SREL - 49
UC - 66e

336

STRESS

(Simulated Toxicant-Related Stress)
Documentation

K.D. Greene, M.C. Newman, and R.H. Jagoe

*University of Georgia
Savannah River Ecology Laboratory
Drawer E
Aiken, SC 29801*

DISCLAIMER

This report was prepared as an account of work sponsored by an agency of the United States Government. Neither the United States Government nor any agency thereof, nor any of their employees, makes any warranty, express or implied, or assumes any legal liability or responsibility for the accuracy, completeness, or usefulness of any information, apparatus, product, or process disclosed, or represents that its use would not infringe privately owned rights. Reference herein to any specific commercial product, process, or service by trade name, trademark, manufacturer, or otherwise does not necessarily constitute or imply its endorsement, recommendation, or favoring by the United States Government or any agency thereof. The views and opinions of authors expressed herein do not necessarily state or reflect those of the United States Government or any agency thereof.

DISTRIBUTION OF THIS DOCUMENT IS UNLIMITED

MASTER

DISCLAIMER

Portions of this document may be illegible in electronic image products. Images are produced from the best available original document.

INTRODUCTION

STResS (Simulated Toxicant-Related Stress) is a program written in DEC FORTRAN v. 6.2. This program can be run either interactively or batch mode. This program is designed to model the effects of toxicant exposure on a simulated population of a specific species, as well as the effects of the toxicant on the demographic and genetic characteristics. The toxic effect on the time-to-death is based on an accelerated failure time model in which the time-to-death depends on size, sex and genotype, toxicant concentration, and frequency and duration of exposure. Sexual, fecundity, and meiotic drive/gametic selection can also be included. Multiple simulations can be run for a user-specified number of gestation periods of user-specified length. The effect of winter can be included, and the exposure duration can be changed once during each simulation, if desired.

INSTRUCTIONS

To run STResS in interactive mode, type RUN STRESS at the prompt. Following the instructions given on the screen, enter the information requested. Data can be entered completely interactively or via a previously entered data file. A previously entered data file can be modified interactively and corrections to a data file can be identified and corrected interactively. (An incorrect data type will cause a fatal error.) Once all the information requested is entered correctly, the simulations will begin running. In interactive mode, the simulations, gestation periods, populations, and median time-to-death are written to the screen as the simulations progress. The program can be terminated at any time by typing [ctrl]Y to interrupt. All outputs are written at the user's request.

To run STResS in batch mode, type SUBMIT STRS at the prompt. The data file must be complete and correct or the program will terminate with errors. If a file is not already created, one can be created by running STResS in interactive mode, saving, interrupting the program, and running Make.exe (type RUN MAKE). However, it is only necessary to run Make if a data file exists for the interactive mode. Following the instructions given on the screen, enter the information requested. Data must be entered via a previously entered data file with the filename STRS.DAT.

STResS is a FORTRAN program designed to model the effects of toxicant exposure on a population of fish. The program can be used to find the effect of the toxicant on the demographic and genetic characteristics of a simulated population. This model incorporates population dynamics specific to mosquitofish (*Gambusia holbrooki*) but could be adapted to describe other species. The toxic effect on the time-to-death is based on an accelerated failure time model in which the time-to-death depends on size, sex and genotype, toxicant concentration, and frequency and duration of exposure. Sexual, fecundity, and meiotic drive/gametic selection can also be included. Multiple simulations can be run for a user-specified number of gestation periods of user-specified length. The effect of winter can be included, and the exposure duration can be changed once during each simulation, if desired.

At the beginning of the program, the data are entered with the aid of the DATA ENTRY module. Counter values are initialized and the maximum population size is set. Next an initial population is generated and the simulation loop is started. The number of males and females in the initial population depends on the user specified sex ratio, and whether the user has designated the reference sex as male or female. The subroutine CREATE assigns characteristics to the initial population. FISH is a two dimensional array, the first element containing ID numbers to identify the individual fish, and the second element containing the eight fish characteristics:

1. sex
2. size (wet weight in milligrams)
3. cumulative survival
4. median time-to-death due to toxicant exposure
5. age
6. natural time-to-death
7. growth rate
8. winter time-to-death

CREATE employs several subroutines. Among these are:

ASSIGNSEX, which randomly assigns a sex to each fish according to the user-specified sex ratio.

WEIGHTS randomly assigns a size to each fish. The user specifies the type of underlying distribution assumed (normal or lognormal), and separate mean weights and standard deviations for males and females.

GROWTH assigns an initial age to each individual in the population. The individual fish's sizes (assigned above) are compared to sizes calculated from the logistic equation (Philippi et al., 1987) in order to determine the individual's age.

$$W_{t+1} = W_t \left[1 + r \left(1 - \left(\frac{W_t}{W_{\max}} \right)^{\text{SHAPE}} \right) \right] \quad (1)$$

where t = timestep (each representing a gestation period of 28 days for mosquitofish)

W_t = the individual's weight at the current timestep

W_{t+1} = the weight at the next timestep
 W_{max} = the user specified maximum allowed weight (different for males and females)
 r = the growth rate assigned by CREATE (different for males and females)
 $SHAPE$ = the user specified shape parameter.

NANDW assigns a time-to-death for each fish based on winter or other natural causes. The equation below (Kennedy and Gentle, 1980) is used to generate a random time-to-death from a Weibull distribution:

$$NATTTD = SCALE[-\ln(1-z)]^{1/\beta} \quad (2)$$

where z is a random number from a normal distribution, and $SCALE$ and β are user-specified scale and shape parameters. There are separate parameters for males and females, and for winter and non-winter.

GROWTHRATE assigns a random growth rate to each fish. The growth rates are assumed to be normally distributed, with separate user-specified means and standard deviations for males and females.

GETGENO assigns genotypes according to user-specified frequencies.

CREATE is also called every time step to assign characteristics to newborn fish and to immigrant fish if applicable.

The subroutine CALC calculates the cumulative survival and median time-to-death of each fish due to toxicant exposure. The approach is based on an accelerated failure time model (Dixon and Newman, 1991, Newman and Aplin, 1992), where the time-to-death due to toxicant exposure is

$$\begin{aligned}
 \log TTD &= \mu + X \cdot \beta + \sigma \cdot \epsilon \\
 TTD &= \exp(\mu + X \cdot \beta + \sigma \cdot \epsilon) \\
 &= \exp(\mu + X \cdot \beta) \exp(\sigma \cdot \epsilon)
 \end{aligned} \quad (3)$$

where: μ = intercept

X = the matrix of covariates (e.g., sex, weight, genotype)

β = a vector of parameters that indicate the effect of X on the hazard (e.g., β_s , β_w , β_g). This is not the same as the β which occurs in Equation 2.

σ = scale factor

ϵ = the assumed error distribution (e.g., normal, exponential, Weibull, log normal, etc.).

The median time-to-death is then

$$MTTD = \exp(\mu + X \cdot \beta) \exp(\sigma \cdot \epsilon_{0.50}) \quad (4)$$

where $\epsilon_{0.50}$ denotes the 50th percentile of the error distribution. For example, for the Weibull distribution, $\epsilon_{0.50} = -0.3665$.

The equation for cumulative mortality depends on the assumed error distribution. For the Weibull distribution, the cumulative mortality is (Pinder, et al., 1978)

$$CUMMORT = \exp(-\alpha t^\gamma) \quad (5)$$

Where $\gamma = 1/\sigma$

$\alpha = [\exp(-\mu + \text{sex} \cdot \beta_s + \text{weight} \cdot \beta_w + \text{genotype} \cdot \beta_g)]/\sigma$

$t = \text{duration of exposure (can be changed once during each simulation, if desired)}$

The fish weights in Equation 5 are assumed to be either normally or log normally distributed. β_w will differ for these two cases. The cumulative survival is

$$CUMSURV = 1 - CUMMORT \quad (6)$$

If multiple insemination and sperm storage occur, the subroutine MALELOC1 assigns male fish to each female. The number of males assigned to each female is between zero and the maximum allowed (an input variable between 1 and 5). The males are partitioned according to the user specified frequencies of occurrence of one male per female, two males per female, etc. The choice of individuals can be influenced by sexual and/or fecundity selection, if desired.

After the initial population has been established, a summary of the input data is generated and the gestation period loop begins. Each iteration, or time step, in this loop represents a gestation period of 28 days (the length of the gestation period can be specified by the user). The population is tested by POPTEST for valid size (at least two fish), and valid number of females (at least one), to continue.

