plot to be written to the file defined by a *Gnuplot* `set output` command.

Additional details on how the *Gnuplot* program is executed, see the description of the *FINISHPLOT* procedure in the procedure summary chapter.

More Examples

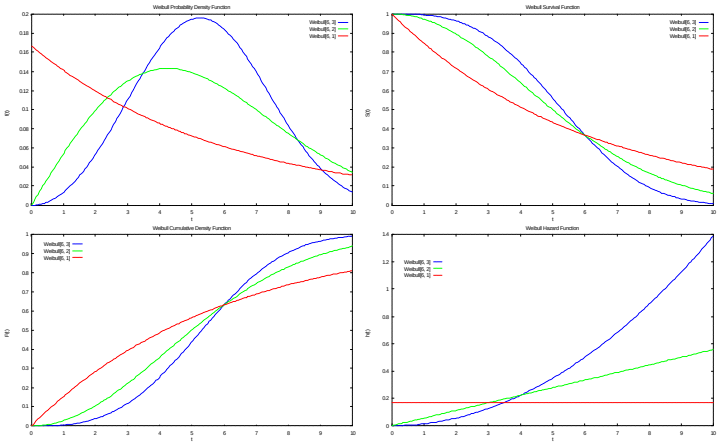
Additional examples of graphical programming in *mle* are given here.

Graphing PDFs, SDF, CDF, and HFs

Here is an example of plotting all four basic probability functions for the Weibull distribution with three different sets of parameters. This example shows multiple plots in one program, and how key titles can be added to the plot. Also note that the keys are moved around for different sets of plots.

```
MLE
  PLOTFILE(DEFAULTPLOTNAME)
  WRITEPLOTLN('set xlabel "t"; set autoscale; set key')
  minz = 0.01
  maxz = 10
  np = 100
  titles : STRING[1 TO 4] =
             ["Probability Density",
              "Survival",
              "Cumulative Density"
              "Hazard"]
  ylab : STRING[1 TO 4] = ["f(t)", "S(t)", "F(t)", "h(t)"]

  MULTIPLOT(2, 2)
    FOR ty = 1 TO 4 DO                      {loop through PDF, SDF, CDF, HF}
      PLOT('set title "Weibull ' + titles[ty] + ' Function"'
           'set ylabel "' + ylab[ty] + '"')
        FOR v = 1 TO 3 DO                   {use three different variances}
          CURVE z (minz, maxz, np)
            KEY 'Weibull[6, ' + INT2STR(z) + ']'
            z, PDF WEIBULL(z,
                           IF ty = 2 THEN 0 ELSEIF ty = 3 THEN oo ELSE z END,
                           IF ty = 3 THEN z ELSE 0 END)
                 6,  v                      {these are the weibull parameters}
               END {pdf}
          END  {curve}
        END  {for v}
      END  {plot}
    END  {for ty}
  END  {multiplot}
END  {mle}
```

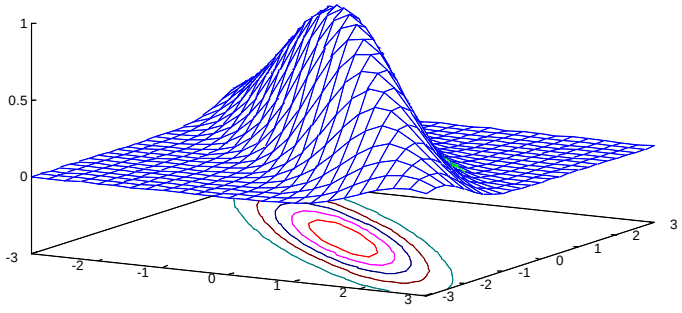
Here is the result of this program:



Contour plots

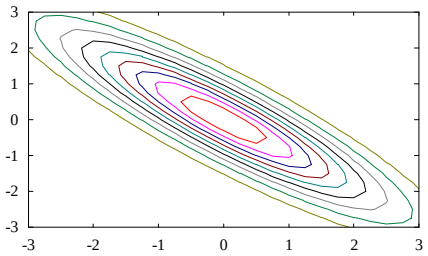
Contours can be drawn beneath the surface of a three-dimensional plot. Here is an example:

```
MLE
  PLOTFILE(DEFAULTPLOTNAME)
  WRITEPLOTLN('set zrange[0:1]; set contour base; set hidden3d; set view 70')
  PLOT
    DO x y (-3  3  25) (-3 3 25)
      x, y, EXP(-(x^2 + 1.8*x*y + y^2))  {a type of bivariate normal}
    END  {do}
  END  {plot}
END
```



A contour plot alone is generated from the previous example by turning off the surface and changing the perspective:

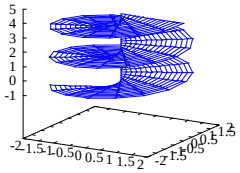
```
MLE
  PLOTFILE(DEFAULTPLOTNAME)
  PLOT('set zrange[0:1]; set contour base; set nosurface'
       'set yrange [] reverse; set view 180, 0')
    CURVE x (-3  3  25) BY y (-3 3 25)
      x,  y,  EXP(-(x^2 + 1.8*x*y + y^2))  {a type of bivariate normal}
    END  {curve}
  END  {plot}
END
```



A Helix

A helix is defined parametrically with simple functions. The following code generates a helix

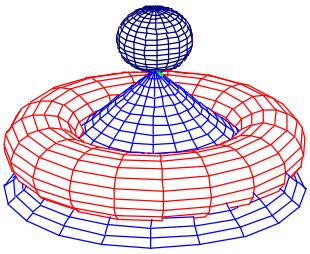
```
MLE
  PLOTFILE(DEFAULTPLOTNAME)
  WRITEPLOTLN('set zrange[-1:]; set view 60, 30, 0.75, 2; set hidden3d')
  PLOT
    CURVE x (0 2 15) BY y (-PI 4*PI 40)
      x*COS(y),  x*SIN(y),  y/3
    END  {curve}
  END  {plot}
END
```



Geometric Figures

Mathematically defined geometric figures can be easily drawn. This example shows a number of useful tricks in *Gnuplot*, including turning off the axis borders, and graphing multiple plots.

```
MLE
  PLOTFILE(DEFAULTPLOTNAME)
  WRITEPLOTLN('set zrange[0:]; set hidden3d; set view 70')
  WRITEPLOTLN('set noborder; set noxtics; set noytics; set noztics')
  PLOT
    CURVE x (0 2*PI 20) BY y (0 4 20)         {plot a cone}
      SIN(x)*y,  COS(x)*y,  (-y + 5)
    END  {curve}
    CURVE x (0 2*PI 20) BY y (0 2*PI 20)      {Now plot a torus around the cone}
      COS(x)*(3 + COS(y)),  SIN(x)*(3 + COS(y)),  SIN(y) + 2.5
    END  {curve}
    CURVE x (0 2*PI 20) BY y (-PI/2 PI/2 20)  {And place a sphere on top}
      COS(x)*COS(y),  SIN(x)*COS(y),  SIN(y) + 6
    END  {curve}
  END  {plot}
END  {mle}
```

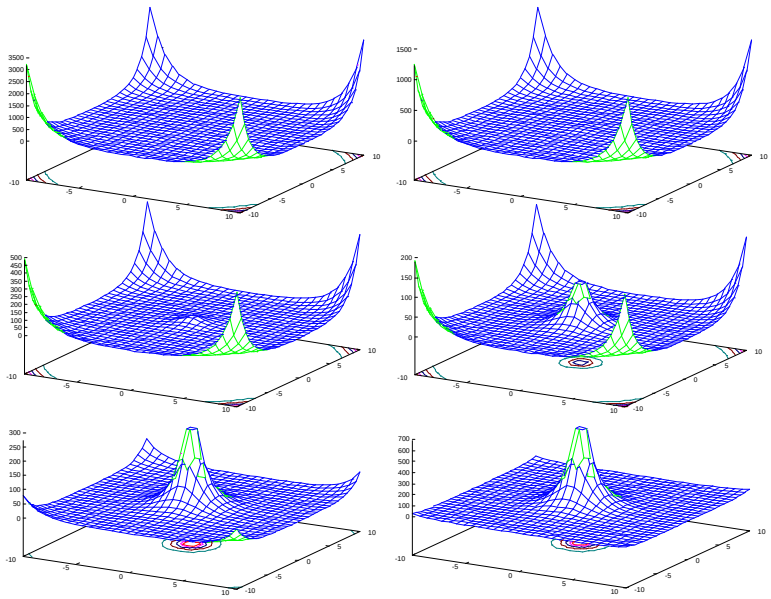


Animation Example

Multiple `PLOT...END` statements can be used to create animation in *mle*. Alternatively, the time dimension can be introduced with the use of a looping statement outside of the `PLOT...END` statement. *Gnuplot* has a `pause` command that helps control the length of time each plot is displayed. Here is an example:

```
MLE
  { -- An animation example }
  PLOTFILE(DEFAULTPLOTNAME)        { open plot file}
  WRITEPLOTLN("set contour both; set hidden3d")
  FOR f = 4 TO 9 DO
    PLOT("pause 2")   {wait two seconds before showing the next plot}
      CURVE x (-10, 10, 30) BY y (-10, 10, 30)
        x, y, BESSELI(0, SQRT(x^2 + y^2) - f)
      END  {curve}
    END  {plot}
  END  {for}
END  {mle}
```

This example produces this sequence of plots:



Creating Plots from the Model Statement

The MODEL statement can create two types of commonly used plots that are related to model estimation. The first plot includes three graphs of distributions: the survival density function, the probability density function and the hazard function. Each of these is graphed with error bars. The second type of plot is a likelihood surface graph in either one or two variables.

Before attempting to plot either one of these special plots, a plotfile must be defined with the PLOTFILE() procedure. This opens the plot file and defines the name of the plot data file. Additionally, the PLOT...END statement must surround the MODEL statement.

Estimated Distributions

The survival function, probability density function and hazard function can be plotted from a MODEL statement by setting the variable PLOT_DISTS to TRUE. (The mechanism is similar to that used for printing the values using the PRINT_DIST variable). In addition to PLOT_DISTS=TRUE, you must set three other values. DIST_T_START defines the lowest value over which the distribution is plotted, DIST_T_END is the highest value over which the distribution is plotted. DIST_T_N is the number of points to plot.

An example of plotting these distributions is given after the description of likelihood surfaces.

Likelihood Surfaces

A likelihood surface can be plotted over one parameter or two parameters of a model. All other parameters are taken at their estimated value.

Surface plots are made by adding SURFACE(<xparam>) or SURFACE(<xparam>, <yparam>) to the end of the RUN or REDUCE list part of the MODEL statement. Here is the format:

```
PLOT            {surrounds the model statement for plotting surfaces}
  MODEL
    <model statement>
  RUN
    FULL  SURFACE(<xparam>)                  {plots a likelihood profile over one parameter}
    FULL  SURFACE(<xparam>, <yparam>)        {plots a likelihood profile over two parameters}
    REDUCE  ... SURFACE(<xparam>)
    REDUCE  ... SURFACE(<xparam>, <yparam>)
  END  {model}
END  {plot}
```

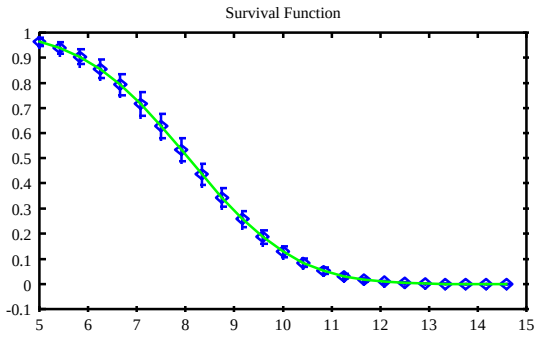
For each parameter being plotted, the minimum plotted value is taken from the PARAM function as the LOW = value, and the maximum is taken from HIGH = value.

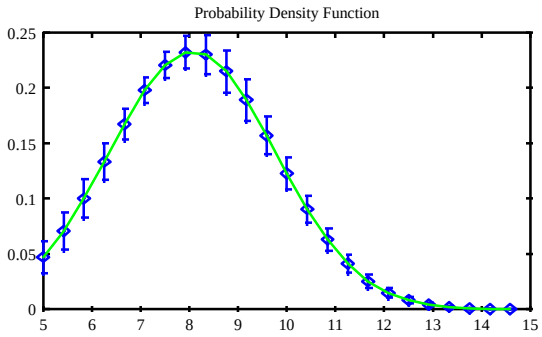
An Example

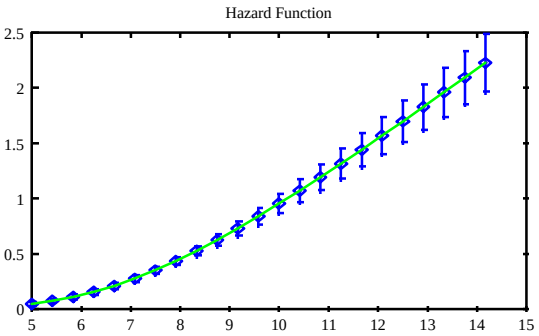
Here is an example of statistical estimation and plotting of distributions and a likelihood surface.

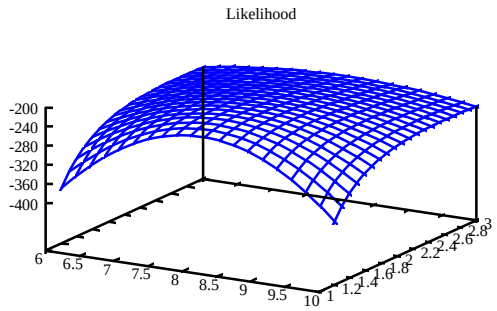
```
MLE
  TITLE = "Japanese tooth eruption: lower first incisor."
  DATAFILE("japan.dat")
  OUTFILE(DEFAULTOUTNAME)
  PLOTFILE(DEFAULTPLOTNAME)
  DATA
      li1o     FIELD 5 LINE 1     {earliest eruption age for lower central incisor}
      li1c     FIELD 6 LINE 1     {latest eruption age}
      sex      FIELD 3  LINE 2    {Child's sex}
  END

  PLOT_DISTS = TRUE
  DIST_T_START = 5.0   {Plot the distribution from 5}
  DIST_T_END = 15.0    {to 10 months}
  DIST_T_N = 25        {in 25 points}

  PLOT            {surrounds the model statement}
    MODEL
      DATA
           PDF NORMAL(li1o, li1c)
             PARAM  mean    LOW = 6  HIGH = 10  START = 8   END
             PARAM  stdev   LOW = 1.2  HIGH = 3   START = 1.7  END
           END  {pdf normal}
      END  {data}
    RUN
      FULL SURFACE(mean, stdev)  {plots the surface for mean and stdev}
    END  {model}
  END  {plot}
END  {mle}
```

The following four plots result:









Chapter 6
Statistical examples

This chapter provides a series of examples in creating likelihood models and estimating parameters of the models. The examples are categorized by the type of likelihood problem being done. Some of the examples include data files.

