Software Survey Section

Editor's Note: The following Software Descriptions have been
submitted by our readers in response to our call for an open
exchange of information on software programs. They are offered
without review or comment to provide a rapidly published, easily
accessible avenue of communication. Other readers with relevant
software packages are invited to complete and submit a Software
Description Form (found at the end of this section).

Software Package BP-027-S90   Lognormal Survival Analysis

Contributor: John W. Gamel, M.D., University of Louisville, Department
of Ophthalmology, 301 East Muhammad Ali Blvd., Louisville, KY 40292

Brief Description: This program the likelihood of survival from any cause
to be subdivided into two categories: probability of cure, and distribution
of time to death from the cause under study. Although designed specifically
for cancer-related deaths, it could be used to assess any event within a
population where an unknown fraction of the population is not at risk for
the specified event. Intrinsic to this analysis is the assumption that the
distribution of times if lognormally distributed. For each case studied,
numerous predictive measurements are entered into the program. The program
will then determine the degree of correlation between each predictive
covariate and the following parameters: likelihood of cure (C), mean log
survival time (M), and standard deviation log survival time (S). Although
the user must make initial estimates of these parameters, the algorithm
yields a final estimate and standard error, provided convergence is achieved.
Although this model has not been widely applied, a description has recently
been published in the statistical literature. Demonstration disk is
available free of charge.

Potential Users: Biostatisticians studying cancer-related survival.
Fields of Interest: Epidemiology and biostatistics.

** This application program in the area of statistics has been developed for
   HP-9836 in BASIC. It is available on 3-1/2", dual-sided, double-density
   floppy diskette. Required memory is 1-2MB.
** Distributed by contributor.
** User training is required. There is extensive external documentation.
   Source code is available.
** The package is fully operational. Collaboration would be welcomed. It
   has been in use at 1 site for approximately 3 years. The contributor is
   available for user inquiries.

Software Package BP-028-S90   Maximum Likelihood Method
                                    for Fitting Dose Response
                                   Curves to Experimental Data

Contributor: John W. Gamel, M.D., University of Louisville, Department
of Ophthalmology, 301 East Muhammad Ali Blvd., Louisville, KY 40292

Brief Description: This algorithm utilizes the maximum likelihood method
to fit any selected differentiable function to the dose response observed
in an experimental setting. Potential parameters including plating
efficiency and fraction of exposed cells completely resistant to the agent
under study. Given initial estimates derived by the user, the algorithm
will yield final estimates of all parameters as well as the standard error
of these parameters. This method is especially useful for cellular dose
response analysis, allowing maximum likelihood methods to be used for
discriminating among various models.

Potential Users: Cell biologists, former cologists, and toxicologists
Fields of Interest: Cell biology, cancer research.

**   This application program in the area of dose response, bioassay,
     toxicology has been developed for HP-9836 in BASIC. It is available
     on 3-1/2", dual-sided, double-density floppy diskette. Required
     memory is 1-2MB.
**   Distributed by contributor.
**   User training is required. There is extensive external documentation.
     Source code is available.
**   The package is fully operational. Collaboration would be welcomed.
     It has been in use at 1 site for approximately 3 years. The contributor
     is available for user inquiries.

JOURNAL NAME _____ BIOCHEMICAL PHARMACOLOGY _____

P E R G A M O N   P R E S S

SOFTWARE DESCRIPTION FORM

Title of Software Program: _____

_____

Contributor: _____

    Institution: _____

    Address: _____

              _____

             Telephone: _____

Type of program: [ ] Application [ ] Utility [ ] Other _____

Category: _____ (ie., Psychological Assessment,

        statistics, thermodynamics, etc.)

Potential users: _____

Field/s of interest: _____

Developed for (name of computer/s): _____

    in (language/s): _____

    to run under (operating system): _____

    available on: [ ] Floppy diskette   Specify:

        Size _____   Density _____   [ ] Single-sided   [ ] Dual-sided

              [ ] Magnetic Tape   Specify:

        Size _____   Density _____   Character set _____

Hardware required: _____

Memory required: _____   User training required: [ ] Yes   [ ] No

Documentation: [ ] None   [ ] Minimal   [ ] Self-documenting

              [ ] Extensive external documentation

Source code available: [ ] Yes   [ ] No

Stage of development: [ ] Design complete   [ ] Coding complete

                [ ] Fully operational   [ ] Collaboration welcomed

Is program in use?   [ ] Yes   How long? _____   How many sites? _____

                [ ] No

Is the contributor available for user inquiries?:   [ ] Yes   [ ] No

Distributed by: _____

    Cost of program: _____

    Demonstration disk available?   [ ] Yes   Cost: _____

                      [ ] No

Description of what software does (maximum of 200 words):

RETURN COMPLETED FORM TO:

                          Dr. David Stagg
                     Department of Pharmacology
                 Yale University School of Medicine
                         333 Cedar Street
                         P.O. Box 3333
                      New Haven, CT   06510

    Reference number _____
                          (assigned by Editor)

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