Next the subroutine EXPOSURE is called to simulate toxicant exposure. The cumulative survival (Equation 6) of each fish is compared to a random number. If the cumulative survival is less than that random number, the fish dies. The population is tested for valid size to maintain itself. The subroutine PRINTRESULT is called to print a summary of results. The user specifies what information is to be included.

The subroutine MORTALITY is then called to determine whether a fish dies of natural causes during the current time step. The natural time-to-death (Equation 2) is multiplied by the factor

$$[1 - (\text{LONGEVITY} \cdot \text{PROBABILITY})] \quad (7)$$

where PROBABILITY is the total population divided by the carrying capacity, and LONGEVITY is a parameter was introduced to adjust the longevity. If winter is scheduled to occur in the current gestation period, the winter time-to-death is used in the above calculation. The fish's age is compared to the adjusted natural (or winter) time-to-death to see if the fish will live for one more gestation period. A test is also made to determine if the fish has exceeded the (user specified) maximum number of gestation periods allowed. The population is tested again for valid size to continue.

If winter does not occur during the current gestation period, breeding is then simulated by the subroutine BREEDING. Male fish must exceed a user-specified lower weight limit before they can breed. This limit can be based on genotype, if desired. In the case that multiple insemination does not occur, one male is assigned to each female (there must be at least one male) by MALELOC1. This choice may be completely random or influenced by sexual selection, according to the user's specification.

The subroutine BROODSIZE assigns a maximum brood size to each breeding female and assigns an age to each brood. A linear relationship is assumed between the weight of the mother fish and the maximum possible number of offspring her brood can contain (Mulvey et al., Vondracek et al ,1988).

$$\text{MAXIMUM BROODSIZE} = \text{SLOPE} \cdot \text{WEIGHT} + \text{INTERCEPT} \quad (8)$$

WEIGHT is the mother's weight and SLOPE and INTERCEPT are user-supplied constants. When fecundity selection is included, there will be a separate set of constants for each genotype per locus in which fecundity selection is a factor.

Actual brood sizes are determined in the main program according to population constraints (Taylor, 1990).

$$\text{ACTUAL BROODSIZE} = \text{MAXIMUM BROODSIZE} \left(1 - \frac{\text{BNMPOP}}{K}\right) \quad (9)$$

where BNMPOP is the population size before natural mortality and K is the carrying capacity. The neonate population is the sum of the actual broods of each adult female in the population. If the addition of the new fish causes the population to exceed the maximum size limit, the program terminates.

The fish from the previous gestation period get one gestation period older. If it is not winter, growth is simulated by the subroutine GROWTH. The growth of individual fish is assumed to follow the logistic equation (Equation 1). The surviving fish are added to the fish born during the new gestation period. The new fish are assigned genotypes by SELECTGENO. A random number generator is initiated to choose the first allele of the genotype of each locus from the female and the second allele from a male assigned to that female. In the case of meiotic drive/gametic selection, the frequency of selection of maternal and/or paternal alleles may be specified. Size, sex, age, growth rate and natural times-to-death (Equation 2) are assigned to each new fish by CREATE. Cumulative survival (Equation 6) and median times-to-death due to exposure (Equation 4) are calculated by CALC for the survivors and the neonates.

The subroutine CANN is called to simulate density and size-dependent mortality. A linear relationship is assumed between a fish's size and the probability that it will succumb to size-dependent predation, including cannibalism. For $W > W_{min}$:

$$C = C_{max} + C_{slope} * W \quad (10)$$

where C = the probability of predation

C_{max} = the user-specified maximum probability of density and size-dependent mortality

C_{slope} = the user-specified slope, always negative

W_{min} = the user-specified minimum weight

For $W \leq W_{min}$, $C = C_{max}$. C is then multiplied by the factor POP/K , or the population size divided by the carrying capacity, to incorporate the effect of competition on density and size-dependent mortality. C is compared to a random number to determine whether the fish is dies.

A user-specified number of migrating fish can be added to the population each gestation period (the number of immigrants can be different in winter). CREATE and CALC are called to assign characteristics to the immigrant fish, then they are added to the native population. If multiple insemination and sperm storage occur, MALELOCI is then called to assign male fish to females for the entire population.

The characteristics of each fish are printed if requested by the user. If the simulation has gone through the desired number of gestation periods, a new simulation is started. Otherwise, control passes to the top of the gestation period loop.

The input variables, in the order that they are read in:

NUMLOCI - number of loci

SELECTION - Does Meiotic drive or Gametic selection occur? (T or F)

SSELECTION - Does Sexual selection occur? (T or F)

FSELECTION - Does Fecundity selection occur? (T or F)

MSELECTION - Does the weight limit in mg for which males may begin to breed differ for each genotype of specific locus? (T or F)

LOCILABEL*10 - loci label(s)

NUMGENO - number of genotypes

REFGENO*2 - reference genotypes

WHICHLOCI - Is sexual selection indicated for this locus? (T or F)

FWHICHLOCI - Is fecundity selection indicated for this locus? (T or F)

MWHICHLOCI - Is male breeding weight limit differ per genotype indicated for this locus? (T or F)

SEXCHAR - Is sexual selection for this locus for the Male, Female, or Both? (M or F or B)

GENOTYPE*2 - genotype label(s)

GENOFREQ - genotype frequencies

GENOBETAS - genotype betas

MALLELE1, FALLELE1 - male and female first allele Meiotic drive/Gametic selection frequency

MALLELE2, FALLELE2 - male and female second allele Meiotic drive/Gametic selection frequency

MSEXFREQ, FSEXFREQ - male and female Sexual selection frequency

FUPPERWGT, FLOWERWGT - female's weight limits, of wet mass in mg for brood relation for fecundity selection

FSLOPE - slope coefficient for brood relation for fecundity selection

FINTERCEPT - intercept coefficient for brood relation for fecundity selection

MWGTLMT - male weight limit in mg for breeding

MBETA, FBETA - male and female betas (natural mortality)

MSCALE, FSCALE - male and female scales (natural mortality)
 LONGEVITY - proportional longevity
 MMAXGEN, FMAXGEN - male and female maximum number of gestation periods
 MWBETA, FWBETA - male and female betas (winter natural mortality)
 MWSCALE, FWSCALE - male and female scales (winter natural mortality)
 WW, WD - frequency and duration of winter
 MMEAN, FMEAN, MSD, FSD - male and female mean weights and standard deviations
 PDF - Is the probability density function lognormal? (T or F)
 MMAX, FMAX, MMIN, FMIN - male and female maximum and minimum weights
 MGRM, FGRM, MGRSD, FGRSD - male and female growth rates and standard deviations
 MSHAPE, FSHAPE - male and female size shape factors (individual growth)
 BASE - hazard model intercept
 SCALE - hazard model scale parameter
 DURATION1, DURATION2 - durations of exposure
 GPT - gestation period in which the duration of exposure changes
 SHIFT - the median shift; usually 0.693147; also the median shift is equivalent to $\exp(w)$
 SIZEBETA - size beta
 SEXBETA - sex beta
 FORM - indicates if sizebeta is in the log transform (T or F)
 EXPOSE - frequency of exposure
 K - carrying capacity
 WGTLM T - minimum male weight (breeding)
 CNTLMT - maximum male breeding per gestation period
 UPPERWGT, LOWERWGT - female's weight limits, of wet mass in mg for brood relation
 SLOPE - slope coefficient for brood relation
 INTERCEPT - intercept coefficient for brood relation

MAXC - density and size-dependent mortality coefficient

CSLOPE - slope coefficient (density and size-dependent mortality)

MULTI - Does multiple insemination and sperm storage occur? (T or F)

CMALES - maximum number of males per female

MALEFREQ - frequencies of occurrence for 1 to 5 males per female

REFSEX - reference sex

SEX RATIO - sex ratio

LENGEN - length of gestation period

If Batch routines are used, additional input variables are read in:

INITPOP - number of individuals in the initial population

IMMPOP - number of individuals migrating into the population

WIMMPOP - number of individuals migrating into the population during winter

NUMSIM - number of simulations

NUMGEN - number of gestation periods

GO, GC, MO, MC, PS - output file indicators

NUMOUT - number of gestation periods to output to Gen_Cut.dat or Gen_Out.dat

SELECTOUT - users selection of output to Gen_Cut.dat and/or Gen_Out.dat, random or multiple

SIMNUM, GENNUM - simulation, gestation period to output to Gen_Cut.dat and/or Gen_Out.dat