Survival analysis—Exact measurements

This first example not only provides an illustration of a simple *mle* program, but also shows the notation that will be used throughout this chapter. The problem at hand is finding one or more parameters q of some distribution $f(t|\mathrm{q})$, given a series of observations, $\mathbf{t}=t_1, t_2, \ldots, t_N$. The values of **t** are known exactly. For an individual observation, t_i, the individual likelihood is $L_i = f(t_i|\mathrm{q})$, and the overall likelihood for the N observations is

$$L(\mathrm{q}\,|\,\mathbf{t}) = \prod_{i=1}^{N} f(t_i\,|\,\mathrm{q})dt\,. \tag{2}$$

Data for this example (Table 6) are a series of 15 observations of times to breakdown for an insulating fluid at 32 kV. The times are arranged as one observation per line in a file named ex1.dat. The underlying distribution is believed to follow a negative exponential probability density function, with a single parameter lambda. The following *mle* program analyses these data. Comments are enclosed in curly brackets.

Here is the code for this problem:

```
MLE
  TITLE = "32 kV Insulating Fluid Example from Nelson (1982:105)"
  DATAFILE("ex1.dat")   {Input data file name}
  OUTFILE("ex1.out")    {Name to which results are written}

  DATA                  {data are read from the data file here}
    failtime   FIELD 1
  END

  MODEL                 {this specifies the likelihood model}
    DATA                {this corresponds to the product in the likelihood equation}
       PDF EXPONENTIAL(failtime)
         PARAM  lambda  LOW=0.00001  HIGH=1  START=0.05  END
       END  {pdf}
    END {data}
  RUN
    FULL
  END {model}
END {program}
```

Here is the abridged output

```
New model:  32 kV Insulating Fluid Example

LogLike= -70.76273 Iterations= 2 Func evals= 26 Del(LL)= 0.0000000000
Converged normally

Results with estimated standard errors.  (7 evals)
Solution with 1 free parameter
         Name Form       Estimate         Std Error          t        against
       lambda LOGLIN   0.024294254090   0.004468859626    5.43634307759   0.0
```

The first part of the output shows the loglikelihood, and information about iterations, function evaluations, and convergence. This is followed a report of parameter estimates and their standard errors.

Table 6 Times to breakdown for an insulating fluid at 32 kV, from Nelson W (1982:105).

0.27	0.4	0.69
0.79	2.75	3.91
9.88	13.95	15.93
27.8	53.24	82.85
89.29	100.58	215.1

Survival analysis—Exact Failure and Right Censored observations

The standard problem in survival analysis is to find parameters of a parametric model when some observations are right censored. Typically we have N exact observations, and N^+ right-censored observations, the likelihood is

$$L(\mathrm{q} \mid \mathbf{t}) = \prod_{i=1}^{N} f(t_i \mid \mathrm{q}) \prod_{i=1}^{N^+} S(t_i \mid \mathrm{q}), \tag{3}$$

where $S(t|\mathrm{q})$ is the survival distribution, which is the area under $f(t|\mathrm{q})$ to the right of t. The area under a right censored observation is specified in the *mle* PDF

function by setting the second time variable to infinity (or something less than the first time variable). So, the function `PDF NORMAL(14,-1) 10, 6 END` would return the area from 14 to infinity of under a normal pdf with parameters $\mu = 10$, and $\sigma = 6$, or about 0.2525. This would correspond to the likelihood of an individual surviving past 14 units of times under the specified model.

For this example, we use the data in Table 6 and suppose that there were three additional observations that had not failed by time 220—the end of the experiment. The data will be coded so that the three right censored times are given as negative times, -220. The `DATA` statement now creates two variables, the first is the absolute value of time to failure, and the second is the unmodified time. Thus, failed observations have two identical failure times, for example [9.88, 9.88], which defines an exact failure. When the two identical observations are used in the `PDF` function, the probability density function at that point is returned. The right-censored observations have a positive and a negative failure times [220, -220]. When the second failure time is less than the first, the `PDF` function gives the area under the pdf from 220 to infinity, which is the survival function.

```
MLE
  TITLE = "32 kV Insulating Fluid Example"
  DATAFILE("ex2.dat")   {Input data file name}
  OUTFILE("ex2.out")    {Name to which results are written}

  DATA
    topen   FIELD 1 = ABS(topen)
    tclose  FIELD 1
  END

  MODEL
    DATA
       PDF EXPONENTIAL(topen, tclose)
         PARAM  lambda  LOW=0.00001  HIGH=1  START=0.05  END
       END  {of the PDF}
    END
  RUN
    FULL
  END  {of the MODEL}

END    {of the MLE program}
```

The abridged output is

```
18 lines read from file ex2.dat
18 Observations kept and 0 observations dropped.

New model:  32 kV Insulating Fluid Example

LogLike= -81.66833 Iterations= 2 Func evals= 28 Del(LL)= 0.0000000000
Converged normally

Results with estimated standard errors.  (8 evals)
Solution with 1 free parameter
         Name Form       Estimate         Std Error          t        against
       lambda LOGLIN   0.011742333138   0.002142967492    5.47947329296   0.0
```

Survival analysis—Interval censored Observations

Interval censored observations, are those collected between two points of time. These observations frequently arise from prospective studies in which periodic observations are collected. The exact times to the event are not known. What is known is t_u, the last time before the event occurred, and t_e, the time of the first observation after the event occurred. The likelihood for interval censored events is the area under the pdf between t_u and t_e,

(4)

$$L(\theta \mid \mathbf{t}_u, \mathbf{t}_e) = \prod_{i=1}^{N} \int_{t_{u_i}}^{t_{e_i}} f(z \mid \theta) dz = \prod_{i=1}^{N} \left[S(t_{u_i} \mid \theta) - S(t_{e_i} \mid \theta) \right]$$

In *mle*, the area under the pdf (that is, the integral over the interval $(t_u, t_e]$ is specified for most distributions as the first two times, with the second time greater than the first. For example, `PDF NORMAL(11, 15) 10, 6 END` returns 0.231, which is the area between 11 and 15 under a normal distribution with μ=10, and σ=6. Here is an *mle* program that finds parameters of a lognormal distribution from interval censored data.

```
MLE
  TITLE = "Example"
  DATAFILE("ex3.dat")
  OUTFILE("ex3.out")

  DATA
    topen   FIELD 1
    tclose  FIELD 2
  END

  MODEL
    DATA
       PDF LOGNORMAL(topen, tclose)
         PARAM  a  LOW=0.00001  HIGH=9  START=1  END
         PARAM  b  LOW=0.00001  HIGH=2   START=0.4  END
       END  {of the PDF}
    END
  RUN
    FULL
  END  {of the MODEL}

END
```

Current status analyses

Current status analysis consists of observations that are collected cross-sectionally. The methods most commonly associated with current status analysis are probit and logit analysis. *mle* makes it easy to do current status analysis with any of the built-in distribution functions.

Under a cross-sectional study design, each observation consists of (1) time of a single observation since the study began (t), (2) an indicator variable to determine whether or not the individual experienced the event. The result of the indicator

variable is that the individual is a responder (*r*) or non-responders (*n*). The likelihood from *N* observations made up of N_r responders and N_n non-responders is

$$L(\mathrm{q} \mid \mathbf{t}) = \prod_{i=1}^{n} S(t_i \mid \mathrm{q}) \prod_{i=1}^{r} F(t_i \mid \mathrm{q}) \tag{5}$$

This likelihood can be interpreted as follows. For the likelihood for the non-responders is the area under the pdf from the time of observation to infinity. Thus, a responder contributes a likelihood that is exactly like a right-censored observation. The likelihood for a responder is the area under the pdf from -∞ (or 0 for pdfs defined to have positive arguments) to the time of observation, which is the probability of the event occurring at some time unknown time before the time of observation. In mle, the area under the likelihood for a responder is specified as `PDF LOGNORMAL(-1, 5) 2, 0.5 END` return 0.217, which is the area between 0 (or anything less than 0) and 5 under a lognormal distribution with μ=2, and σ=0.5.

Consider a data set that contains a time of observation and an indicator variable that is 0 if the observation was a non-responder and 1 for a responder. One way of coding this model is to place an `IF...THEN...ELSE...END` statement to switch between responder and nonresponder likelihoods as appropriate for each observation:

```
MLE
  TITLE = "Example"
  DATAFILE("ex4.dat")
  OUTFILE("ex4.out")

  DATA
    t       FIELD 1  {time of observation}
    resp    FIELD 2  {1 if responder, 0 if nonresponder}
  END

  MODEL
    DATA
      IF resp = 1 THEN        {it is a responder}
        PDF LOGNORMAL(0, t)
          PARAM  a  LOW=0.00001  HIGH=9  START=1    END
          PARAM  b  LOW=0.00001  HIGH=2  START=0.4  END
        END  {of the PDF}
      ELSE  {non-responder}
        PDF LOGNORMAL(t, oo) a, b END
      END  {of if then else}
    END {data}
  RUN
    FULL
  END  {of the MODEL}

END
```

Alternatively, The following *mle* data statement will transform the observation time into a set of two times. For a responder, `topen` will be set to zero and `tclose` will take the value of the observed time. For a non-responder, `topen` will take the value of the observed time and `tclose` will be set to zero. Note that when the second time is set to zero, it will be less than `topen`, so *mle* returns the area from `topen` to infinity.

```
MLE
  TITLE = "Example"
  DATAFILE("ex4.dat")
  OUTFILE("ex4.out")

  DATA
    time     FIELD 1    {read in observation time}
    resp     FIELD 2    {1 if responder, 0 if nonresponder}
    topen     = IF resp == 1 THEN 0 ELSE time END
    tclose    = IF resp == 1 THEN time ELSE -1 END
  END

  MODEL
    DATA
       PDF LOGNORMAL(topen, tclose)
         PARAM  a  LOW=0.00001  HIGH=9  START=1    END
         PARAM  b  LOW=0.00001  HIGH=2  START=0.4  END
       END  {of the PDF}
    END
  RUN
    FULL
  END  {of the MODEL}

END
```

Survival analysis—Left-truncated observations

Left truncation arises in survival analysis when some early portion of an individual's period of risk is not observed. For example, in a prospective study of mortality, we might want to follow all living people in some area, instead of just following individuals from birth. This type of data collection can lead to unbiased results, provided observations are left-truncated at the age at which people are enrolled in the study. The idea is that, had the someone died prior to being enrolled in the study, that would not have been enrolled; therefore, their risk of mortality is know to be zero.

For this example, we will use the Siler competing hazards mortality model for a fictitious prospective study of mortality. We will two types of observations: those who died and those who are right censored. For each observation we know three times: the time an individual was enrolled for prospective observation (t_α), the last time an individual was observed as alive (t_u), and the first time the individual was known to be dead (t_e). The first time, t_α, defines the left truncation point, t_u and t_e define an interval within which death took place. For right censored observations, t_e is set to infinity (or a number greater than the human lifespan). The likelihood is

(6)
$$L(\mathrm{q}, \mathbf{t}_u, \mathbf{t}_e, \mathbf{t}_\alpha) = \prod_{i=1}^{N} \frac{S(t_{u_i} \mid \mathrm{q}) - S(t_{e_i} \mid \mathrm{q})}{S(t_{\alpha_i} \mid \mathrm{q})}.$$

From this likelihood it can be seen that an individual's probability of death is the area under pdf between t_u and t_e and divided by the area from t_α to infinity, which renormalizes the pdf for the period of actual observation. An individual likelihood is constructed in *mle* as `PDF SILER(14, 15, 6) 0.05, 0.3, 0.0, 0.001, 0.05 END`, which represents a person who died between ages 14 and 15, and were enrolled in the study at age 6.

```
MLE
  TITLE = "Example"
  DATAFILE("ex5.dat")
  OUTFILE("ex5.out")

  DATA
    talpha    FIELD 1  {Left truncation time}
    topen     FIELD 2  {time last known alive}
    tclose    FIELD 2  {time first known dead, or oo if censored}
  END

  MODEL
    DATA
       PDF SILER(topen, tclose, talpha)
         PARAM  a1  LOW=0.00001  HIGH=0.5 START=0.01   END
         PARAM  b1  LOW=0.01     HIGH=2   START=0.1    END
         PARAM  a2  LOW=0        HIGH=1   START=0.001  END
         PARAM  a3  LOW=0.0000   HIGH=1   START=0.001  END
         PARAM  b3  LOW=0.00001  HIGH=1   START=0.001  END
       END  {of the PDF}
    END
  RUN
    FULL
  END  {of the MODEL}

END
```

Survival analysis—Right-truncated observations

Right truncation arises in survival analysis when the later risk is determined by the study design. For example, we might have data on child mortality for analysis. Each child was followed from birth to age five, and the only children available in the data set were those who died from birth to five. This type of data collection can lead to unbiased results, provided child's observations are right-truncated at age five.

For this example, we will use the Gompertz competing hazards mortality model for a fictitious prospective study of mortality. We will have observations selected for mortality by age five and no right-censoring. A single age at death is known. The likelihood for exact times to death with right truncation is

(7)

$$L(\mathrm{q}, \mathbf{t}, \mathbf{t}_{\omega}) = \prod_{i=1}^{N} \frac{f(t_i \mid \mathrm{q})}{1 - S(t_{\omega i} \mid \mathrm{q})}.$$

From this likelihood it can be seen that an individual's probability of death is the pdf at the age of death, divided by the area from 0 to t_{ω}, which renormalizes the pdf for the period of actual observation. An individual likelihood is constructed in *mle* as `PDF GOMPERTZ(2.1, 2.1, 6) 0.05, 0.3 END`, which is a death at the age of 2.1.

```
MLE
  TITLE = "Example"
  DATAFILE("ex6.dat")
  OUTFILE("ex6.out")

  DATA
    tdeath    FIELD 1  {Left truncation time}
  END

talpha = 5.0     {set a constant for right truncation}

  MODEL
    DATA
       PDF GOMPERTZ(tdeath, tdeath, talpha)
         PARAM  a1  LOW=0.00001  HIGH=0.5  START=0.01  END
         PARAM  b1  LOW=-2       HIGH=-0   START=0.1   END
       END  {of the PDF}
    END
  RUN
    FULL
  END  {of the MODEL}

END
```

Survival analysis—Left-and right-truncated observations

This example extends the previous one by including both left and right truncation, as well as interval censored observations. We will use a child mortality example again, but now each children is recruited at some age from 0 to 5 years. Their risk will be left-truncated at the age of entry. Again, only children who die before age 5 would be included in the analysis, so that all exposures are right-truncated. Finally, children are periodically visited, so all observations are interval censored. Again, we will use the Gompertz competing hazards mortality model for this fictitious prospective study of child mortality. The likelihood is

(8)
$$L(\mathrm{q}, \mathbf{t}_u, \mathbf{t}_e, \mathbf{t}_\alpha, \mathbf{t}_\omega) = \prod_{i=1}^{N} \frac{S(t_{u_i} \mid \mathrm{q}) - S(t_{e_i} \mid \mathrm{q})}{S(t_{\alpha_i} \mid \mathrm{q}) - S(t_{\omega_i} \mid \mathrm{q})}.$$

From this likelihood it can be seen that an individual's probability of death is the area under pdf between t_u and t_e and divided by the area from t_α to t_ω, which renormalizes the pdf for the period of actual observation. An individual likelihood is constructed in *mle* as `PDF GOMPERTZ(topen, tclose, talpha, tomega) 0.05, 0.3 END`. For example `PDF GOMPERTZ(2.1, 2.4, 1.0, 5.0) 0.05, 0.3 END` returns the probability that a child, enrolled in the study at age one and selected for having died by age five, died between the ages of 2.1 and 2.4.

```
MLE
  TITLE = "Example"
  DATAFILE("ex7.dat")
  OUTFILE("ex7.out")

  DATA
    talpha    FIELD 1  {Left truncation time}
    topen     FIELD 2  {time last known alive}
    tclose    FIELD 2  {time first known dead, or oo if censored}
  END

tomega = 5.0

  MODEL
    DATA
       PDF GOMPERTZ(topen, tclose, talpha, tomega)
         PARAM  a1  LOW=0.00001  HIGH=0.5 START=0.01  END
         PARAM  b1  LOW=0.01     HIGH=2   START=0.1   END
       END  {of the PDF}
    END
  RUN
    FULL
  END  {of the MODEL}

END
```

Survival analysis—Accelerated failure time model

Frequently, one is interested in modeling the effects of covariates on the time to failure. A common model of this type is call the accelerated failure time model (AFT), in which covariates shift the time to failure to the right or the left. *mle* has a general mechanism for modeling the effects of covariates on any parameter that is defined, so that accelerated failure time models can be easily constructed.

In this example, the mean of a normal distribution has two covariates that shift the failure time.

```
MLE
  TITLE = "Example"
  DATAFILE("ex8.dat")
  OUTFILE("ex8.out")

  DATA
    topen     FIELD 1  {Last observation time prior to the event}
    tclose    FIELD 2  {First observation time after the event}
    weight    FIELD 3  {the first covariate}
    age       FIELD 4  {the second covariate}
  END

  MODEL
    DATA
       PDF NORMAL(topen, tclose)
         PARAM  mu  LOW=0.00001  HIGH=100 START=25  FORM=LOGLIN
            COVAR weight PARAM b_weight LOW=-20 HIGH=20  START=0  END
            COVAR age    PARAM b_age    LOW=-20 HIGH=20  START=0  END
         END     {param mu}
         PARAM  s  LOW=0.01  HIGH=50  START=3  END
       END  {of the PDF}
    END
  RUN
    FULL
  END  {of the MODEL}

END
```

From this specification of covariates, the μ intrinsic parameter of the normal distribution will be computed for the *i*th observation as μ_i = `mu`×`exp(weight`$_i$ × `b_weight + age`$_i$ × `b_age)`.

Survival analysis—Hazards model

An alternative to the accelerated failure time model is the hazards model. Under the hazards model, the effects of covariates is to raise or lower the hazard by some amount[9]. In general, if $h(t)$ is the hazard function, covariates for the *i*th individual, $x_i\beta$, are modeled on the hazard as $h_i(t) = h(t)\exp(x_i\beta)$.

Most of the probability density functions in *mle* provide a mechanism for modeling the effects of covariates on the hazard. You can find out for any particular pdf by typing, for example, `mle -h lognormal`. A message will tell you whether or not covariates can be modeled on the hazard.

In this example, the same normal distribution used in the previous example has had the two covariates moved from affecting μ to affecting the hazard.

```
MLE
  TITLE = "Example"
  DATAFILE("ex8.dat")
  OUTFILE("ex8.out")

  DATA
    topen     FIELD 1  {Last observation time prior to the event}
    tclose    FIELD 2  {First observation time after the event}
    weight    FIELD 3  {the first covariate}
    age       FIELD 4  {the second covariate}
  END

  MODEL
    DATA
       PDF NORMAL(topen, tclose)
         PARAM  mu  LOW=0.00001  HIGH=100  START=25  END
         PARAM  s   LOW=0.01     HIGH=50   START=3   END
         HAZARD COVAR weight PARAM b_weight LOW=-20 HIGH=20  START=0  END
                COVAR age    PARAM b_age    LOW=-20 HIGH=20  START=0  END
         END     {hazard}
       END  {of the PDF}
    END
  RUN
    FULL
  END  {of the MODEL}

END
```

Survival analysis—Immune subgroup

When observing times to events, there may be an unidentifiable subgroup for whom risk of experiencing the event is zero. These make up a so-called *immune fraction*, a *sterile subgroup*, or a *contaminating fraction*. It is possible to model

[9] Except for the exponential and the Weibull distributions, accelerated failure time models are not proportional hazards models.

some fraction of individuals who are not at risk, so to statistically identify the subgroup.

If complete records are available for all individuals, one could simply remove the sterile individuals from the analysis of the non-sterile fraction. When complete records are not available (i.e. we cannot tell a sterile individual from a right-censored individual) maximum likelihoods methods are easily adapted to include estimation of an unknown fraction of individuals who are not susceptible to failure.

The effect of the sterile subgroup on the survival distribution can be seen in Figure 5. Call *s* the non-susceptible fraction. Then the proportion of individuals who are susceptible at the start of risk is $p(0)=1-s$. Inspection of Figure 5 suggests that the fraction of surviving individuals at time *t* must be made up of two fractions. One is $S_f(t)$ weighted by the fraction not sterile, $(1-s)$. The second fraction is constant at *s*:

$$S(t) = (1-s)S_f(t) + s\,.$$

The overall hazard at time t is simply the hazard of the non-susceptible subgroup weighted by the proportion of that group at time *t*. The proportion of susceptible individuals at time *t* will decrease as fecund individuals fail, and must depend on survivorship of the non-sterile group to time *t* and the initial fraction of sterile individuals, *s*. This fraction at time *t* is

$$p(t) = \frac{(1-s)S_f(t)}{s+(1-s)S_f(t)}\,.$$

The hazard at time *t* is

$$h(t) = p(t)h_f(t) = \frac{(1-s)S_f(t)}{s+(1-s)S_f(t)}\frac{f_f(t)}{S_f(t)} = \frac{(1-s)\,f_f(t)}{s+(1-s)S_f(t)}$$

and the probability density function is found as

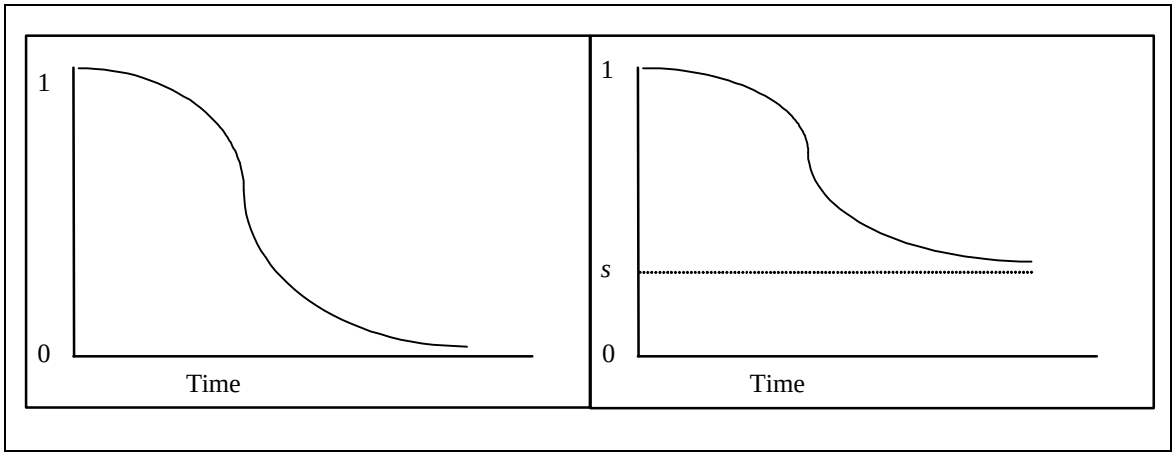


Figure 5. The effect of contamination by a sterile subgroup on the survivorship distribution. The subgroup makes up fraction s *of the initial population at risk. The left panel shows survivorship for the uncontaminated group and the right panel shows the same distribution contaminated by the sterile subgroup.*

$$f(t) = h(t)S(t) = (1-s)S_f(t)h_f(t) = (1-s)\,f_f(t).$$

These forms for the PDF, SDF, and hazard function provide for reasonably straight-forward maximum likelihood estimation of the parameters of the distribution for the susceptible observations as well as *s*. The general form of the likelihood when sterility is included, becomes

$$(9)\quad L(\mathrm{q}, s \mid t_u, t_e) = \prod_{i=1}^{N}\left[(1-s)\left[f(t_{e_i} \mid \mathrm{q})\right]^{\delta\{t_{u_i}, t_{e_i}\}}\left[S(t_{u_i} \mid \mathrm{q}) - S(t_{e_i} \mid \mathrm{q})\right]^{1-\delta\{t_{u_i}, t_{e_i}\}} + s\delta\{t_{e_i}, t_{\omega_i}\}\right],$$

where the $\delta\{x,y\}$ is the Kronecker's delta function, which equals one when $x=y$, and zero when $x \neq y$.

The following example estimates one such model. The likelihood begins with the `MIX()` function, which produces an average of the second and third arguments, weighted by first argument (which is a probability). The first PDF is `PDF STERILE() END`, which returns one if `tclose` is infinity or less than `topen`. Covariates are modeled on both the non-susceptible fraction as well as the hazard of the susceptible fraction.

```
MLE
  TITLE = "Example"
  DATAFILE("ex.dat")
  OUTFILE("ex.out")

  DATA
    topen     FIELD 1  {Last observation time prior to the event}
    tclose    FIELD 2  {First observation time after the event}
    weight    FIELD 3  {the first covariate}
    age       FIELD 4  {the second covariate}
  END

  MODEL
    DATA
       MIX( PARAM s LOW=-100  HIGH=100 START=0  FORM=LOGLIN    {define the immune
fraction}
               COVAR  weight  PARAM b_s_weight  LOW=-20  HIGH=20  START=0  END
               COVAR  sex     PARAM b_s_sex     LOW=-20  HIGH=20  START=0  END
            END  {param s}

            PDF STERILE(topen, tclose) END,     {returns 1 for right censored
observations}

            PDF LNNORMAL(topen, tclose)
              PARAM  a  LOW=0.00001  HIGH=100 START=25  END
              PARAM  b  LOW=0.01     HIGH=50   START=3  END
              HAZARD COVAR weight PARAM b_weight LOW=-20 HIGH=20  START=0  END
                     COVAR sex    PARAM b_sex    LOW=-20 HIGH=20  START=0  END
              END  {hazard}
            END  {of the PDF}
       )  {mix function}
    END
  RUN
    FULL
  END  {of the MODEL}

END
```

Linear regression in the likelihood framework

This example shows how linear regression is treated within the framework of likelihood models. The linear regression model with *n* covariates specifies that the value of the *i*th observation is a combination of a *y* intercept term (α) an additive covariate-parameter term ($x_{i1}\beta_1 + x_{i2}\beta_2 + ... + x_{in}\beta_n$) plus an error ($e_i$). Furthermore, distribution among all error terms (ε) is normally distributed with a mean of zero and a standard deviation of σ. The formal specification is:

$$y_i = a + x_{i1}b_1 + x_{i2}b_2 + ... + x_{in}b_n + e_i$$

$$e \sim N(0, s)$$

Under the likelihood model, the equivalent specification can be given in a very different format.

$$Y \sim f(\mu_i, \sigma)$$

$$\mu_i = \alpha + x_{i1}\beta_1 + x_{i2}\beta_2 + ... + x_{in}\beta_n$$

The difference in the two specifications exemplifies the two different philosophies in the methods. Under regression, difference between each observation and the line defined by parameters and covariates is treated as "error". Under the likelihood model, the observations are normally distributed, with a mean that is determined by a series of covariates.

The data for this example are fictitious. The third column contains the values of y_i, column 1 is x_{i1} and x_{i2}.

```
0.4 53 64
0.4 23 60
3.1 19 71
0.6 34 61
4.7 24 54
1.7 65 77
9.4 44 81
10.1 31 93
11.6 29 93
12.6 58 51
10.9 37 76
23.1 46 96
23.1 50 77
21.6 44 93
23.1 56 95
1.9 36 54
29.9 51 99
```

The following shows the output from a regression analysis

```
     VARIABLE               MEAN      STD. DEVIATION COEF. VARIAT.
Indept Variable: Y        76.17647059   16.63293154    0.21834736
Depent Variable:  1       11.07058824    9.74453467    0.88021833
Depent Variable:  2       41.17647059   13.43612339    0.32630585

 VAR.    COEFFICIENT   STD ERROR    T STATISTIC
Alpha   66.46540496
B(1)     1.29019050    0.34276468    3.76407073
B(2)    -0.11103677    0.24858973   -0.44666675

              SUM OF               MEAN         F
SOURCE       SQUARES      DF      SQUARE      RATIO
REGRESS.    2325.1795      2   1162.5897      7.7458
RESIDUAL    2101.2911     14    150.0922
TOTAL       4426.4706     16    276.6544

R SQUARE =     0.5253
STANDARD ERROR OF ESTIMATE =    12.251213
```

The following shows the *mle* code for the equivalent likelihood model. Notice that this program is similar to the accelerated failure time model, except that the form for modeling covariates on the mean is additive (`FORM = ADD`).

```
MLE
  TITLE = "Test regression"
  DATAFILE("eg.dat")
  OUTFILE("eg.out")

  DATA
    y       FIELD 3
    x1      FIELD 1
    x2      FIELD 2
  END

  MODEL
    DATA
      PDF NORMAL(y)
        PARAM  mu   LOW = 7   HIGH = 500   START = 50 FORM = ADD
          COVAR  x1  PARAM  b1  LOW=-10  HIGH=10  START=0  END
          COVAR  x2  PARAM  b2  LOW=-10  HIGH=10  START=0  END
        END   {param}
        PARAM  sig  LOW=0.1   HIGH=200   START=10  END
      END   {pdf}
    END   {data}
  RUN
    FULL
  END

END
```

The following output fragment shows the result from this model.

```
LogLike= -65.06725 Iterations= 334 Func evals= 25383 Del(LL)=  9.745E-0011
Converged normally

Results with estimated standard errors.  (27 evals)
Solution with 4 free parameters
         Name Form       Estimate         Std Error          t        against
           mu ADD      66.46589883575   9.596050356992    6.92638078825   0.0
           b1          1.290194199465   0.453901547297    2.84245384742   0.0
           b2          -0.11104975496   0.202022074279    -0.5496911927   0.0
          sig          11.11779472801   2.630810510011    4.22599601366   0.0
```

The results are nearly identical to the regression results presented earlier. All parameters of the likelihood model are given with a standard error.