REFERENCES

- Diamond, S.A., M.C. Newman, M. Mulvey, P.M. Dixon and D. Martinson. 1989. Allozyme genotype and time to death of mosquitofish, *Gambusia affinis* (Baird and Girard), during acute exposure to inorganic mercury. *Environ. Toxicol. and Chem.* 8:613-622.
- Dixon, P.M. and M.C. Newman. 1991. Analyzing toxicity data using statistical models for time-to-death: an introduction. In *Metal Ecotoxicology, Concepts and Applications*. Newman, M.C. and McIntosh, A.W. (Chelsea, MI: Lewis Publishers) pp. 207-242.
- Hernandez-Martich, J.D. and M.H. Smith. 1990. Patterns of genetic variation in eastern mosquitofish (*Gambusia holbrooki* Girard) from the piedmont and coastal plain of three drainages. *Copeia* 1190:619-630.
- Kennedy, W.J., Jr. and J.E. Gentle. 1980. *Statistical Computing*. (New York: Marcel Dekker, Inc.) pp. 211-212.
- Krumholz, L.A. 1948. Reproduction in the western mosquitofish *Gambusia affinis affinis* (Baird and Girard) and its use in mosquito control. *Ecol. Monogr.* 18(1):3-42.
- Mulvey, M. et al. Unpublished data.
- Newman, M.C., S.A. Diamond, M. Mulvey and P. Dixon. 1989. Allozyme and time to death of mosquitofish, *Gambusia affinis* (Baird and Girard) during acute mercury exposure: a comparison of arsenate and inorganic mercury. *Aquat. Toxicol.* 15:141-156.
- Newman, M.C. and M.S. Aplin. 1992. Enhancing toxicity data interpretation and prediction of ecological risk with survival time modeling: an illustration using sodium chloride toxicity to mosquitofish (*Gambusia holbrooki*). *Aquat. Toxicol.* 23: 85-96.
- Philippi, T.E., M.P. Carpenter, T.J. Case and M.E. Gilpin. 1987. *Drosophila* population dynamics: chaos and extinction. *Ecology* 68:154-159.
- Pinder, J.E. III, J.G. Wiener and M.H. Smith. 1978. The Weibull distribution: a new method of summarizing survivorship data. *Ecology* 59:175-179.
- Taylor, B.E. 1990. Personal communication.
- Vondracek, B., W.A. Wurtsbaugh and J. J. Cech, Jr. 1988. Growth and reproduction of the mosquitofish, *Gambusia affinis*, in relation to temperature and ration level: consequences for life history. *Environ. Biol. Fishes* 21:45-57.

Outline of files and routines for STResS

Main Program - STResS.for

- I. Data_Entry.for
 - Edit_Data
 - Get_Data
 - Cat_One
 - Cat_Two
 - Cat_Three
 - Cat_Four
 - Cat_Five
 - Cat_Six
 - Cat_Seven
 - Cat_Eight
 - Cat_Nine
 - Test_Data
- II. Select.for
 - Select_Output
 - TestResults
- III. IandM.for
 - Random_Gen
 - I_Random
 - Handler
 - Create_Contig
 - Read_Contig
- IV. CreatePop.for
 - Create
 - AssignSex
 - GetGeno
 - GrowthRate
 - NandW
 - Weights
 - Calc
 - Growth
- V. Cause_Death.for
 - Exposure
 - Cann
 - Mortality
- VI. Breeding.for
 - SelectGeno
 - BroodSize
 - CalcBrood_A
 - CalcBrood_B
 - MaleLoc

- VII. Util.for
SwitchFish
PopTest
SortGeno
- VIII. Print_All.for
PrintResult
PrintChar
SummaryOne
SummaryTwo
SortMTTD

PROGRAM :

STress

Simulated Toxicant - Related Stress

WRITTEN BY :

DAWN GREENE

PROGRAM SPECIFICATIONS :

DEC FORTRAN v. 6.2

This program receives the genetics and population data, the number of simulations to be done and the number of gestation periods to be processed for each simulation. A complete list of definitions and ranges for each variable are listed in the tables near the end.

Each simulation uses random number generators to create the characteristics of the initial population. For each gestation period the individuals are exposed to a toxicant (based on the frequency and duration of exposure; however, the duration can be changed once after a user specified number of gestation periods), the survivors are subjected to natural mortality or winter mortality (dependent on the frequency and duration of winter). These survivors are then allowed to breed, grow, and age; however, during winter they do not breed or grow. The population as a whole is subjected to density and size-dependent mortality. Finally, by using the same random process used to create the initial population, a migrating group of a specific number of individuals is created and added to the final population. Thus one gestation period is completed.

Abnormal termination occurs when the population is less than is required for the next step. Also, when the population exceeds the set maximum limit of 20,000 individuals, termination occurs.

PROGRAM DESIGN :

The initial data are received from either a prepared or modified data file, or interactively. When the data are entered interactively, a data file of a given name can then be created. Modifications can be made to the data file once it's entered. These modifications are made interactively. The following is entered interactively: number of simulations, number of gestation periods, initial population, migrating population, winter migrating population and the outputs desired.

The simulated initial population is created by randomly selecting and assigning a genotype for each locus (based on the genotype frequency) to each individual, assigning sex to each individual (based on the sex ratio), assigning weight (which is randomly calculated according to sex, mean, standard deviation, and pdf) to each individual, assigning an initial age in days, cumulative survival for exposure, median time to death, natural time to death, growth rate, and winter time to death for each individual in the initial population. Each gravid female, determined by female sexual selection, is assigned a brood size, which is linearly related to her weight which may be effected by fecundity selection; and an initial age for her brood is also assigned. If multiple insemination and

sperm storage takes place, adult male(s) of adequate size are selected at random, based on male sexual selection, whose genotypes are assigned to each gravid female with brood size greater than zero in the initial population.

The first gestation period of each simulation, the initial population is exposed to the stressor; otherwise, the current population is exposed according to the frequency of exposure. The survivors are subjected to natural or winter mortality, based on the frequency and duration of winter, every gestation period. If there is no multiple insemination and sperm storage, the genes of one randomly selected adult male are assigned for each gravid female in the current population. Using the percentage of deaths from natural mortality, and the percentage of births possible, the carrying capacity and the sum of the assigned brood sizes, the number of new individuals to be born is calculated. Each individual of this new population of juveniles is assigned genotypes chosen randomly or as affected by meiotic drive/gametic selection, from a female and her assigned male. Each juvenile is assigned an initial weight, in relation to age; and sex, natural time-to-death, winter time-to-death, growth rate, cumulative survival, and median time-to-death during toxicant exposure using the same process as the initial population. The original individuals who survived exposure and mortality are allowed to grow, age, and receive updated cumulative survival and median time-to-death. This surviving population is subjected to density and size-dependent mortality. The migrating populations are created in the same way as the initial population. The dead individual's characteristics are deleted from the current population and the new individual's characteristics are added to the current population and the current population is continually updated. If multiple insemination and sperm storage occur, gravid female(s) are subjected to the process of assigning male genotypes, brood sizes, and brood ages; this process is repeated every gestation period, with the exception of winter gestation periods when new births, individual growth, and sperm storage do not occur.

MODULE SPECIFICATIONS :

MAIN PROGRAM: STResS.For

PURPOSE: The purpose of this program is to initialize counters; call the subroutines required to obtain the initial data, create the initial population, simulate death from exposure to a stressor, natural or winter mortality, simulate breeding, growth, death by density and size-dependent mortality and create a migrating group, maintain the simulation and the gestation period loops, and update the population and its characteristics.

INPUT: See Input Data File Format or the table of definitions at the end.

OUTPUT: In the main program, the current simulation and gestation period being processed, the number of males, and the number of females, the current population, and the median time-to-death for each gestation period is written to the screen. At the user's request, the above mentioned information is written to a file called PT_SN.DAT. Also, at the user's request, the median times to death for 25%, 50%, and 75%, and the population for every gestation period of every simulation, before and after exposure are written to two possible files; one with headings called MTTD_OUT.DAT, the other without headings called MTTD_CUT.DAT. The file produced without headings may be conveniently analyzed with standard statistical software, such as SAS, without editing

NORMAL EXITS: Completes process of all the simulations and gestation periods requested by user.

ERROR CONDITIONS: The population is less than required for the next step.

I. DATA_ENTRY.FOR

SUBROUTINE: EDIT_DATA

PURPOSE: The purpose of this subroutine is to receive the initial data either interactively or from a data file, call the subroutines required to modify, correct or edit the data file (at user request), test each data item for correct form and range, determine the output files needed by the user, and write INIT_OUT.DAT file.

USAGE: CALL EDIT_DATA (parameters)

PARAMETERS: NumLoci, NumGeno, Duration1, Duration2, Expose, K, MShape, FShape, MaxBrood, CMales, GenoBetas, MaleFreq, GenoFreq, SexBeta, SizeBeta, Sexratio, LenGen, MBeta, FBeta, MMax, FMax, MMin, FMin, MGRM, FGRM, MGRSD, FGRSD, MScale, FScale, MMean, FMean, MSD, FSD, LowerWgt, UpperWgt, Intercept, Slope, Base, Scale, PDF, RefSex, LociLabel, GenoType, RefGeno, Multi, ImmPop, InitPop, NumSim, NumGen, Longevity, MMaxGen, FMaxGen, MaxC, CSlope, CntLmt, WgtLmt, FWBeta, FWScale, MWBeta, MWScale, WW, WD, WImmPop, Shift, GPt, Form, Selection, MAllele1, FAllele1, MAllele2, FAllele2, SSelection, WhichLoci, SexChar, MSexFreq, FSXFreq, FLowerWgt, FUpperWgt, FSlope, FIntercept, FMaxBrood, FSelection, FWhichLoci, MSelection, MWhichLoci, MWgtLmt

NORMAL EXITS: All data items, either read in from a data file or entered interactively, are within the appropriate ranges and of the correct form.

ERROR CONDITIONS: A data item is not within the appropriate ranges or it is not listed as the correct type. The first will produce an error message and the user is allowed to correct the error interactively. The other will terminate the program abruptly and a systems error message will appear on the screen.

SUBROUTINE: GET_DATA

PURPOSE: The purpose of this routine is to allow the user to modify or correct the previously entered file, or to edit a file interactively.

USAGE: CALL GET_DATA (parameters)

PARAMETERS: Ch, Errs, ErrorNum, GenoError, FreqError, BetaError, RefError, NumLoci, NumGeno, Duration1, Duration2, Expose, K, MShape, FShape, CMales, GenoBetas, MaleFreq, GenoFreq, SexBeta, SizeBeta, SexRatio, LenGen, MBeta, FBeta, MWBeta, FWBeta, MWScale, FWScale, WW, MMax, FMax, MMin, FMin, MGRM, FGRM, MGRSD, FGRSD, MScale, FScale, MaxC, CSlope, WgtLmt, CntLmt, MMean, FMean, MSD, FSD, LowerWgt, UpperWgt, Intercept, Slope, Base, Scale, PDF, RefSex, LociLabel, GenoType, RefGeno, Multi, Longevity, MMaxGen, FMaxGen, WD, GPt, Shift, Form, Selection, MAllele1, FAllele1, MAllele2, FAllele2, SSelection, WhichLoci, SexChar, MSexFreq, FSXFreq, FLowerWgt, FUpperWgt, FSlope, FIntercept, FMaxBrood, FSelection, FWhichLoci, MSelection, MWhichLoci, MWgtLmt

NORMAL EXITS: All data items, changes, or corrections required are successful, within their respective ranges, and any errors found are reported to the user to be corrected.

ERROR CONDITIONS: If a data item is not the correct type, then the program will terminate abruptly and a system's error message is written to the screen. Also, if there is an error when writing the new data to the data file, the program will terminate, the data file may be destroyed, and a system's error message will be written to

the screen.

SUBROUTINE: CAT_ONE

PURPOSE: The purpose of this routine is to prompt the user and accept data interactively for modification or correction of the genotype and loci information. In the case of meiotic drive/gametic selection, it prompts the user and accepts the required data. This is also true in the case of sexual selection, fecundity selection, and male weight selection.

USAGE: CALL CAT_ONE (parameters)

PARAMETERS: Ch, NumLoci, NumGeno, GenoBetas, GenoFreq, LociLabel, GenoType, RefGeno, Selection, MAllele1, FAllele1, MAllele2, FAllele2, SSelection, WhichLoci, SexChar, MSexFreq, FSexFreq, FLowerWgt, FUpperWgt, FSlope, FIntercept, FMaxBrood, FSelection, FWhichLoci, MSelection, MWhichLoci, MWgtLmt

NORMAL EXITS: All data items requested are received and accepted.

ERROR CONDITIONS: If a data item is not the correct data type, then the program will terminate abruptly and a system's error message is written to the screen.

SUBROUTINE: CAT_TWO

PURPOSE: The purpose of this routine is to prompt the user and accept data interactively for modification, correction, or interactive data entry of the natural mortality factors.

USAGE: CALL CAT_TWO (parameters)

PARAMETERS: Ch, MBeta, FBeta, MScale, FScale, Longevity, MMaxGen, FMaxGen

NORMAL EXITS: All data items requested are received and accepted.

ERROR CONDITIONS: If a data item is not the correct data type, then the program will terminate abruptly and a system's error message is written to the screen.

SUBROUTINE: CAT_THREE

PURPOSE: The purpose of this routine is to prompt the user and accept data interactively for modification, correction, or interactive data entry of the winter mortality factors.

USAGE: CALL CAT_THREE (parameters)

PARAMETERS: Ch, MWBeta, FWBeta, MWScale, FWScale, WW, WD

NORMAL EXITS: All data items requested are received and accepted.

ERROR CONDITIONS: If a data item is not the correct data type, then the program will terminate abruptly and a system's error message is written to the screen.

SUBROUTINE: CAT_FOUR

PURPOSE: The purpose of this routine is to prompt the user and accept data interactively for modification, correction, or interactive data entry of the growth and size factors.

USAGE: CALL CAT_FOUR (parameters)

PARAMETERS: Ch, MMean, FMean, MSD, FSD, PDF, FGRM, MGRM, FGRSD, MGRSD, FMax, MMax, FMin, MMin, FShape, MShape

NORMAL EXITS: All data items requested are received and accepted.

ERROR CONDITIONS: If a data item is not the correct data type, then the program will terminate abruptly and a system's error message is written to the screen.

SUBROUTINE: CAT_FIVE

PURPOSE: The purpose of this routine is to prompt the user and accept data interactively for modification, correction, or interactive data entry of the exposure coefficients.

USAGE: CALL CAT_FIVE (parameters)

PARAMETERS: Ch, Base, Scale, Duration1, Duration2, GPt, Shift, SexBeta, SizeBeta, Form, Expose

NORMAL EXITS: All data items requested are received and accepted.

ERROR CONDITIONS: If a data item is not the correct data type, then the program will terminate abruptly and a system's error message is written to the screen.

SUBROUTINE: CAT_SIX

PURPOSE: The purpose of this routine is to prompt the user and accept data interactively for modification, correction, or interactive data entry of the breeding and brood relation coefficients. However, in the case of fecundity selection, the brood relation coefficients are accepted in CAT_ONE and only the breeding coefficients are required. Also, in the case of male weight selection, the weight limit for males to begin to breed is accepted in CAT_ONE.

USAGE: CALL CAT_SIX (parameters)

PARAMETERS: Ch, K, UpperWgt, LowerWgt, Slope, Intercept, WgtLmt, CntLmt, FSelection, MSelection

NORMAL EXITS: All data items requested are received and accepted.

ERROR CONDITIONS: If a data item is not the correct data type, then the program will terminate abruptly and a system's error message is written to the screen.

SUBROUTINE: CAT_SEVEN

PURPOSE: The purpose of this routine is to prompt the user and accept data interactively for modification, correction, or interactive data entry of the density and size-dependent mortality coefficients.

USAGE: CALL CAT_SEVEN (parameters)

PARAMETERS: Ch, MaxC, CSlope

NORMAL EXITS: All data items requested are received and accepted.

ERROR CONDITIONS: If a data item is not the correct data type, then the program will terminate abruptly and a system's error message is written to the screen.

SUBROUTINE: CAT_EIGHT

PURPOSE: The purpose of this routine is to prompt the user and accept data interactively for modification, correction, or interactive data entry of the multiple insemination and sperm storage related information.

USAGE: CALL CAT_EIGHT (parameters)

PARAMETERS: Ch, Multi, CMales, MaleFreq

NORMAL EXITS: All data items requested are received and accepted.

ERROR CONDITIONS: If a data item is not the correct data type, then the program will terminate abruptly and a system's error message is written to the screen.

SUBROUTINE: CAT_NINE

PURPOSE: The purpose of this routine is to prompt the user and accept data interactively for modification, correction, or interactive data entry of the reference sex, the sex ratio, and the length of a gestation period.