For a series of data that are complete, as given in this example, there is little advantage to using maximum likelihood for parameter estimation. Maximum likelihood methods are most useful under some simple modificatons of the data or model used above. Suppose, that in addition to the above observations we had several observations that were less than the minimum or greater than the maximum value of y that could be measured by our instrumentation. The maximum likelihood model could accomodate such observations with ease. Another modification might be to change the underlying distribution to something other than a normal. For example, ε could take on an extreme value distribution or a Laplace distribution. Again, the likelihood framework easily accomodates such modifications.

Case study —Mortality models

Estimation of age-at-death distributions from skeletal indicators is an important task for ecologists and anthropologists alike. This case study discusses some likelihood models to estimate such distributions. The simplest case arises when exact skeletal ages at death are known for a representative sample of N skeletons covering the entire life span. Call $f(a|\mathrm{q})$ the probability density function that represents the age-at-death distribution with parameters q. For example, it might be the `SILER` model, if individuals span the entire lifespan, or it might be the `MAKEHAM` (Gompertz-Makeham) model if the entire sample consists of adults. Under either model, the likelihood given a series of skeletal ages is

Table 7. Ages at death for 608 Dall mountain sheep. Source: Deevey (1947).

Minimum age	Maximum age	Number dying in interval
0	0.5	33
0.5	1	88
1	2	7
2	3	8
3	4	7
4	5	18
5	6	28
6	7	29
7	8	42
8	9	80
9	10	114
10	11	95
11	12	55
12	13	2
13	14	2

(10)
$$L = \prod_{i=1}^{N} f(t_i \mid \mathrm{q})$$

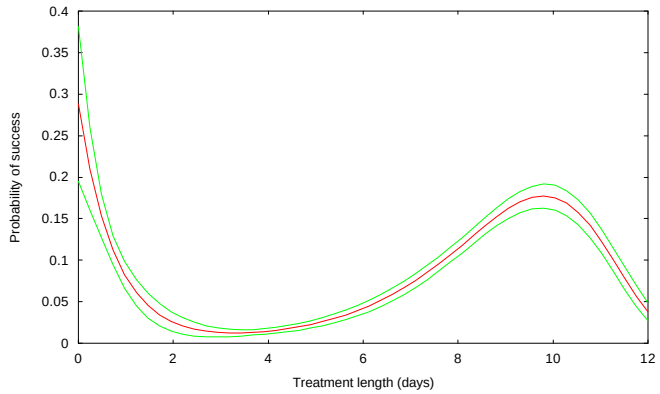
if exact ages are known, or

(11)
$$L = \prod_{i=1}^{N} \left[S(t_u \mid \mathrm{q}) - S(t_e \mid \mathrm{q}) \right]$$

if ages are known over intervals.

The data of Murie (1944) as reported in Deevey (1947) will serve as our example. The raw data consist of 608 Dall mountain sheep skulls collected in the Mt. McKinley Park (Table 7). The ages at death were determined from the annual growth rings on the horns. Causes of death were not determined, but predation by wolves was quite common.

The data were fit by maximum likelihood to the mixed-makeham model. The most parsimonious model had all parameters except the α_2 parameter. The following parameter estimates (and standard error) were found: p = 0.221 (0.018), α_1 = 1.297 (0.211), α_3 = 0.00146 (0.00032), β_3 = 0.618 (0.023). The log-likelihood was -1461.350.



The interpretation of the mixed-makeham model is that there are two subgroups: a high-risk (infant-mortality) subgroup and low-risk (normal) subgroup. The results suggest that 22% of the deaths were to individuals in the first subgroup. The expected age at death can be found by taking

(12)
$$E(a) = \int_0^{\infty} S(a \mid \hat{\mathrm{q}}) da$$

where $\hat{\mathrm{q}}$ denotes that we are using the parameter estimates. Additionally, the expectation can be taken for each of the subgroups by fixing p = 0 or p = 1. The expectation comes to 7.11 years for the full sample, which is very close to the 7.09 years found by Deevey (1947) using the life table method.. For the first subgroup, the expectation of life is 0.77 years, and for the low risk subgroup the expectation of life is 8.90 years.

A plot of the survival distribution for the most parsimonious model is shown in the following figure.

The following code show the final analysis and other statistics computed for this model.

```
MLE
  {Analysis of the data from Murie (1944) as reported in Deevey
   (1947). The raw data consist of 608 Dall mountain
   sheep skulls collected in the Mt. McKinley Park.  Ages at death
   were determined from the annual growth rings on the horns.}

  INPUT_SKIP = 2
  TITLE = "Murie skull data -- Siler model"
  EPSILON = 0.0000001
  DATAFILE("murie.dat")
  OUTFILE(DEFAULTOUTNAME)
  PLOTFILE(DEFAULTPLOTNAME)
  MAXITER = 500

  DATA
      frequency   FIELD 3
      last_alive  FIELD 1
      first_dead  FIELD 2
  END

  MODEL
    DATA
      PDF MIXMAKEHAM(last_alive, first_dead)
        PARAM p   LOW = 0  HIGH = 1   START = 0.25   END
        PARAM a1  LOW = 0  HIGH = 2   START = 0.5    END
        0
        PARAM a3  LOW = 0  HIGH = 4   START = 0.001  END
        PARAM b   LOW = 0  HIGH = 3   START = 0.5    END
      END
    END
  RUN  THEN
         e2  = INTEGRATE z (0, 120)
                  z * PDF MIXMAKEHAM(z) p, a1, 0, a3, b END
               END
         e2a = INTEGRATE z (0, 120)
                  z * PDF MAKEHAM(z) a1, a3, b END
               END
         e2b = INTEGRATE z (0, 120)
                  z * PDF MAKEHAM(z) 0, a3, b END
               END
         PRINTLN("Expectation of life: MixedMakeham model    = ", e2)
         PRINTLN("Expectation of life: Subgroup 1    = ", e2a)
         PRINTLN("Expectation of life: Subgroup 2    = ", e2b)
         plotoptions =   "set ylabel 'Probability of success'; "
                       + "set xlabel 'Treatment length (days)'; "
         lo = 0  hi = 12  pts = 50
         PLOT (plotoptions)
           CURVE
             x (lo, hi, pts)  x,  PDF MIXMAKEHAM(x) p a1 0 a3 b END
           END {curve}
           CURVE WITH "lines linetype 2"
             x (lo, hi, pts)  x,  PDF MIXMAKEHAM(x) p a1 0 a3 b END
                + 1.96*SETRANSFORM(PDF MIXMAKEHAM(x) p a1 0 a3 b END)
           END {curve upper CI}
           CURVE WITH "lines linetype 2"
             x (lo, hi, pts)  x,  PDF MIXMAKEHAM(x) p a1 0 a3 b END
                - 1.96*SETRANSFORM(PDF MIXMAKEHAM(x) p a1 0 a3 b END)
           END {curve lower CI}
         END {plot}
       END {run}
    FULL
  END

END
```

Logistic regression

Tanner (1996) gives an example of logistic regression using data from Mendenhall et al. (1989). Twenty four patients were given radiotherapy for some number of days to treat a tongue carcinoma. Three years later, the treatment is classified as success, by the absence of the tumor after three years, or failure if the disease recurs. The observations are given in the file `RADIOT.DAT`, and the *mle* program file is `RADIOT.MLE`.

```
MLE
  INPUT_SKIP = 8   {skip comments}
  TITLE = "Radiotherapy success"
  DATAFILE("radiot.dat")     {Input data file name}
  OUTFILE(DEFAULTOUTNAME)
  METHOD = CGRADIENT1
  EPSILON = 1E-10

  DATA
    days       FIELD 1  {Days of treatment}
    success    FIELD 2  {Success of treatment at 3 years}
  END

  ALT_LOGISTIC = TRUE        { use         exp(xb)/[1 + exp(xb)]
                               instead of        1/[1 + exp(xb)]}

  MODEL
    DATA
      PDF BERNOULLITRIAL(success)
         PARAM b_0 LOW = -500 HIGH = 500 FORM = LOGISTIC
           COVAR days PARAM b_days LOW = -10 HIGH = 10 START = 0 END
         END  {param}
      END {pdf}
    END  {data}
  RUN
    FULL
  END  {model}

END    {of the MLE program}
```

In this model, the variable *days* is the covariate of interest and the outcome is the variable *success*. The logistic regression model specifies the probability of success as

$$p_i = \frac{\exp(\beta_0 + \beta_1 x_i)}{1 + \exp(\beta_0 + \beta_1 x_i)}, \tag{13}$$

where x_i is the number of days of treatment and the b coefficients are parameters to be estimated. Note that the variable ALT_LOGISTIC is set to TRUE for this particular form of the logistic model. The likelihood under the logistic model is probability p_i for each patient for whom therapy is successful, and $1 - p_i$ for each patient for whom therapy is unsuccessful. Hence, each observation is treated as a Bernoulli trial for success with parameter p modeled as (13). The likelihood is

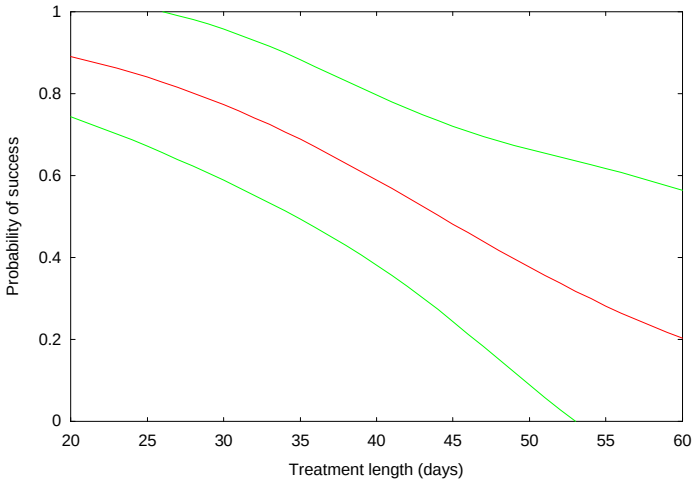
$$L = \prod_{i=1}^{N} B\left[t, \frac{\exp\left(\beta_0 + \beta_1 x_{1i}\right)}{1 + \exp\left(\beta_0 + \beta_1 x_{1i}\right)}\right].$$

The resulting parameter estimates suggest the log odds of recurrence by year 3 with zero days of treatment are 3.819. Paradoxically, the log odds of success decrease with each extra day of treatment by about 8.6 percent!

```
Convergence at EPSILON =  1.000E-0010
LogLikelihood: -13.89411 AIC: 31.788220 Del(LL):  1.367E-0014
Iterations: 8 Function evaluations: 824 Converged normally

Results with estimated standard errors.  (10 evals)
Solution with 2 free parameters
         Name Form       Estimate         Std Error          t        against
          b_0 LOGISTIC 3.819417361125   1.739572481596    2.19560691005   0.0
       b_days          -0.08648243176   0.041100225123    -2.1041838944   0.0
```

The resulting logistic curve can be plotted with a 95% confidence interval by replacing the RUN…FULL part of the model statement with the following code:

```
  RUN
    FULL THEN  {Code for plotting the logistic curve with CIs}
           PLOT ("set ylabel 'Probability of success'; " +
                 "set xlabel 'Treatment length (days)'; "  +
                 "set yrange[0:1];")
             CURVE
               x = 20 to 60  x,  LOGISTIC(p + x * b_days)
             END {curve}
             CURVE WITH "lines linetype 2"
               x = 20 to 60   x,  LOGISTIC(p + x * b_days) +
                              1.96*SETRANSFORM(LOGISTIC(p + x * b_days))
             END {curve upper CI}
             CURVE WITH "lines linetype 2"
               x = 20 to 60   x,  LOGISTIC(p + x * b_days) -
                              1.96*SETRANSFORM(LOGISTIC(p + x * b_days))
             END {curve lower CI}
           END {plot}
         END {full then}
```




```
  END  {model}
```

Case study: Extended Poisson for modeling species abundance

This example shows the use of a user-defined function for programming a pdf that is not built into *mle*. In fact, the Thomas distribution is available in *mle*, but we will ignore the built-in implementation for this example. This example also shows some graphics programming in *mle*.

Thomas (1949) discusses the problem of clustering among a given species of plants in ecological surveys. Ecologists were using the Poisson distribution to describe the number of plants found in randomly selected square quadrats. The Thomas distribution (Thomas 1949; Christensen 1984) models the count of *k* plants in a quadrat as resulting from one or more clusters of plants, and is given by

(14)

$$f(k;a,b) = e^{-a}\sum_{j=0}^{k}\frac{a^j}{j!}e^{-jb}\frac{(jb)^{k-j}}{(k-j)!}$$

Data are counts of *Armeria maritima* plants surveyed in 100 quadrats on Blakeney Marsh: 57 quadrats with 0 plants; 6 with 1 plant; 12 with 2; 5 quadrats each with 3, 4, and 5 plants; 7 quadrats with 6 plants; and 1 quadrat each with 7, 9 and 10 plants.

The following *mle* program fits these data to the Thomas distribution as well as the Poisson distribution and graphs the distributions of observed versus expected number of plants.

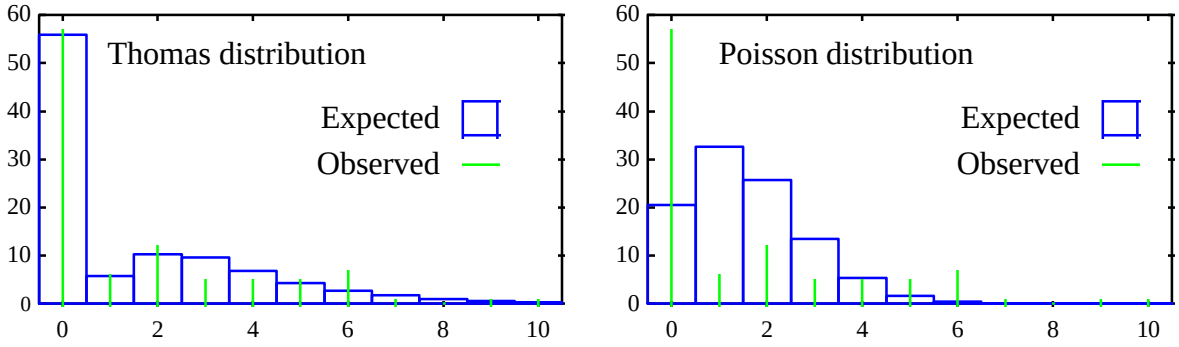
```
MLE
  {Distribution of Ameria maritima in Blakeney Marsh  using the Thomas distribution
   or Double Poisson distribution. Data are given by M Thomas (1949) A generalization
   of Poisson's Binomial Limit for use in Ecology, Biometrika 36:18-25.}

  FUNCTION thomas(k:INTEGER, a:REAL, b:REAL):REAL
    { -- returns the pdf for the thomas dist count k and parameters a and b}

    RETURN = EXP(-a)*SUMMATION j (0, k)
                       ((a^j)/FACT(j))*EXP(-j*b)*
                       (((j*b)^(k - j))/FACT(k - j))
                     END  {summation}
  END  {function thomas}

  DATAFILE("armeria.dat")
  OUTFILE(DEFAULTOUTNAME)
  PLOTFILE(DEFAULTPLOTNAME)
  INPUT_SKIP = 3

  DATA
    numb_plants    FIELD 1
    numb_quadrants FIELD 2
    FREQUENCY     = numb_quadrants
  END

  TITLE = 'Thomas distribution'
  MODEL
    PREASSIGN
      BEGIN
         a = PARAM aa LOW=0.0001 HIGH=20 START=2.0 END
         b = PARAM bb LOW=0.0001 HIGH=40 START=0.5 END
      END
      DATA thomas(ROUND(numb_plants), a, b) END
    END  {preassign}
  RUN
    FULL
  END

  {Plot obs & exp # of quadrants with k plants under the Thomas distribution}

  PLOT ("set title 'Thomas distribution'","set xrange [-0.5:10.5]; set key top right")
    CURVE KEY "Expected" WITH "boxes"
      i = 0 TO 10   i, 100*thomas(i, aa.1.1, bb.1.1)
    END
    CURVE KEY "Observed" WITH "impulses"
      d_idx = 1 TO 11   numb_plants, numb_quadrants
    END
  END  {plot}

  TITLE = 'Poisson distribution'
  MODEL
    DATA
      PDF POISSON(numb_plants)
        PARAM m LOW = 0.001  HIGH = 100  START = 1.5 END
      END
    END
  RUN
    FULL
  END

  {Plot the obs & exp # of quadrants with k plants under the Poisson distribution}

  WRITEPLOTLN("pause -1")
  PLOT ("set title 'Poisson distribution'",
        "set xrange [-0.5:10.5]; set key top right")
    CURVE KEY "Expected" WITH "boxes"
      i = 0 TO 10   i, 100*PDF POISSON(i) m.2.1 END
    END
    CURVE KEY "Observed" WITH "impulses"
      d_idx = 1 TO 11   numb_plants, numb_quadrants
    END
```

```
  END  {plot}

END
```

The resulting parameter output are given in annotated form below. The difference in AIC between the two modesl suggests that the Thomas distribution fits the data much better than the Poisson. The plots in Figure 6 show how much better the Thomas distribution fits compared to the Poisson.

```
11 lines read from file armeria.dat
11 Observations kept and 0 observations dropped.

NAME   numb_plant  numb_quadr   FREQUENCY
MEAN   5.00000000  9.09090909  9.09090909
VAR    11.0000000  264.690909  264.690909
STDEV  3.31662479  16.2693242  16.2693242
MIN    0.00000000  0.00000000  0.00000000
MAX    10.0000000  57.0000000  57.0000000

Model 1 Run 1 : Thomas distribution

LogLikelihood: -158.0639 AIC: 320.12784 Del(LL): 0.0000016017
Iterations: 6 Function evaluations: 158 Converged normally

Results with estimated standard errors.  (6 evals)
Solution with 2 free parameters
         Name Form       Estimate         Std Error          t        against
           aa          0.581452489433   0.088149263241    6.59622631041   0.0
           bb          1.717416986359   0.258883747023    6.63393127652   0.0

Model 2 Run 1 : Poisson distribution

LogLikelihood: -225.3173 AIC: 452.63465 Del(LL): 0.0000000000
Iterations: 2 Function evaluations: 26 Converged normally

Results with estimated standard errors.  (3 evals)
Solution with 1 free parameter
         Name Form       Estimate         Std Error          t        against
            m          1.579996571411   0.069292424625    22.8018658598   0.0
```

Figure 6. Plots of observed and expected numbers of plant counts under two different distributions.



Chapter 7
Programming tutorial

The *mle* programming language is a general purpose algebraic programming language. This chapter provides a tutorial and examples of some of the language tools that can be used for many types of programming.

Introduction to programming in *mle*

People get passionate about programming languages the way they get passionate about religion.[10] There are thousands of programming languages that have been written. Why should you use *mle*? Why indeed. With so many good general purpose programming languages available in the world, I will not try to make strong arguments that *mle* is the best general purpose programming language, and I will not even claim that it is the single best language for any specific purpose. Rather, I will argue that there some pretty good reasons to use *mle*. But, if you are already a crack Ada, Basic, COBOL, Fortran, Python, SAS, SNOBOL, Java, perl, or COBOL programmer, by all means use that language you know best.

If you are an experienced programmer in any conventional programming language, the learning *mle* will be simple—the syntax is straightforward, and punctuation is minimal. If you are learning a programming language for the first time, *mle* is a good language beginner's language.

If not, here are some reasons to learn and use *mle*.

- It will make it easier to develop and estimate statistical models in *mle*. This is perhaps the biggest reason to learn *mle* instead of another language. Learning general-purpose computer programming in *mle* will simultaneously provide tools for scientific computing, model development and statistical estimation.

[10] Okay, this is an exaggeration. After all, hundreds, if not thousands, of wars have been fought over religion. Fortunately, programming language bigotry does not quite rise to that level of fanaticism!

- It is free for non-commercial use.
- It is a simple language. It is almost as simple as early versions of Basic, but with some nice programming features like those found in Pascal. So many newer languages are badly bogged down with widget libraries, object oriented constructs, and other complexities; it makes it difficult to do simple data manipulation or calculation.
- It recognizes many different number formats. This can be helpful when you need to read in, say, Roman numerals, time formats, dates, etc.
- It comes with many useful numerical and mathematical functions.
- It comes with many useful statistical functions and predefined probability density functions.
- It can work with complex numbers.
- It has built-in help.
- Learning how to program in *mle* will make it easy to move to another programming language.

There is no single language that is good at handling all programming problems. All languages have strengths and weaknesses for particular programming tasks. *mle* is good for doing straightforward manipulation of data and scientific computation, and developing simple simulations. The extensive library of pre-defined functions is what makes *mle* useful for these tasks. The language is not suited for building complex interfaces (using the mouse, graphics, menus, etc.), and is not good for low-level development (like for writing an operating system). Additionally, *mle* is an interpreted language. Hence, if speed is an important criterion, then conventionally-compiled languages like C or Pascal should be used instead of *mle*.

Elements of *mle* programming

The first program

The outline of an *mle* program looks like this:

```
MLE
  <statement 1>
  <statement 2>
  <statement 3>
  .
  .
  .
END {mle}
```

Between the keywords `MLE` and `END` comes a series of statements. When the program is run, each statement is executed in turn. Let's put a statement in. Type the following text into an editor, save it, and run it.

```
MLE
  WRITELN('Hello Universe!')
END
```

This program consists of a single `WRITELN()` procedure. `WRITELN()` takes a list of zero or more arguments, writes them to the screen (or to a file in some circumstances), and puts the cursor at the start of the next line on the screen. The single argument is the string `'Hello Universe!'`. The term *string* refers to a sequence of text characters. The single quote marks on each side serve to define the extent of the string. As it happens, you can also use double quote marks, so that `"Hello Universe!"` does the same thing. You cannot mix the two types of marks for a string.

If all went well when you ran the program, the message `Hello Universe!` was sent to the screen, and you have successfully written your first *mle* program. If not, you have probably gotten an error message. For example, if you left off the second quote mark, the message is returned:

```
Unclosed ' at end of a line or file
 Error found while parsing "("
 line 2 column 10 in file eg1.mle
```

mle, like all programming languages, requires you to follow some very strict rules. Here are a few to get you started.

- Arguments to simple functions and procedures are enclosed in a set of parentheses (not square brackets or curly braces).

- Keywords and variables cannot have spaces and most punctuation within them. *mle* is a free-fromat language. Indentation, spacing and formatting are ignored, with some exceptions. The previous program could be written on a single line as:

```
MLE   WRITELN ( "Hello Universe!" )   END
```

- A space or valid punctuation mark must separate keywords. The program `MLEWRITELN("Hello Universe!")END` is not valid because `MLE` and `WRITELN` are run together. The program `MLE WRITELN("Hello Universe!")END` is a valid program. Notice that the `)END` does not require an additional space, because ')' is punctuation.

Identifiers, assignment statement, and functions

Let's expand on the first program a bit. The second program introduces assignment statements, identifiers, function calls, and comments.

```
MLE
  { -- Writes a greeting card to the universe.
       Written 29 Mar 2003
  }
  population = 6.3     {update from http://www.ibiblio.org/lunarbin/worldpop}

  greeting = 'Hello Universe!'

  { -- now create a signature that includes everyone}
  signature = ' -- from ' + REAL2STR(population, 3, 1) + '+ billion of us on earth.'

  { -- write the message here}
  WRITELN(greeting)
  WRITELN(signature)
END
```

The first thing to notice about this program is that it contains comments. The comments are contained within curly brackets, {}. Comments are ignored and are there to help programmers makes sense of the program months or years later. As a programmer, you should develop the discipline to document your program with comments. Try to develop a consistent and descriptive style for formatting your programs, including informative comments sprinkled throughout.

In this program, we have created some variables. Variables are named "objects" that take on a value. In a spreadsheet program, there are "cells" available that can take on values. Variables are like the cells in a spreadsheet program, except that they are not laid out in a visual grid.

The first variable created above is called `population`. The value 6.3 is assigned to this variable. Since 6.3 is a real number rather than an integer or a string of characters, the variable will be created to be a real number and initially assigned the value 6.3.

The variable `greeting` is assigned to a string of characters: '`Hello Universe!`'. Consequently, the `greeting` is created as a `STRING` variable. The single-quotation marks are not actually part of the string. Rather, they serve to delimit where the string starts and where it ends. The quote marks can be single quote marks (') or double quote marks ("), but they must match. `'Hello"` is not a valid way to specify a string. However, you can specify the string `People's world` as `"People's world"`.

What goes into a variable name? There are several rules that must be followed.

- First, a variable name must begin with a letter. The letter can be upper-case or lower-case, it does not matter—*mle* treats uppercase and lowercase as identical for identifier names and keywords.

- After at least one letter, other letters, numbers, a period or an underscore may be used.

- You should avoid using predefined keywords, function names, and procedure names. Sometimes you will get an error (i.e. using a keyword) and other times, you will simply add confusion and disable the original purpose of the keyword (e.g. using a predefined function).

- An additional point of good programming practice is to create variable names that are meaningful. Choose `subject_birthdate` over something less descriptive like `sbd`. Doing so will pay off in the extra time many times over. The payoff comes when you look at your program weeks, months or years later, and are able to quickly understand what the program does. On the other hand, some abbreviation is warranted, particularly if you do so consistently for all variables. If you always use `subj` in place of `subject`, the variable name `subj_birthdate` might work just as well.

The variable `signature` is also assigned a string value. In this case, the string value is computed as the concatenation of three separate elements: first a string constant, secondly a string value returned by the `REAL2STR()` function, and third a string constant.

Assignment statements serve two purposes. First, they create new variables. The variables `population`, `greeting`, and `signature` did not exist until they were defined in the assignment statement. When each variable is first used in an assignment statement, its type is determined by the type returned from the expression on the right-hand side of the assignment statement. The other purpose of assignment statements is to assign values to variables, as is done here. Once a variable is created, it can be assigned other values of the same type (or values that can be converted into the same type, an integer into a real, for example).

Types

Variables (and expressions, for that matter) in *mle* can take on one of the following *types*: `REAL`, `INTEGER`, `COMPLEX`, `BOOLEAN`, `STRING`, `CHAR` (character), and `FILE`. A detailed discussion of these types is given in the reference manual. A summery is given here.

A variable's *type* refers to the domain of values that the variable can take on. For example, `INTEGER` variables can take on a limited range of integer values, `BOOLEAN` variables can only take on the values `TRUE` and `FALSE`. Variables can be defined for each of the seven types and expressions always take on one of these types. Here is an explanation of each:

- ***Real*** variables represent the continuous real number line. For example, 3.5, 1E-23, 7.0, and -19.999 are all real numbers.

- ***Integer*** variables take on whole number values over a machine-dependent range of numbers. For most versions of *mle* this range is [-2,147,483,648 to 2,147,483,647].

- ***Complex*** variables include a real number part and an imaginary part. Complex numbers are specified by expressions such as `1.2 + 0.4i`, or `0+ 1i`.

- ***Boolean*** variables take on one of two states: `TRUE` or `FALSE`. No other value is allowed or recognized. Boolean expressions are frequently used to test conditions in the `IF...THEN...ELSE...END` function or statement.

- ***String*** variables hold a sequence of character constants. A string written as a constant is a sequence of characters, enclosed within quotes ("). The single quote character (') can be used as well for strings greater than one character. String variables are typically used to assign file names, titles, etc.

- ***Character*** variables take on the value of a single character. When written as a constant in a program, character constants consist of a single character enclosed within single quotes ('). Character constants are not typically used within a user's program, but are available if needed. Usually, character constants and variables can be used anywhere string variables are allowed.

- ***File*** variables are used to reference files. Most of the time, file variables are transparent, and you need not explicitly define or manipulate file variables. This is because *mle* defines and does the bookkeeping for the data file, the output file, the plot file, and the screen (or standard output) file. File variables can be created should you wish to create and manipulate other files.

Here are some examples, largely self explanatory, of typical assignment statements:

```
large_data = N_OBS > 5000               {large_data is declared as type BOOLEAN}
subtitle   = "Analysis of " + INFILE    {subtitle is declared as type STRING}
nine       = 3 * 3.0                    {nine is type REAL}
five       = 2 + 3                      {five is type INTEGER}
one        = SIN(23)^2 + COS(23)^2      {one is type real}
onealso    = SIN(23+0i)^2 + COS(23)^2   {onealso is type COMPLEX}
```

You can explicitly define a variable's type when the variable is first referenced in an assignment statement. Here are some examples:

```
c:STRING  = 'x'           {c would otherwise be CHAR}
nine:REAL = 3 * 3         {nine would otherwise be INTEGER}
t:BOOLEAN = TRUE          {t is explicitly declared BOOLEAN, it is the default}
ang:REAL = SIN(2*pi)      {ang is explicitly declared REAL, it is the default}
ang2:COMPLEX = GAMMA(1.5) {force ang2 to COMPLEX}
```

Table 8. Algebraic, boolean, and logical operators.