USAGE: CALL CAT_NINE (parameters)

PARAMETERS: Ch, RefSex, SexRatio, LenGen

NORMAL EXITS: All data items requested are received and accepted.

ERROR CONDITIONS: If a data item is not the correct data type, then the program will terminate abruptly and a system's error message is written to the screen.

SUBROUTINE: TEST_DATA

PURPOSE: The purpose of this routine is to test each data item received either from a data file or interactive entry for a given range and return any errors to the EDIT_DATA.

USAGE: CALL TEST_DATA (parameters)

PARAMETERS: NumLoci, NumGeno, Duration1, Duration2, Expose, K, MShape, FShape, CMales, GenoBetas, MaleFreq, GenoFreq, SexBeta, SizeBeta, SexRatio, LenGen, MBeta, FBeta, MWBeta, FWBeta, MWScale, FWScale, WW, MMax, FMax, MMin, FMin, MGRM, FGRM, MGRSD, FGRSD, MScale, FScale, MaxC, CSlope, WgtLmt, CntLmt, MMean, FMean, MSD, FSD, LowerWgt, UpperWgt, Intercept, Slope, Base, Scale, PDF, RefSex, LociLabel, GenoType, RefGeno, Multi, Longevity, MMaxGen, FMaxGen, WD, GPt, Shift, Form, Ch, Selection, MAllele1, FAllele1, MAllele2, FAllele2, Errs, ErrorNum, GenoError, FreqError, BetaError, RefError, AlleleError, SSelection, WhichLoci, SexChar, MSexFreq, FSexFreq, SexError, FecError, FLowerWgt, FUpperWgt, FSlope, FIntercept, FMaxBrood, FSelection, FWhichLoci, MSelection, MWhichLoci, MWgtLmt

NORMAL EXITS: All data items are within their respective ranges and the errors found are reported to the user to be corrected.

ERROR CONDITIONS: If a data item is not the correct type, then the program will terminate abruptly and a system's error message is written to the screen.

II. SELECT.FOR

SUBROUTINE: SELECT_OUTPUT

PURPOSE: This routine writes a menu of output files and their descriptions to the screen. The user is allowed to select the specific output files needed and the specific simulation and gestation periods for GEN_OUT.DAT and/or GEN_CUT.DAT.

USAGE: CALL SELECT_OUTPUT (parameters)

PARAMETERS: NumSim, NumGen, GO, GC, PS, MO, MC, N, Results

NORMAL EXITS: The user has selected the output files and simulations and gestation periods needed.

ERROR CONDITIONS: If the first number entered here is not the exact number of output files the user requests or if this number or any of the output file id numbers are not within their range, then an error message is written to the screen and the user is allowed to make corrections.

SUBROUTINE: TEST_RESULTS

PURPOSE: This routine is used only if the GEN_OUT or the GEN_CUT file is requested by the user. The simulations and gestation periods required for these files are tested and put in ascending order.

USAGE: CALL TESTRESULTS (parameters)

PARAMETERS: N, Results

NORMAL EXITS: The data are data type integer and within the respective ranges.

ERROR CONDITIONS: If the above condition is not true, then an error message is written to the screen and user is allowed to make corrections.

III. IANDM.FOR

SUBROUTINE: RANDOM_GEN

REFERENCE: IMSL User's Manual, Stat/Library
Vol. 3, Ch. 16 - 20, Version 1.0, April 1987
18.2 Basic Uniform Generators, pg. 963+

PURPOSE: Generates pseudorandom numbers from a uniform (0,1) distribution. The routine RNOPT is used to select the form of the generator. (This routine actually contains four pseudorandom number generators; a normal distribution, a log normal distribution, and two uniform distributions.)

USAGE: CALL RANDOM_GEN (parameters)

PARAMETERS: NR, Mean, SD, Code, R

EXTERNALS: RNOPT, RNSET, RNUN, UMACH, RNNOR, SSCAL, SADD, RNLNL, RNUNF

NORMAL EXITS: All requested random numbers are generated.

ERROR CONDITIONS: The number of random numbers to be generated must be greater than or equal to 1.

SUBROUTINE: I_RANDOM

REFERENCE: IMSL User's Manual, Stat/Library
Vol. 3, Ch. 16 - 20, Version 1.0, April 1987
18.2 Basic Uniform Generators, pg. 963+

PURPOSE: Generates pseudorandom numbers from a uniform (1, K) distribution. (K being any integer.) The routine RNOPT is used to select the form of the generator.

USAGE: CALL I_RANDOM (parameters)

PARAMETERS: NR, IR, K

EXTERNALS: RNOPT, RNSET, RNUN, UMACH

NORMAL EXITS: All requested random numbers are generated.

ERROR CONDITIONS: The number of random numbers to be generated must be greater than or equal to 1.

SUBROUTINE: HANDLER

REFERENCE: Condition - Handling Facilities, 9-17
Vax Fortran users manual

PURPOSE: This routine is a condition handler for system service failures.

USAGE: INTEGER*4 FUNCTION HANDLER (SIGARGS, MECHARGS)

PARAMETERS: INTEGER*4 SIGARGS(*), MECHARGS(5)
INCLUDE '\$SSDEF'
INCLUDE '\$MTHDEF'

NORMAL EXITS: System service failures are corrected.

SUBROUTINE: CREATE_CONTIG

REFERENCE: Using VMS Record Management Services, 7-5
Vax Fortran Users Manual

PURPOSE: USEROPEN routine to set block I/O bit and create the block I/O file.

USAGE: INTEGER FUNCTION CREATE_CONTIG (FAB, RAB, LUN)

PARAMETERS: INCLUDE '\$FABDEF'
INCLUDE '\$RABDEF'
INCLUDE '\$SYSSRVNAM'
RECORD /FABDEF/FAB, /RABDEF/RAB

NORMAL EXITS: File is created and opened.

ERROR CONDITIONS: The above conditions are not true, then the program terminates and a systems error message appears on the screen.

SUBROUTINE: READ_CONTIG

REFERENCE: Using VMS Record Management Services, 7-5
Vax Fortran Users Manual

PURPOSE: USEROPEN routine to set block I/O bit and open the block I/O file for reading.

USAGE: INTEGER FUNCTION READ_CONTIG (FAB, RAB, LUN)

PARAMETERS: INTEGER LUN
 INCLUDE '\$FABDEF'
 INCLUDE '\$RABDEF'
 INCLUDE '\$SYSSRVNAM'
 RECORD /FABDEF/ FAB, /RABDEF/ RAB

NORMAL EXITS: File is found and opened for reading.

ERROR CONDITIONS: The above conditions are not true, then the program terminates and a systems error message appears on the screen.

IV. CREATEPOP.FOR

SUBROUTINE: CREATE

PURPOSE: This routine randomly selects and assigns a genotype for each locus, sex, weights, growth rates, age, natural and winter time-to-death to each individual in the initial population or the migrating populations. Also this routine assigns sex, weights, growth rates, natural, and winter time-to-death to each individual in the new population of juveniles.

USAGE: CALL CREATE (parameters)

PARAMETERS: S, ID, Tot, NumLoci, NumGeno, GenoFreq, GenoType, FishGeno, FTot, RefSex, FMean, FSD, MMean, MSD, PDF, FMin, FMax, MMin, MMax, FGRM, FGRSD, MGRM, MGRSD, LenGen, FMaxGen, MMaxGen, FShape, MShape, FBeta, MBeta, FScale, MScale, FWBeta, FWScale, MWBeta, MWScale, Fish, ErrorCode

NORMAL EXITS: The required characteristics are assigned to each individual in the initial population, the migrating populations or the new population.

SUBROUTINE: ASSIGNSEX

PURPOSE: This routine assigns a sex, based on the sexratio, to each individual of either the initial population, the migrating populations, or the new population.

USAGE: CALL ASSIGNSEX (parameters)

PARAMETERS: I, Pop, Q, RefSex, Fish

NORMAL EXITS: A sex value is assigned to each individual in the initial population, the migrating populations, or the new population.

SUBROUTINE: GETGENO

PURPOSE: This routine randomly selects and assigns a genotype for each locus, based on it's frequency, to each individual in the initial population or the migrating populations.

USAGE: CALL GETGENO (parameters)

PARAMETERS: I, InitPop, NumLoci, NumGeno, GenoFreq, GenoType, FishGeno

NORMAL EXITS: One genotype for each locus is selected and assigned to each individual in the initial population or in the migrating populations.