Operator	Function	Example	Equivalent function
-	uniary negation	-x	NEGATE(x)
+	uniary positive	+x	
^	power function	x^y	POWER(x, y)
*	multiply function	x*y	MULTIPLY(x, y)
/	divide function	x/y	DIVIDE(x, y)
DIV	integer divide function	x DIV y	IDIV(x, y)
MOD	integer modulo function	x MOD y	MODF(x, y)
AND	boolean and logical and function	x AND y	ANDF(x, y)
SHL	logical shift left function	x SHL y	SHIFTLEFT(x, y)
SHR	logical shift right function	x SHR y	SHIFTRIGHT(x, y)
+	addition	x + y	ADD(x, y)
-	subtraction	x - y	SUBTRACT(x, y)
OR	boolean and logical or function	x OR y	ORF(x, y)
XOR	boolean and logical xor function	x XOR y	XORF(x, y)
== or =	boolean "is equal" function	x == y	ISEQ(x, y)
<>	boolean "not equal" function	x <> y	ISNE(x, y)
<	boolean "less than" function	x < y	ISLT(x, y)
>	boolean "greater than" function	x > y	ISGT(x, y)
<=	boolean "less than or equal to" function	x <= y	ISLE(x, y)
>=	boolean "greater than or equal to" function	x >= y	ISGE(x, y)

Statements with numeric, boolean, and logical expressions

Algebraic expressions are expressions are created using a series of special operators and calls to functions. Operators include algebraic symbols like +, –, *, /, ^, and a series of algebraic keywords for integer operations, DIV, MOD, SHL, SHR (See Table 8). The right hand side of an assignment statement is an expression. Examples of valid assignment statements with expressions on the right-hand side are:

```
n = 2*3
n = (HOURS/60)^2
n = 12.5*first - 10*second
n = SIN(2*PI)
i = mask SHL 4
i = 23 DIV 4
```

Boolean expressions evaluate to either TRUE or FALSE. The operators for creating boolean expressions are >, <, >=, <=, ==, <>, and boolean keywords, AND, OR, XOR, and NOT and some simple functions. These operators are used in the same way as they are in many other programming languages.

```
b = a <> 42^2
b = (a <> 12) AND (a >= 0)
```

The difference between boolean and logical expressions is that boolean expressions work with the values `TRUE` and `FALSE` only, whereas logical expressions work with bits on integers. For example, `NOT TRUE` is equal to `FALSE`; but `NOT 767` is equal to `-768`. How does this work? The number 767 is represented by the computer as the binary sequence `00000000000000000000001011111111`. The logical `NOT` operator flips all 1s to 0s and 0s to 1s, so that the number becomes `11111111111111111111110100000000`. The first (left most) bit denotes a negative value, so the value is –768. The logical `AND`, `OR`, and `XOR` functions act bit by bit, as well. Thus the binary values `2X101101 AND 2X111000` (which is the same as `45 AND 56`) evaluates to 40 (or `2X101000`).[11] The `SHL` and `SHR` operators shift bits to the left and right. So, `2X000111 SHL 3` (i.e. `7 SHL 3`) evaluates to 56 (or `2X111000`). See Table 9 defines the logical operators.

Table 9. Definition of logical operators.

Operator	Descritpion	Example	Result
NOT	Flips all 0s to 1s and 1s to 0s	NOT 142	-143
AND	Returns 1 if both bits are 1. 1 AND 1 → 1, 0 AND 1 → 0, 0 AND 0 → 0	2x1010 AND 2x1100	8 [2x1000]
OR	Returns 1 if either bit is a 1. 1 OR 1 → 1, 0 OR 1 → 1, 1 OR 0 → 1, 0 OR 0 → 0	2x1010 OR 2x1110	14 [2x1110]
XOR	Exclusive OR function. Returns a 1 if one of the bits is 1 and the other is 0. 1 XOR 1 → 0, 0 XOR 1 → 1, 1 XOR 0 → 1, 0 XOR 0 → 0	2x1010 OR 2x1110	6 [2x0110]

You might be wondering how *mle* decides whether an operator is boolean or logical. The answer is simple: if both operands are boolean types, the operator will be boolean. If both operands are integers, the operator will be logical. If one operator is boolean and one is logical, an error results. For the expression `(x >= 4) OR (y <= 2)`, each of the expressions in parenthesis will evaluate to `TRUE` or `FALSE`, so that the `OR` will be a boolean operator.

Operator precedence

Mathematicians have developed a series of conventions on operator precedence. When you see the expression `4x2 + 2x + 3`, you know, by convention, that the exponentiation occurs first, the multiplications take place second, and the addition is third. The built in operators in *mle* follow a more or less standard precedence. That is, an expression like `4+2*3` will evaluate `2*3` first and then

[11] The 2X… notation is how numbers are specified in other bases (base 2 or binary in this case). For base 2 numbers, only the digits 0 and 1 are permitted on the right-hand side of the X. Octal (base 8) numbers can be specified as 8X…, where digits from 0 to 7 are permitted on the right hand side of X.

add 4. The precedence of operators are defined in Table 10. Higher precedence

Table 10. Operator precedence.

Operator(s)	Precedence	Category
`- + not`	high	Uniary operators
`^`		Exponent operator
`* / div mod and shl shr`		Multiplying operators
`+ - or xor`		Adding operators
`= (or ==)  <> < > <= >=`	low	Relational operators

operators will always be evaluated before lower precedence operators

More on strings

String constants are values that are enclosed within quotes. Here are a few rules for string constants:

- when you specify a string constant, you can use either the `"` or the `'` characters.
- If you open a string constant with `"`, you must close it with `"`. If you open the string with `'` you must close with `'`.

Hence, the statements:

```
foo = "My name is "
bar = 'Kilroy'
WRITELN(foo bar)
```

are legal and produce the output: `My name is Kilroy`. The statements

```
foo = "My name is '
bar = 'Kilroy"
```

are invalid because the quote types do not match. Some languages do not allow this flexibility. In BASIC, for example, all string constants must be enclosed in the `"` character. In Pascal, all string constants must be enclosed in the `'` character. *mle* allows either.

Commas in lists of arguments

Commas are always optional in *mle*. Hence, both

```
WRITELN(foo, bar)
WRITELN(foo bar)
```

are valid. and they work exactly the same. There are several good reasons to use commas, however. First, they make it easier to read. Secondly, they are helpful when working with negative numbers. Consider the following:

```
WRITELN(3, -1)
```

This statement produces the output: `3-1` (There is no space between the `3` and the `-1` because it is not asked for). Now, what if you leave the comma out?

```
WRITELN( 3  -1 )
```

This program produces the output: `2`. This is because `3 -1` was taken as a mathematical expression! The expression evaluated to the number `2`. So the comma was useful in this context. You could, however, still avoid using the comma. Here are some ways of getting the same result:

```
WRITELN( 3 (-1) )       {put the -1 inside parentheses}
WRITELN( 3 NEGATE(1) )  {creates -1 with the negate function}
```

Now, once you understand all that, you can make sense of statements like:

```
WRITELN("My name is ", first, ' ' middle ' ', last)
```

The "call" to procedure `WRITELN` has 6 arguments (some separated by commas, others not). Can you identify each of the six arguments? They are:

```
"My name is "       # This is a string constant.
first               # This is a variable (defined earlier in the program)
' '                 # This is a one character string constant
middle              # This is another variable
' '                 # Another one character string constant
last                # This is a third variable
```

Suppose earlier in the program there was the statements:

```
first = 'Thomas'
middle = 'A.'
last = 'Edison'
```

Then the `WRITELN` statement above will write 6 different things to the screen. Here is a murkier statement:

```
WRITELN("'", " " ',', ' ',"'")
```

If you look carefully, you can deduce that the output is the 5-character sequence: `' , '`

The same as if you had typed `WRITELN("' , '")`. A programmer with a more developed sense of aesthetics would do neither of the above two statements. Rather, s/he would recognize that it is very confusing and write the program this way:

```
singlequote = "'"
space = ' '
comma = ','
WRITELN(singlequote, space, comma, space, singlequote)
```

As an aside, you can use the + operator to concatenate strings. So another way of writing the program is

```
singlequote = "'"
space = ' '
comma = ','
WRITELN(singlequote + space + comma + space + singlequote)
```

Better yet, it could be written

```
singlequote = "'"
space = ' '
comma = ','
confusingstring = singlequote + space + comma + space + singlequote
WRITELN(confusingstring)
```

With so many ways of doing the same thing, you might well ask, "what is the best way?" The answer is that the best way is to write it in the way that is clearest to you, so that you can read the program a year later and be able to make sense of what you were doing.

Reading from the keyboard

Reading from the keyboard is sometimes very useful. Here is a program that prompts a user for information from the keyboard. It asks for sample sizes, means and standard deviations from two studies, computes a pooled standard deviation, and computes a paired *t*-test.

```
MLE
  { -- This program computes a paired t test}
  { -- Define the variables to read}
  n1  : INTEGER
  n2  : INTEGER
  u1  : REAL
  u2  : REAL
  s1  : REAL
  s2  : REAL

  { -- Read in the sample sizes, means, and standard deviations}
  WRITELN("Paired t test")
  WRITE("Sample size 1: ")
  READLN(n1)
  WRITE("Sample size 2: ")
  READLN(n2)

  WRITE("Mean 1: ")
  READLN(u1)
  WRITE("Mean 2: ")
  READLN(u2)

  WRITE("Stdev 1: ")
  READLN(s1)
  WRITE("Stdev 2: ")
  READLN(s2)

  { -- Compute the values of interest}
  df1 = n1 - 1
  df2 = n2 - 1
  dfp = df1 + df2
  s_pooled = SQR((df1*s1^2 + df2*s2^2)/dfp)
  t = (u1 - u2)/(s_pooled*SQR(1/n1 + 1/n2))
  p = STUDENTT(t, dfp)

  { -- Now write the results to the screen}
  WRITELN("Pooled: t = ", t, " df = ", dfp, "  One-tailed p = ", p)
END
```

The prompts for information are written using the `WRITE` procedure. This means that the cursor does not go to the next line when waiting for input from the keyboard. The `READLN` statements each read a value from the keyboard, and it expects the line to be terminated by the <Enter> key. In fact, the `READLN` statement (like `WRITELN`) can read multiple arguments in one statement. Write a program to see what the behavior is when multiple arguments are given to a `READLN` statement.

Mathematical computation

mle contains many common and some uncommon functions for doing mathematical computation.

Summation

Summation over a series of number is a commonly needed function in scientific programming. For example, the value n^2 can be computed from the series $\sum_{i=1}^{|n|}(2i-1)$. Here is a program that reads an integer from the keyboard and computes the series in this way.

```
MLE
  { -- computes the square of an integer using a series }
  n : INTEGER
  WRITE("Integer to square: ")
  READLN(n)
  n2 = SUMMATION i (1, ABS(n)) 2*i - 1 END
  WRITELN(n, '^2 is ', n2)
END
```

The `SUMMATION` function takes four arguments. The first argument is an integer variable that is the variable of summation. In this program, `i` is used as the variable of summation. It is not previously defined, so it will be implicitly defined by the `SUMMATION` function. The next two arguments are in parentheses. They define the upper and lower limits of the summation. The fourth argument is the expression of summation. Notice that `i` appears within the function. Its value will be updated with each iteration of the function.

Products

Like summation, taking a product over a series of number is a commonly needed function in scientific programming. For example, the factorial function $n! = 1 \times 2 \times \ldots \times (n-1) \times n$ can be computed as $\prod_{i=1}^{n} i$. Here is a program that reads an integer from the keyboard and computes the series in this way.

```
MLE
  { -- computes factorial function }
  n : INTEGER
  WRITE("Find factorial of what integer: ")
  READLN(n)
  factn = PRODUCT i (1, n) i END
  WRITELN(n, '! is ', factn)
END
```

Like the SUMMATION function, PRODUCT function takes four arguments.

Integration

Suppose you want to compute the integral $\int_{-\sqrt{\pi}}^{\sqrt{\pi}} \sin(x^2 + 2x)dx$. Here is an example of how that can be coded: `myvalue = INTEGRATE x (-SQRT(PI), SQRT(PI)) SIN(x^2 + 2*x) END`. (The expression assigns the result, about -1.525, to `myvalue`). Here is a description of the meaning of each part of the expression:

```
MLE
  myvalue = INTEGRATE x  (      {x is the variable of integration}
              -SQRT(PI),        {This is the lower limit of integration}
               SQRT(PI)         {This is the upper limit of integration}
                        )       {Close of the argument list}
             SIN(x^2 + 2*x)  {The function to be integrated}
           END                 {Integrate}
  writeln(myvalue)
END                 {End of the integrate function}
```

Like the SUMMATION and PRODUCT functions, there are four arguments to the INTEGRATE function (actually there can be more, see the reference manual). The first is x, the variable of integration, within parenthesis come the lower and upper limits of integration, followed by the integrand.

Probabilities

One of the strengths of *mle* is that it contains a large number of predefined probability density functions and functions derived from the PDF. Any of the predefined probability density functions can be used as part of an expression. For example, the following program will give the area between user-specified limits for a normal distribution with user-specified parameters.

```
MLE
  a  : REAL
  b  : REAL
  mu : REAL
  sig: REAL

  WRITELN("Returns the area under a Normal distribution")
  WRITE("Lower and upper limits of the area: ")
  READLN(a, b)
  WRITE("Mean and Standard deviation: ")
  READLN(mu, sig)
  WRITELN(PDF NORMAL(a, b) mu, sig END)
END
```

Notice that the PDF function is called within the WRITELN function. This is perfectly valid. The arguments to WRITELN can be any expression no matter how complicated. Here is an example of what happens when this program is run.

```
Returns the area under a Normal distribution
Lower and upper limits of the area: 3, 4
Mean and Standard deviation: 10, 3
0.0129347552
```

Random numbers

Simulation programming often times requires drawing numbers from particular probability densities. Random numbers can be generated for nearly all of the densities supported by *mle*. The `QUANTILE` function facilitates this. Essentially, the `QUANTILE` will accept a value drawn from a uniform distribution and return a value that is randomly drawn from the base density.

A uniform variate from zero to one is generated by the `RAND` function. Before the `RAND` function can be called, the random number generator must be seeded. This is done by a call to procedure `SEED()` with a positive integer argument. If you prefer not to choose an initial seed value, the function `CLOCKSEED` will generate one using the computer's date and time.

Here is an example of a program that prints out a number randomly drawn from a Weibull density with user-specified parameters.

```
MLE
  a  : REAL
  b  : REAL

  SEED(CLOCKSEED)
  WRITELN("Returns a value drawn from a WEIBULL distribution")
  WRITE("a and b parameters of the WEIBULL distribution: ")
  READLN(a, b)
  WRITELN(QUANTILE WEIBULL(RAND) a, b END)
END
```

Flow control

Normally, statements are executed, one at a time, in the order in which they appear. Frequently it is necessary to loop, branch, and otherwise modify the flow of programs. This section introduces statements and techniques that allow you to modify the flow of program statements. First the `IF` statement is introduced, followed by several looping statements.

A loop is a programming concept that allows segments of code to be repeatedly executed. This allows the computer to do what computers do best: perform repetitive tasks. Almost all programs of any significance contains some type of looping (or iteration). *mle* has the `FOR` statement, the `REPEAT` statement and the `WHILE` statement for this purpose.

IF statement

The `IF` statement provides the means to conditionally executing statements. Here is a simple example

```
MLE
  age : REAL
  WRITE("How old are you? ")
  READLN(age)
  IF age < 0 THEN
    WRITELN("That's not possible!")
  ELSEIF age < 4 THEN
    WRITELN("Perhaps you were you giving your age in decades.")
  ELSEIF age >= 115 THEN
    WRITELN("Perhaps you are giving your age in months.")
  ELSE
    WRITELN("Live long and prosper.")
  END {if}
END
```

The IF statement will execute only one of the WRITELN statements, depending on the range of values entered. The statement works this way. First, it evaluates the expression after the IF. If the expression is true the first WRITELN will be executed and then flow will jump to the end of the IF statement. That is, all the other parts of the IF statement will be skipped. If the expression after IF is FALSE, the first ELSEIF expression will be evaluated. Again, if it evaluates to true the statement(s) that follows will be executed and control will jump to the end of the IF statement. As a last resort, when all IF and ELSEIF expressions evaluate to FALSE, the statement between ELSE and END will be executed.

Generically, this is what the statement looks like.

```
IF <bexpr> THEN
  <statements>
ELSEIF <bexpr> THEN
  <statements>
ELSEIF <bexpr> THEN
  <statements>
ELSE
  <statements>
END
```

Notice that any number of statements can come within each section of the IF statement. The ELSEIF and ELSE clauses are always optional. When there is no ELSE clause, the IF statement doesn't necessarily end up executing any of the statements. That is, if all IF and ELSE expressions evaluate to FALSE, the IF statement will skip to the end of the statement. Here is another example of using the IF statement:

```
IF SYSTEM = "MS-DOS" THEN
  PRINTLN("Run from an MS-DOS system")
  SEP = '\'
  DATAFILE("C:" + SEP + DIR + SEP + NAME)
ELSE
  PRINTLN("Run on a unix system")
  SEP = '/'
  DATAFILE(DIR + SEP + NAME)
END
```

FOR statement

The FOR statement provides a means of looping through statements for some fixed number of iterations. *mle* contains several different types of FOR statements. Three of them are introduced here. The rest are introduced in the section on arrays.

Here is an example program that creates a table of sine and cosine values:

```
MLE
  FOR x = 0 TO 359 DO
    r = DTOR(x)
    WRITELN(x " degrees (" r " radians): SIN()=" SIN(r) ", COS()=" COS(r))
  END  {for}
END  {mle}
```

The variable x is called the index variable. Its value will change with each pass through a loop. In this example, x is initially set to zero, and the statements sandwiched between the DO and the END are executed. The value of x is incremented by one and the statements are executed again, and so on until x is 359. After the last pass through the loop, execution continues after the END.

Generically, the simplest form of the FOR statement looks like this

```
FOR <v> = <expr> TO <expr> DO
  <statements>
END
```

The variable <*v*> must either not be previously defined or, if it already exists, it must be an INTEGER or a REAL variable. Its value will change as the FOR statement is executed. The first <*expr*> will be executed once at the beginning of the loop, and will define the starting value of *v*. The second <*expr*> will also be executed once and will define the last value of *v*.

Here is another example. This program reads an integer and prints it out backwards.

```
MLE
  { -- read an integer and print it out backwards}
  i : INTEGER
  WRITE('Type an integer: ')
  READLN(i)

  FOR x = 1 TO LOG10(i) + 1 DO
    tmp = i           {temporarily save i}
    i = i DIV 10      {get rid of last digit}
    WRITE(tmp - i*10) {compute and print the least significant digit}
  END {for}
  WRITELN             {with no argument, writeln goes to the next line}
END {mle}
```

FOR…STEP statement

There are several variations on the FOR. The first, the STEP clause, allows the index variable to be incremented by something other than one. Here is an example that prints the sequence 9, 18, 27….

```
MLE
  FOR x = 9 TO 99 STEP 9 DO
    WRITELN(x)
  END {for}
END {mle}
```

The initial value of the index variable (here, x) is set to the first value (9 in this case), and x is incremented by the STEP value each iteration so long as x is less than or equal to the final value (99 here). The STEP value can be negative, providing a countdown statement.

FOR…STEPS statement

Another variation on the FOR statement includes the STEPS clause. This allows for a fixed number of steps between the first and last values of the loop. For example here is a program that prints the cumulative area under a standard normal PDF from -1 to 1 in 10 steps:

```
MLE
  FOR x = -1 TO 1 STEPS 10 DO
    WRITELN(x, ' ', NORMALCDF(x))
  END {for}
END {mle}
```

Here is the resulting output:

```
-1.000000000 0.1586552595
-0.777777778 0.2183499460
-0.555555556 0.2892573259
-0.333333333 0.3694414036
-0.111111111 0.4557640673
0.1111111111 0.5442359327
0.3333333333 0.6305585964
0.5555555556 0.7107426741
0.7777777778 0.7816500540
1.0000000000 0.8413447405
```

The index variable of a FOR…STEPS statement is always type REAL.

REPEAT statement

The REPEAT statement provides a means of looping through statements until some condition is met. The REPEAT statement differs from the FOR statement in that there is no index variable and no start variable. Generically, the statement looks like this:

```
REPEAT
  <statements>
UNTIL <bexpr>
```

The <*statements*> are executed and then the boolean expression<*bexpr*> is evaluated. If the result is FALSE, the loop repeats and <*statements*> are executed again. When <*bexpr*> evaluates to TRUE, the loop terminates. A REPEAT statement always executes <*statements*> at least once.

The next example is a program that converts polar to rectangular coordinates. The REPEAT statement is used to verify that the angle falls in the proper range.

```
MLE
  { -- Program to convert polar coordinates to rectangular coordinates}
  angle  : REAL
  radius : REAL
  twopi = 2*PI

  REPEAT
    WRITE('Angle in radians? ')
    READLN(angle)
    good = (angle >= 0) AND (angle <= twopi)
    IF not good THEN
      WRITELN('Angle must be >= 0 and <= ', twopi)
    END
  UNTIL good

  WRITE('Radius? ')
  READLN(radius)

  x = POLARTORECTX(angle, radius)
  y = POLARTORECTY(angle, radius)
  WRITELN("Rectangular coordinates are ", x, ", ", y)
END {mle}
```

WHILE statement

The `WHILE` statement provides a means of looping through statements while some condition is met. The format is

```
WHILE <bexpr> DO
  <statements>
END
```

The boolean expression <*bexpr*> is executed first. If the value is `TRUE`, the <*statements*> are executed once and <*bexpr*> is evaluated again. The sequence continues until <*bexpr*> evaluates to `FALSE`. That is, when <*bexpr*> is `FALSE`, the loop terminates.

The chief difference between a `WHILE` loop and a `REPEAT` loop is that the `REPEAT` loop is *always* executed at least once. The `WHILE` loop may be skipped the first time. Here is an example of a small program using a while loop:

```
{Compute factorial}
n : INTEGER
WRITE("Enter an integer: ")
READLN(n)
tmp : REAL = 1
WHILE n > 1 DO
  tmp = tmp*n
  n = n - 1
END
WRITELN(tmp)
```

The Break Statement

The `BREAK` statement is a special statement that works with `FOR`, `WHILE`, and `REPEAT` statements. When a `BREAK` statement is encountered, the loop is immediately exited. The behavior of a `BREAK` statement outside of a loop causes the current "scope" to be exited. This means that within the main program (outside of a user-defined procedure or function) a `BREAK` acts like a `HALT` and causes the program to terminate. Within a user-defined procedure or function, the procedure or function is exited back to the place from where it was called.

Here is an example of how the BREAK statement can be used to shorten the section of code given in an earlier example.

```
  REPEAT
    WRITE('Angle in radians? ')
    READLN(angle)
    IF (angle >= 0) AND (angle <= twopi) THEN
      BREAK  {exit the REPEAT loop}
    END
    WRITELN('Angle must be >= 0 and <= ', twopi)
  UNTIL 1=0   {that is, loop forever}
```

The Continue Statement

Like the BREAK statement, the CONTINUE statement works within loops (WHILE, REPEAT, and FOR). When a CONTINUE statement is encountered, all further statements are skipped until the end of the current loop. The CONTINUE statement is a convenient way to skip over sections of code and force another iteration of the loop.

Arrays

An "array" is a series of contiguous memory locations referenced by a single variable name. Arrays have many important uses in computer programming. They are almost always used with FOR loops or other looping structures. The important idea behind arrays is that an integer value serves as an offset (or index) to the array elements.

For example, consider an array called myarray that is defined to be 20 REAL elements long. Each element of the array can be indexed by placing an integer expression within square brackets; e.g., myarray[3] = 3^2. Suppose we wish to create a table of squared values, and later in the program print the values out. The following code will accomplish this:

```
MLE
  myarray:REAL[1 TO 20]
  FOR i = 1 TO 20 DO
    myarray[i] = i^2
  END {for}
  {...}
  FOR i = 1 TO 20 DO
    WRITELN(i "^2 = " myarray[i])
  END {for}
END
```

In this last example, a one-dimensional array was defined as a REAL and indexed over the range from 1 to 20. Arrays must always be explicitly declared in *mle*. They must be defined the first time the variable is mentioned in the program. A lower and upper index must be specified as integer constants.

Multidimensional arrays of all types are supported by *mle*, as well. The format is *var* : *type*[*min1* TO *max1*, *min2* TO *max2*, . . .]. Some examples of declarations are:

```
s : STRING[1 TO 5]                    {Defines a one-dimensional array of strings}
r : REAL[1 TO 10, 1 TO 10]            {Defines a 10 x 10 matrix}
b : BOOLEAN[0 TO 1, 0 TO 1, 0 TO 1]   {Defines a 3 dimensional array}
```

An entire array can be initialized to a single value in an assignment statement. Examples are:

```
s : STRING[1 TO 5] = ''        {Defines s and initializes all values to ''}
r : REAL[1 TO 10, 1 TO 10] = 0 {Defines a 10 x 10 matrix and initializes to 0}
```

Arrayed variables are accessed by using brackets for subscripting:

```
r : REAL[0 TO 359]
FOR i = 0 TO 359 DO
  r[i] = DTOR(i)
  writeln("Sin(" i ") = " SIN(r[i]) )
END
```

Files

Text files are widely used in computer programming, for statistical analysis, and for data files. *mle* provides tools for creating, reading, writing and appending to text files.

There are four steps to working with files:

- First step, a variable must be declared as type `FILE`. The variable will be used to refer to a file; it acts as a, so-called, “file handle.”

- Next, a file must be “opened.” You must call one of the procedures: `OPENREAD()`, `OPENWRITE()`, `OPENAPPEND()`. Each of these procedures take two arguments. The first is the file variable, and the second is a string expression that is the name of the file.

- Now the file can be read from or written to (depending on how it was opened). The `READ()` and `READLN()` procedures can be used to read from a file. The first argument to the procedures must be the file variable. Likewise, `WRITE()` and `WRITELN()` procedures can be used to write (or append) to files. Again, the file variable must be the first argument.

- After operations on a file have been completed, the `CLOSE()` procedure ensures the file is properly closed. The close procedure forces the operating system to flush any buffers and update the directory information for a file.

Here is a simple program that reads in a file and reverses the characters in each line. Notice the use of the `EOF()` function to check for the end of the file, and the `EXISTS()` function for checking to see if a file exists.

```
MLE
  { -- reads text from a file and reverses the text}
  filename : STRING
  f        : FILE
  textline : STRING

  READDELIMITERS = ''        {read the whole line including spaces}
  REPEAT
    WRITE('File name: ')
    READLN(filename)
    ok = EXISTS(filename)
    IF NOT ok THEN
      WRITELN("Couldn't find ", filename)
    END {if}
  UNTIL ok

  OPENREAD(f, filename)
  WHILE NOT EOF(f) DO
    READLN(f, textline)
    FOR x = STRINGLEN(textline) TO 1 STEP -1 DO
      WRITE(SUBSTRING(textline, x, 1))
    END {for}
    WRITELN
  END  {while}
END  {mle}
```

User-defined procedures

mle allows users to define their own procedures and functions. This section discusses procedure writing and variable passing. The next section discusses the related concept of user-defined functions.

User-defined procedures serve a number of purposes.

- Procedures can be used to extend the languages. Essentially, you can write your own "statements" that take a list of zero or more arguments.

- Procedures provide a way to collect commonly defined operations into a single place. This addresses the frequent need to have the same set of operations performed on different variables or in different parts of a program.

- Procedures provide a way to modularize programs. That is, programs can be composed of a small set of general operations, each that is a separate procedure. Each of those, in turn, can call a set of other procedures. This programming style (called top-down programming) can lead to more robust and readable code.

Procedures must be completely defined prior to their first reference in a program. For example, suppose you want to write a procedure that returns the roots of a quadratic equation. You would first define the procedure `quadratic` (say) that takes 5 arguments: three real coefficients as inputs, and two complex numbers that are the roots as the outputs. Your program could then call that procedure repeatedly in your program with different inputs.

Here is how the procedure could be written:

```
MLE
  PROCEDURE quadratic( a:REAL, b:REAL, c:REAL,
                       VAR root1:COMPLEX, VAR root2:COMPLEX
                       )
    tmpc : COMPLEX
    { -- This procedure takes coefficients a, b, and c, and returns the roots
         as complex roots root1 and root2
    }
    tmpc = SQRT(b^2 – 4*a*c)     {compute an intermediate result}
    root1 = (-b + tmpc)/(2*a)
    root2 = (-b - tmpc)/(2*a)
  END
  . . .
END
```

Defining the procedure

The procedure definition begins with the word `PROCEDURE` and ends with a corresponding `END`. The word following `PROCEDURE` is the name of the procedure, in this case `quadratic`. The name is followed by a list, enclosed in parenthesis, of formal arguments—five in this case. The argument name and type must be specified for each of the argument. In this example, three arguments (`a`, `b`, and `c`) are defined to be type `REAL`, and two are defined as type `COMPLEX`.