SUBROUTINE: GROWTHRATE

PURPOSE: This routine assigns a growth rate to each individual in either the initial population, the migrating populations or the new population. A random number generator is called to determine the growth rate to be assigned. This random number is based on the male or female growth rate means and standard deviations.

USAGE: CALL GROWTHRATE (parameters)

PARAMETERS: I, Pop, Mean, SD, Fish

NORMAL EXITS: Each individual has been assigned a growth rate.

SUBROUTINE: NANDW

PURPOSE: The purpose of this routine is to determine natural and winter time-to-death for each individual of either the initial population, the migrating populations, or the new population. A random number generator is used to chose normally distributed random numbers which are calculated with scale and beta coefficients to determine the natural and winter times to death.

USAGE: CALL NANDW (parameters)

PARAMETERS: MB, FB, MS, FS, J, Fish, FPop, Pop, ID

NORMAL EXITS: Each individual is assigned a natural and winter times to death.

SUBROUTINE: WEIGHTS

PURPOSE: This program assigns randomly chosen weights to each individual in either the initial population, the migrating populations or the new population. This process, based on the PDF, chooses a random number generator which randomly chooses its weight in mg of wet mass.

USAGE: CALL WEIGHTS (parameters)

PARAMETERS: InitPop, Pop, Mean, SD, PDF, Min, Max, I, Fish

NORMAL EXITS: Each individual is assigned a reasonable size and is returned to the main program.

SUBROUTINE: CALC

PURPOSE: The purpose of this routine is to calculate and assign the Cumulative Survival and the Median Time-to-death due to exposure to a stressor to each individual. This routine also calculates the individual's own betas. **NOTES:** Shift = exp (W). Also, if FishGeno is equal to the RefGeno then its GenoBeta is treated as equaling zero when determining the sum for the XBeta for calculating the Cumulative Survival and the Median Time-to-death.

USAGE: CALL CALC (parameters)

PARAMETERS: Pop, P, NumLoc, NumGeno, FishGeno, GenoType, RefGeno, GenoBetas, SexBeta, SizeBeta, Base, Scale, Duration, Shift, Form, Fish

NORMAL EXITS: All individuals are assigned cumulative survival rates and median times to death.

SUBROUTINE: GROWTH

PURPOSE: This routine uses the growth rate, shape, and the individual's current weight to calculate a new weight for each individual, allowing each to grow. Also, this routine calculates the age of each individual in the initial or the migrating populations, based on the individual's weight.

USAGE: CALL GROWTH (parameters)

PARAMETERS: Flag, Pop, FPop, I, LenGen, FMaxGen, MMaxGen, FMin, MMin, FMax, MMax, FShape, MShape, Fish

NORMAL EXITS: Each individual is given a new weight or assigned an initial age.

V. CAUSE_DEATH.FOR

SUBROUTINE: EXPOSURE

PURPOSE: This routine simulates death due to exposure to a stressor. A random number generator is used to find a number to compare with the individual's cumulative survival rate.

USAGE: CALL EXPOSURE (parameters)

PARAMETERS: NumLoc, Pop, FPop, Male, Fish, FishGeno, Brood, BAg, Assign

NORMAL EXITS: Each individual is tested, its survival is determined, and all survivors are replaced in the array.

SUBROUTINE: CANN

PURPOSE: This routine simulates death due to density and size-dependent mortality. A random number generator is used to find a number to compare with an individual's calculated C to determine if that individual lives or dies.

USAGE: CALL CANN (parameters)

PARAMETERS: Pop, ANMPop, FPop, K, MaxC, CSlope, FMin, MMin, Fish, Assign, Male, Brood, Bages, FishGeno

NORMAL EXITS: Each individual is tested, its survival is determined, and all survivors are replaced in the array.

SUBROUTINE: MORTALITY

PURPOSE: This routine simulates death due to natural causes or natural causes during winter. This is done by testing age and natural time-to-death. If the length of a gestation period plus the natural time to death multiplied by one minus longevity multiplied by population divided by carrying capacity is greater than the age then the individual dies.

USAGE: CALL MORTALITY (parameters)

PARAMETERS: X, NumLoci, LenGen, Pop, FPop, K, Longevity, FMaxGen, MMaxGen, Brood, Bages, Fish, FishGeno, Assign, Male

NORMAL EXITS: Each individual is tested, its survival is determined and all survivors are replaced in the array.

VI. BREEDING.FOR

SUBROUTINE: SELECTGENO

PURPOSE: The purpose of this routine is to assign genotypes to each individual in the new population. A random number generator is initiated to chose the first portion of a genotype of each locus from the female and the second portion of that genotype from a male whose genotypes have been assigned to that female. This genotype selection may be affected by Meiotic drive/Gametic selection.

USAGE: SELECTGENO (parameters)

PARAMETERS: NewPop, FPop, Brood, Bages, NumLoci, CMales, FishGeno, Assign, Male, Multi, NewFish, NewGeno, Selection, MAllele1, FAllele1, MAllele2, FAllele2, ErrorCode

NORMAL EXITS: All individuals in the new population is assigned one genotype for each locus.

ERROR CONDITIONS: The new population exceeds the total number possible for all broods.

SUBROUTINE: BROODSIZE

REFERENCE: "GROWTH AND REPRODUCTION OF THE MOSQUITOFISH, GAMBUSIA AFFINIS, IN RELATION TO TEMPERATURE AND RATION LEVEL: CONSEQUENCES FOR LIFE HISTORY"
BY BRUCE VONDRACEK, WAYNE A. WURTSBAUGH, AND JOSEPH J. CECHE, JR.
ENVIRONMENTAL BIOLOGY OF FISHES, VOL. 21, NO. 1, PP. 45 - 57, 1988

PURPOSE: This routine uses the relation of female weight in mg of wet mass to brood size and assigns a brood size to each gravid female. Also, an age between 0 days and length of the gestation period is assigned to each gravid female, this age is given to each individual in her brood. Sexual selection and fecundity selection determines the chances for a female to be gravid. In the case that she is not gravid, then she does not receive a brood size.

USAGE: CALL BROODSIZE (parameters)

PARAMETERS: FPop, LenGen, Fish, LowerWgt, UpperWgt, MaxBrood, Slope, Intercept, BAgess, Brood, SSelection, WhichLocs, SexChar, FSexFreq, GenoType, NumLocs, NumGeno, FLowerWgt, FUpperWgt, FSlope, FIntercept, FMaxBrood, FSelection, FWhichLocs

NORMAL EXITS: All gravid females are assigned a brood size and age.

SUBROUTINE: CALCBROOD_A

PURPOSE: This routine, which is called by BROODSIZE, uses the relation of female weight in mg of wet mass to broodsize and assigns a brood size to each gravid female. Also, an age between 0 days and length of the gestation period is assigned to each gravid female, this age is given to each individual in her brood. Fecundity selection determine the chances for a female to be gravid. In the case that she is not gravid, then she does not receive a brood size.

USAGE: CALL CALCBROOD_A (parameters)

PARAMETERS: Id, Fish, BAgess, Brood, GenoType, NumLocs, NumGeno, FLowerWgt, FUpperWgt, FSlope, FIntercept, FMaxBrood, FWhichLocs

NORMAL EXITS: All gravid females are assigned a brood size.

SUBROUTINE: CALCBROOD_B

PURPOSE: This routine, which is called by BROODSIZE, uses the relation of female weight in mg of wet mass to brood size and assigns a brood size to each gravid female. Also, an age between 0 days and length of the gestation period is assigned to each gravid female, this age is given to each individual in her brood.

USAGE: CALL CALCBROOD_B (parameters)

PARAMETERS: Id, Fish, LowerWgt, UpperWgt, MaxBrood, Slope, Intercept, BAgess, Brood

NORMAL EXITS: All gravid females are assigned a brood size.

SUBROUTINE: MALELOCI

PURPOSE: This routine randomly selects an adult male or males, determined by sexual selection, from the whole population and assigns that male's genotypes to a given gravid female. This is done every gestation period for every gravid female. This routine calls BROODSIZE first to determine whether or not the female is gravid.

USAGE: CALL MALELOCI (parameters)

PARAMETERS: Multi, CntLmt, WgtLmt, MaleFreq, CMales, Pop, FPop, NumLoci, FishGeno, Fish, LenGen, LowerWgt, UpperWgt, Slope, Intercept, BAgess, Brood, Male, Assign, Availability, SSelection, WhichLoci, SexChar, MSexFreq, FSexFreq, FLowerWgt, FUpperWgt, FSlope, FIntercept, FMaxBrood, FSelection, FWhichLoci, MSelection, MWhichLoci, MWgtLmt

NORMAL EXITS: All gravid females are assigned male genotypes.

VII. UTIL.FOR

SUBROUTINE: SWITCHFISH

PURPOSE: This routine switches the individual's characteristics from the temporary arrays to the original arrays.

USAGE: CALL SWITCHFISH (parameters)

PARAMETERS: Pop, NewFish, NumLoci, NewGeno, FPop, NewMale, NewAssign, Fish, FishGeno, Male, Assign

NORMAL EXITS: The arrays are successfully transferred.

SUBROUTINE: POPTEST

PURPOSE: The purpose of this routine is to test the male and the female populations, and the population as a whole for valid amounts of individuals to continue the simulation.

USAGE: CALL POPTEST (parameters)

PARAMETERS: Pop, FPop, Multi, PS, ErrorFound

NORMAL EXITS: The populations are valid.

ERROR CONDITIONS: The populations are below the valid limits; in which, a message is written to the screen and the error found indicator returns to the main program.

SUBROUTINE: SORTGENOS

PURPOSE: The purpose for this routine is to put the brood relation coefficients for fecundity selection, the sex frequencies for sexual selection, the allele frequencies for meiotic drive/gametic selection, the geno types, betas, and frequencies for each locus in ascending order according to the genotypes' frequency.

USAGE: CALL SORTGENOS (parameters)

PARAMETERS: NumGeno, GenoBetas, GenoFreq, GenoType, Loci, Selection, MAllele1, FAllele1, MAllele2, FAllele2, SSelection, SexChar, MSexFreq, FSexFreq, FLowerWgt, FUpperWgt, FSlope, FIntercept, FMaxBrood, FSelection, MSelection, MWgtLmt

NORMAL EXITS: All the geno types, betas, and frequencies, etc. are correctly sorted in ascending order according to their frequencies.

VIII. PRINT_ALL.FOR

SUBROUTINE: PRINTRESULT

PURPOSE: This routine calls PRINTCHAR to format and write the characteristics of each individual to the specified file as requested. Then the MTTD files are formatted and written, as requested.

USAGE: CALL PRINTRESULT (parameters)

PARAMETERS: GO, GC, MO, MC, PS, Sim, Gen, S, Pop, Fish, FishGeno, NumLoci, NumGeno, GenoType, Multi, FPop, Male, Assign, LociLabel, Results, X, PageNum, Winter

NORMAL EXITS: The characteristics of each individual are written to the specified file.

SUBROUTINE: PRINTCHAR

PURPOSE: This routine formats and writes the characteristics of each individual to the specified file.

USAGE: CALL PRINTCHAR (parameters)

PARAMETERS: GO, GC, Sim, Gen, String, Ch, Ch2, Pop, Fish, FishGeno, NumLoci, NumGeno, GenoType, Multi, FPop, Male, Assign, LociLabel, Results, X, PageNum, Winter

NORMAL EXITS: The characteristics of each individual are written to the specified file.

SUBROUTINE: SUMMARYONE

PURPOSE: This routine is called by PRINTCHAR to sort and to determine the median weights (mg) of the female population and of the male population.

USAGE: CALL SUMMARYONE (parameters)

PARAMETERS: Pop, FPop, Fish, Wgts

NORMAL EXITS: The 25%, 50%, and 75% medians of weight for sex are returned to PRINTCHAR.

SUBROUTINE: SUMMARYTWO

PURPOSE: This routine is called by PRINTCHAR to find the genotype frequencies for each locus for the current population.

USAGE: CALL SUMMARYTWO (parameters)

PARAMETERS: NumGeno, NumLoci, Pop, FishGeno, GenoType, Freq

NORMAL EXITS: The frequencies are found and returned to PRINTCHAR.

SUBROUTINE: SORTMTTD

PURPOSE: This routine sorts the Median Times To Death of each individual and determines the 25%, 50%, and 75% medians and returns these values to the main program.

USAGE: CALL SORTMTTD (parameters)

PARAMETERS: Fish, Pop, MTTD

NORMAL EXITS: The values above are found and returned.

Outline of files and routines for STRS (Batch routines)

Satellite Program - STRS.com

Main Program - STRS.for

- I. STRS_Data.for
 - Edit_Data
 - Test_Data
 - TestResults
- II. IandM.for
 - Random_Gen
 - I_Random
 - Handler
 - Create_Contig
 - Read_Contig
- III. CreatePop.for
 - Create
 - AssignSex
 - GetGeno
 - GrowthRate
 - NandW
 - Weights
 - Calc
 - Growth
- IV. Cause_Death.for
 - Exposure
 - Cann
 - Mortality
- V. Breeding.for
 - SelectGeno
 - BroodSize
 - CalcBrood_A
 - CalcBrood_B
 - MaleLoci
- VI. STRS_Util.for
 - SwitchFish
 - PopTest
 - SortGeno
- VII. STRS_Print.for
 - PrintResult
 - PrintChar
 - SummaryOne
 - SummaryTwo

SortMTTD

Satellite Program - Make.for

I. Make.for
SelectOutput
TestResults

MODULE SPECIFICATIONS :

MAIN PROGRAM: STRS.Com

PURPOSE: The purpose of this program, a command routine, is to actually preform the batch run of STRS.Exe.

NORMAL EXITS: Completes batch run of STRS.Exe.

ERROR CONDITIONS: Error in data file or batch job is interrupted.

MAIN PROGRAM: STRS.For

PURPOSE: The purpose of this program is to initialize counters; call the subroutines required to obtain the initial data, create the initial population, simulate death from exposure to a stressor, natural or winter mortality, simulate breeding, growth, death by density and size-dependent mortality and create a migrating group, maintain the simulation and the gestation period loops, and update the population and its characteristics.

INPUT: See Input Data File Format or the table of definitions at the end.

OUTPUT: In the main program, at the user's request, the current simulation and gestation period being processed, the number of males, and the number of females, the current population, and the median time-to-death for each gestation period is written to a file called PT_SN.DAT. Also, at the user's request, the median times to death for 25%, 50%, and 75%, and the population for every gestation period of every simulation, before and after exposure are written to two possible files; one with headings called MTTD_OUT.DAT, the other without headings called MTTD_CUT.DAT.

NORMAL EXITS: Completes process of all the simulations and gestation periods requested by user.

ERROR CONDITIONS: The population is less than required for the next step.

I. STRS_DATA.FOR

SUBROUTINE: EDIT_DATA

PURPOSE: The purpose of this subroutine is to receive the initial data from a data file, call the subroutine required to test each data item for correct form and range, and write INIT_OUT.DAT file.

USAGE: CALL EDIT_DATA (parameters)

PARAMETERS: NumLocs, NumGeno, Duration1, Duration2, Expose, K, MShape, FShape, MaxBrood,

CMales, GenoBetas, MaleFreq, GenoFreq, SexBeta, SizeBeta, Sexratio, LenGen, MBeta, FBeta, MMax, FMax, MMin, FMin, MGRM, FGRM, MGRSD, FGRSD, MScale, FScale, MMean, FMean, MSD, FSD, LowerWgt, UpperWgt, Intercept, Slope, Base, Scale, PDF, RefSex, LociLabel, GenoType, RefGeno, Multi, ImmPop, InitPop, NumSim, NumGen, Longevity, MMaxGen, FMaxGen, MaxC, CSlope, CntLmt, WgtLmt, FWBeta, FWScale, MWBeta, MWScale, WW, WD, WImmPop, Shift, GPt, Form, Selection, MAllele1, FAllele1, MAllele2, FAllele2, SSelection, WhichLoci, SexChar, MSexFreq, FSexFreq, FLowerWgt, FUpperWgt, FSlope, FIntercept, FMaxBrood, FSelection, FWhichLoci, MSelection, MWhichLoci, MWgtLmt, GO, GC, MO, MC, PS, N, Results

NORMAL EXITS: All data items read in from a data file are within the appropriate ranges and of the correct form.

ERROR CONDITIONS: A data item is not within the appropriate ranges or it is not listed as the correct type. The first will produce an error message. The other will terminate the program abruptly and a systems error message will appear on the screen.

SUBROUTINE: TEST_DATA

PURPOSE: The purpose of this routine is to test each data item received from a data file and return any errors to the EDIT_DATA.