The argument names and, for that matter, all of the variables defined within the procedure (like `tmpc`) are "private" to the procedure. Names of preexisting variables outside of the procedure are not affected by and do not affect declarations of variables using the same name inside the procedure. Thus, the following bit of code causes no problems. Outside of the procedure `a`, `b`, and `c` refer to one set of variables, but the names have different meanings within the procedure.

```
MLE
  a : STRING
  b : BOOLEAN
  c : CHAR
  tmpc : CHAR

  PROCEDURE quadratic( a:REAL, b:REAL, c:REAL,
                       VAR root1:COMPLEX, VAR root2:COMPLEX
                       )
    tmpc : COMPLEX
    . . .
  END
```

Any reference to the variables a, b, and c inside the procedure, refers to the local variable within the procedure, not the global variables defined at the top.

The keyword `VAR` has a very important effect on the arguments root1 and root2. These arguments, once they are modified in the body of the procedure, will pass the modifications back to the original calling argument. Without the `VAR` keyword, changing the value of an argument has *no* effect on the calling arguments. In other words, `VAR` makes the argument variable—or changeable.

Calling the procedure

To call the procedure, the code might include something like this:

```
MLE

  a  : REAL
  a2 : REAL
  a3 : REAL
  r1 : COMPLEX
  r2 : COMPLEX
  PROCEDURE quadratic( a:REAL, b:REAL, c:REAL,
                       VAR root1:COMPLEX, VAR root2:COMPLEX
                       )
    tmpc : COMPLEX
    ...
  END

  { -- The main body of the program starts here -- }
  quadratic(2, 3, -4, r1, r2)
  ...
  a=-4
  a2=1.5
  a3=-1
  quadratic(a, a2, a3, r1, r2)
END
```

The statements within the procedure are executed, the values of root1 and root2 are updated, and control is passed back to the main program. In the main program, the variables r1 and r2 have been updated with the results from root1 and root2.

Nested procedures

New procedure and function definitions can be defined within existing procedures. In the same way that variables defined inside a procedure are "visible" from within a procedure, procedures defined within procedures are only visible from within that procedure. Here is an example of nested procedures:

```
MLE
  PROCEDURE printthings(s1:STRING s2:STRING)

    PROCEDURE indent(VAR s:STRING  n:INTEGER)
      {Indents a string by n spaces}
      FOR i = 1 TO n DO
        s = ' ' + s
      END {for}
    END  {proc indent}

    indent(s1, 6)
    indent(s2, 12)
    WRITELN(s1)
    WRITELN(s2)
  END  {proc printthings}
  ...
END
```

EXIT statement

The `EXIT` statement causes the immediate exit of the current procedure or function. If `EXIT` is called from the main program, it has the same effect as a `HALT` statement—the program is exited.

User-defined functions

mle allows users to define their own functions. User-defined functions serve a number of very important purposes.

- Functions are used to extend the types of expressions that can be created.
- Functions provide a way to collect commonly computed operations into a single place. This addresses the frequent need to have the result computed on different variables or in different parts of a program.
- Functions also help modularize programs into smaller, more maintainable components.

Functions must be completely defined prior to their first reference in a program (just like procedures). For example, suppose you want to write a function that returns the average of two integers. You would first define a function that takes two integer arguments. The return type of the function must also be defined. The body of the function does the computation and then returns the results through the predefined variable `RETURN`.

Here is how the function could be written:

```
MLE
  FUNCTION average( v1:INTEGER, v2:INTEGER ): REAL
    { -- This function returns the average of two integers}
    RETURN = (v1 + v2)/2
  END
  . . .
END
```

Defining the function

The function definition begins with the word `FUNCTION` and ends with a corresponding `END`. The word following `FUNCTION` is the name of the function, in this case `average`. The name is followed by a list, enclosed in parenthesis, of formal arguments—two in this case. The argument name and type must be specified for each of the argument. In this example, both are defined to be type `INTEGER`.

The argument names and, for that matter, any variables that might be defined within the function are "private" to the function (the same is true for procedures). Names of preexisting variables outside of the procedure are not affected by and do not affect declarations of variables using the same name inside the function.

As with procedures, arguments can be preceded by the `VAR` keyword. This would have the side-effect of allowing the function to modify the argument. Without `VAR` keywords, changing the value of an argument within a function has *no* effect on the calling arguments. On general principles, it is considered bad programming practice to allow functions to modify arguments.

Calling the function

To call the function, the main program might include something like this:

```
MLE

  FUNCTION myfunc( a:REAL, b:REAL):REAL
    ...
    RETURN = ...
  END

  { -- The main body of the program starts here -- }
  FOR x = 1 TO 20 DO
    a = myfunc(x, -x^2)
    WRITELN(a)
  END
END
```

The statements within the procedure are executed, the values of root1 and root2 are updated, and control is passed back to the main program. In the main program, the variables r1 and r2 have been updated with the results from root1 and root2.

Nested procedures

New procedure definitions can be defined within existing procedures. In the same way that variables defined inside a procedure are "visible" from within a procedure, procedures defined within procedures are only visible from within that procedure. Here is an example of nested procedures:

```
MLE
  PROCEDURE printthings(s1:STRING s2:STRING)

    PROCEDURE indent(VAR s:STRING  n:INTEGER)
      {Indents a string by n spaces}
      FOR i = 1 TO n DO
        s = ' ' + s
      END {for}
    END  {proc indent}

    indent(s1, 6)
    indent(s2, 12)
    WRITELN(s1)
    WRITELN(s2)
  END  {proc printthings}
  ...
```

Example programs

This section contains a few examples of programs written in *mle*.

A simple simulation program

```
MLE
  { This program simulates a simple data set.
    The output is an id and an age at which some developmental
    landmark is attained, drawn from a normal pdf.}

  nkids = 1000   {number of kids to simulate}
  mu = 6         {mean age of reaching the landmark}
  sig = 1        {stddev in reaching the landmark}

  fout : FILE
  SEED(CLOCKSEED)

  OPENWRITE(fout, "kids.dat")

  FOR cid = 1 TO nkids DO
    age = QUANTILE NORMAL(RAND)  mu  sig  END
    WRITELN(FOUT, cid, ' ', age)
  END
  CLOSE(fout)
END
```

A less simple simulation program

Rather than just simulating a data set, this program creates multiple data sets and also does analyses of each data set. This simulation program deals with aspects of study design (study length, censoring, and duration between prospective follow-ups) as well as the underlying parametric model. The last segment of the program computes some summary statistics for the repeated estimates of the model parameters.

```
MLE
  { -- This program does 4 things:

       1. It creates data sets, each with a single
       variable age, and observations of age.  The
       observations are drawn from a normal distribution.

       2. It fits a model (Normal) to each data set.

       3. It simulates aspects of the study observation:
          a. children are initially recruited from ages minrage
             to maxrage months of age--uniformly distributed.
          b. Children are visited every obswidth months for
             studylength months
          c. censorprob % of children drop out between mincensor
             and maxcensor months
       4. It computes the mean and standard deviation
          of the repeated parameter estimates
  }

  OUTFILE(DEFAULTOUTNAME)

  { -- seed the random number generator}
  s = CLOCKSEED
  SEED(s)
  PRINTLN('Clock seeded with ', s)

  { -- SEs must be computed with the alternative method
    because we are not using a DATA statement}

  info_method1 = FALSE
  info_method2 = TRUE

  minrage = 0        {minimum age of recruitment}
  maxrage = 0        {maximum age of recruitment}
  censorprob = 0.20  {probability of dropping out}
  obswidth = 4.0     {width of the observation interval}
  studylength = 10   {max # of months to observe over}
  mincensor = 1      {min number of months to censor at}
  maxcensor = 9      {max number of months to censor at}
  sitmean = 6        {mean age at sitting}
  sitsd = 1          {sd of age at sitting}
  { -- array for "observations"}
  ageo : REAL[1 TO 500]  {last interval before sitting}
  agec : REAL[1 TO 500]  {first observation after sitting}
  numbobs = 500

  { -- save the estimates of mu and sig, one for each simulation}
  savemu : REAL[1 TO 200]
  savesig: REAL[1 TO 200]
  numbsims = 200

  { -- Loop through data sets}
  FOR sim = 1 TO numbsims DO

    { -- create a new data set}
    FOR cid = 1 TO numbobs DO
      s_age = QUANTILE NORMAL(RAND) sitmean sitsd END  {get age at sitting}
      r_age = RRAND(minrage, maxrage)                  {age at recruitment}

      { -- now determine how long to observe children}
      o_len = IF RAND < censorprob THEN
                RRAND(mincensor, maxcensor)
              ELSE
                studylength
              END {if function}

      { -- Now figure out open and closing interval }
      IF s_age < r_age THEN                 {cross-section responder}
        ageo[cid] = 0
        agec[cid] = r_age
```

```
    ELSEIF s_age > (r_age + o_len) THEN   {right censored}
      ageo[cid] = r_age + o_len
      agec[cid] = -1
    ELSE
      FOR x = r_age TO o_len STEP obswidth DO
        IF (s_age >= x) AND (s_age < (x + obswidth)) THEN
          ageo[cid] = x
          agec[cid] = x + obswidth
          BREAK
        END  {if}
      END  {for}
    END { if }

  end {for cid}

  { -- now estimate params from the current simulated data}
  MODEL
    SUMMATION j (1, numbobs)
      LN(PDF NORMAL(ageo[j], agec[j])
           PARAM mu LOW=1 HIGH=10  START=3 END
           PARAM sig LOW=0.01 HIGH=5 START=2 END
         END
      )
    END {summation}
  RUN
    FULL THEN
           { -- save parameter estimates}
           savemu[sim] = mu
           savesig[sim] = sig
         END {then}
  END {model}

END {for sim}
{ -- Now do two models: one to tally the mu's and one sig's }
PRINTLN('Finding mean and stdev for mu parameters')
MODEL
  SUMMATION j (1, numbsims)
    LN(PDF NORMAL(savemu[j])
         PARAM mu_mean LOW=1 HIGH=10  START=3 TEST=6.0 END
         PARAM mu_sd LOW=0.0001 HIGH=5  START=2 END
       END {pdf}
    ) {ln}
  END {summation}
RUN
  FULL
      THEN { print out simulation stats}
         PRINTLN('mu mean = ' , mu_mean,
                 ', mu SD = ', mu_sd,
                 ', true = ', sitmean)
         PRINTLN('Absolute bias = ', sitmean - mu_mean,
                 ', % bias = ', 100*mu_mean/sitmean)
         PRINTLN('t test: (param<>0)  t = ', mu_mean/mu_sd)
         PRINTLN('t test: (param=' sitmean, ')  t = ',
                (mu_mean-sitmean)/mu_sd)
       END {then}
end {model}

{ -- Now, collect info for the estimates of sig}
PRINTLN('Finding mean and stdev for sig parameters')
MODEL
  SUMMATION j (1, numbsims)
    LN(PDF NORMAL(savesig[j])
         PARAM sig_mean LOW=0.00001 HIGH=6  START=3 TEST=1.0 END
         PARAM sig_sd LOW = 0.000001 HIGH = 2 START = 0.5 END
       END {pdf}
    ) {ln}
  END {summation}
RUN
  FULL
      THEN { print out simulation stats}
         PRINTLN('sig mean = ' , sig_mean,
```

```
                    ', sig SD = ', sig_sd,
                    ', true = ', sitsd)
            PRINTLN('Absolute bias = ', sitsd - sig_mean,
                    ', % bias = ', 100*sig_mean/sitsd)
            PRINTLN('t test: (param<>0)  t  = ', sig_mean/sig_sd)
            PRINTLN('t test: (param=', sitsd, ') t = ',
                      (sig_mean - sitsd)/sig_sd)
          END {then}
  END {model}

END
```

An even more complicated simulation program

This program simulates repeated datasets, each containing observations of a bilateral morphological trait. The simulation includes the ability to add, for example, a directional size bias. “Noise” of development is superimposed on the underlying trait, and different variances in the noise can be specified for each side.

```
MLE
  { This program simulates Fluctuating Asymmetry data.  It
    creates 200 simulations with 150 subjects each }

  SEED(CLOCKSEED)          { pick a random seed }
  outdir = 'sim\'          { directory where output goes }
  outfilebase = 'sim'      { base name for output file }
  nsims = 200              { Number of simulations to do }
  nsubjects = 150          { Number of subject in each simulation }
  trait_a = 2.688          { Trait mean parameter }
  trait_b = 0.1979         { Trait dispersion parameter }
  da = 0.0                 { this param controls da (AS if prob_AS <> 0) }
  sd_left = 1              { asymmetrical dispersion param }
  sd_right = 1             { asymmetrical diserpsion param }
  prob_AS = 0.0            { da = 0.0; antisymmetry = 0.5 }
  fout:FILE                { the output file }

  FUNCTION drawtrait(dist:INTEGER a:REAL b:REAL):REAL
    { -- draws a random value from the trait distribution
         dist selects the distribution to use }
    IF dist = 1 THEN
      RETURN = QUANTILE NORMAL(RAND) a b END
    ELSEIF dist = 2 THEN
      RETURN = QUANTILE LOGNORMAL(RAND) a b END
    ELSEIF DIST = 3 THEN
      RETURN = QUANTILE EXPONENTIAL(RAND) a END
    ELSE
      WRITELN('Error: dist is invalid')
      HALT
    END {if}
  END  {drawtrait}

  FUNCTION DRAWNOISE(mu:REAL sigma:REAL):REAL
    { -- draws a random developmental noise value }
    RETURN = QUANTILE NORMAL(RAND) mu sigma END
  END {drawnoise}

  PROCEDURE openoutfile(i:INTEGER)
    dig:STRING
    IF NOT DIREXISTS(outdir) THEN
      MKDIR(outdir)
    END  {if}
    IF i < 10 THEN
      dig = '00' + INT2STR(i)
    ELSEIF i < 100 THEN
      dig = '0' + INT2STR(i)
    ELSE
      dig = INT2STR(i)
    END
    OPENWRITE(fout, outdir + outfilebase + '.' + dig)
  END {openoutfile}

  FOR s = 1 TO nsims DO    {create nsims files}
    openoutfile(s)
    FOR j = 1 TO nsubjects DO
      { -- pick the individual's baseline trait}
      size = drawtrait(2, trait_a, trait_b)

      { -- create right and left measures }
      IF RAND > prob_AS THEN
        right = size + drawnoise( da, sd_right)
        left  = size + drawnoise(-da, sd_left)
      ELSE
        left  = size + drawnoise( da, sd_right)
        right = size + drawnoise(-da, sd_left)
      END {if}

      { -- write this observation to the file}
      WRITELN(fout, j, ' ', left, ' ', right)
    END  {for j}
```

```
    CLOSE(fout)
  END {for s}
END  {mle}
```

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