USAGE: CALL TEST_DATA (parameters)

PARAMETERS: NumLoci, NumGeno, Duration1, Duration2, Expose, K, MShape, FShape, CMales, GenoBetas, MaleFreq, GenoFreq, SexBeta, SizeBeta, SexRatio, LenGen, MBeta, FBeta, MWBeta, FWBeta, MWScale, FWScale, WW, MMax, FMax, MMin, FMin, MGRM, FGRM, MGRSD, FGRSD, MScale, FScale, MaxC, CSlope, WgtLmt, CntLmt, MMean, FMean, MSD, FSD, LowerWgt, UpperWgt, Intercept, Slope, Base, Scale, PDF, RefSex, LociLabel, GenoType, RefGeno, Multi, Longevity, MMaxGen, FMaxGen, WD, GPt, Shift, Form, Ch, Selection, MAllele1, FAllele1, MAllele2, FAllele2, Errs, ErrorNum, GenoError, FreqError, BetaError, RefError, AlleleError, SSelection, WhichLoci, SexChar, MSexFreq, FSexFreq, SexError, FecError, FLowerWgt, FUpperWgt, FSlope, FIntercept, FMaxBrood, FSelection, FWhichLoci, MSelection, MWhichLoci, MWgtLmt

NORMAL EXITS: All data items are within their respective ranges and the errors found are reported to the user to be corrected.

ERROR CONDITIONS: If a data item is not the correct type, then the program will terminate abruptly and a system's error message is written to the screen.

SUBROUTINE: TEST_RESULTS

PURPOSE: This routine is used only if the GEN_OUT or the GEN_CUT file is requested by the user. The simulations and gestation periods required for these files are tested and put in ascending order.

USAGE: CALL TESTRESULTS (parameters)

PARAMETERS: N, Results

NORMAL EXITS: The data are data type integer and within the respective ranges.

ERROR CONDITIONS: If the above condition is not true, then an error message is written to the screen and user is allowed to make corrections.

II. STRS_UTIL.FOR

SUBROUTINE: SWITCHFISH

PURPOSE: This routine switches the individual's characteristics from the temporary arrays to the original arrays.

USAGE: CALL SWITCHFISH (parameters)

PARAMETER: Pop, NewFish, NumLoci, NewGeno, FPop, NewMale, NewAssign, Fish, FishGeno, Male, Assign

NORMAL EXITS: The arrays are successfully transferred.

SUBROUTINE: POPTEST

PURPOSE: The purpose of this routine is to test the male and the female populations, and the population as a whole for valid amounts of individuals to continue the simulation.

USAGE: CALL POPTEST (parameters)

PARAMETERS: Pop, FPop, Multi, PS, ErrorFound

NORMAL EXITS: The populations are valid.

ERROR CONDITIONS: The populations are below the valid limits; in which, a message is written to the file PT_SN.DAT, at user request, and the error found indicator returns to the main program.

SUBROUTINE: SORTGENOS

PURPOSE: The purpose for this routine is to put the brood relation coefficients for fecundity selection, the sex frequencies for sexual selection, the allele frequencies for meiotic drive/gametic selection, the genotypes', betas, and frequencies for each locus in ascending order according to the genotypes' frequency.

USAGE: CALL SORTGENOS (parameters)

PARAMETERS: NumGeno, GenoBetas, GenoFreq, GenoType, Loci, Selection, MAllele1, FAllele1, MAllele2, FAllele2, SSelection, SexChar, MSexFreq, FSexFreq, FLowerWgt, FUpperWgt, FSlope, FIntercept, FMaxBrood, FSelection, MSelection, MWgtLmt

NORMAL EXITS: All the genotypes, betas, and frequencies, etc. are correctly sorted in ascending order

according to their frequencies.

III. STRS_PRINT.FOR

SUBROUTINE: PRINTRESULT

PURPOSE: This routine calls PRINTCHAR to format and write the characteristics of each individual to the specified file as requested. Then the MTTD files are formatted and written, as requested.

USAGE: CALL PRINTRESULT (parameters)

PARAMETERS: GO, GC, MO, MC, PS, Sim, Gen, S, Pop, Fish, FishGeno, NumLoci, NumGeno, GenoType, Multi, FPop, Male, Assign, LociLabel, Results, X, PageNum, Winter

NORMAL EXITS: The characteristics of each individual are written to the specified file.

SUBROUTINE: PRINTCHAR

PURPOSE: This routine formats and writes the characteristics of each individual to the specified file.

USAGE: CALL PRINTCHAR (parameters)

PARAMETERS: GO, GC, Sim, Gen, String, Ch, Ch2, Pop, Fish, FishGeno, NumLoci, NumGeno, GenoType, Multi, FPop, Male, Assign, LociLabel, Results, X, PageNum, Winter

NORMAL EXITS: The characteristics of each individual are written to the specified file.

SUBROUTINE: SUMMARYONE

PURPOSE: This routine is called by PRINTCHAR to sort and to determine the median weights (mg) of the female population and of the male population.

USAGE: CALL SUMMARYONE (parameters)

PARAMETERS: Pop, FPop, Fish, Wgts

NORMAL EXITS: The 25%, 50%, and 75% medians of weight for sex are returned to PRINTCHAR.

SUBROUTINE: SUMMARYTWO

PURPOSE: This routine is called by PRINTCHAR to find the genotype frequencies for each locus for the current population.

USAGE: CALL SUMMARYTWO (parameters)
PARAMETERS: NumGeno, NumLoci, Pop, FishGeno, GenoType, Freq
NORMAL EXITS: The frequencies are found and returned to PRINTCHAR.

SUBROUTINE: SORTMTTD

PURPOSE: This routine sorts the Median Times To Death of each individual and determines the 25%, 50%, and 75% medians and returns these values to the main program.

USAGE: CALL SORTMTTD (parameters)

PARAMETERS: Fish, Pop, MTTD

NORMAL EXITS: The values above are found and returned.

OUTPUT FILES DESCRIPTIONS

GEN_OUT.DAT: This file list the characteristics of each individual in the populations of any gestation period of any simulation. In this file the user is given the simulation and the gestation period numbers, the event (that is Before exposure, After exposure, and Final), the current population, and the current female population. This is followed by a list of all the characteristics if each individual (ID number, sex, size in mg, cumulative survival, median time-to-death, age in days, natural time-to-death, growth rate, the winter time-to-death, and the genotype for each of that individual's loci, and if that individual is female then the genotype for each locus belonging to the male assigned to that female is listed). Once the entire population for an event is listed, a summary is printed for that population. This summary contains the median weights for both males and females, and the frequencies for each genotype in each locus for that specific population.

GEN_CUT.DAT: This file is simply the cut version of GEN_OUT.DAT. However, this file only list simulation and gestation period numbers, the event (B, A, F), the population, ID number, sex, rounded size in mg, rounded median time-to-death, rounded age in days, rounded natural time-to-death, rounded winter time-to-death, and the genotypes for each locus. This file does not contain headings or summaries.

MTTD_OUT.DAT: This file outputs the median time-to-death for the 25%, the 50%, and the 75%, for each event of each gestation period of each simulation.

MTTD_CUT.DAT: This file outputs the rounded median time-to-death for the 25%, the 50%, and the 75%, for each event of each gestation period of each simulation. This file does not contain headings.

PT_SN.DAT: This file outputs simulation and gestation period numbers, event, male population, female population, entire population, 50% median time-to-death, and any messages (what appears on the screen during an interactive run of the program).

MAIN PROGRAM: **MAKE.For**

PURPOSE: The purpose of this program is to create the data file for the batch routines to read. This file is converted from the data file read into the interactive routines.

INPUT: User's data file from interactive routines, and additional data entered interactively to create the new data file. (See Input Data File Format for Batch or the table of definitions at the end.)

OUTPUT: The new data file in the new format.

NORMAL EXITS: Completes process and saves new data file named STRS.DAT.

ERROR CONDITIONS: User's input data file cannot be found or the format of the user's input data file is incorrect.

SUBROUTINE: **SELECTOUTPUT**

PURPOSE: This routine writes a menu of output files and their descriptions to the screen. The user is allowed to select the specific output files needed and the specific simulation and gestation periods for GEN_OUT.DAT and/or GEN_CUT.DAT.

USAGE: **CALL SELECTOUTPUT (parameters)**

PARAMETERS: NumSim, NumGen, GO, GC, PS, MO, MC, N, Results

NORMAL EXITS: The user has selected the output files and simulations and gestation periods needed.

ERROR CONDITIONS: If the first number entered here is not the exact number of output files the user requests or if this number or any of the output file id numbers are not within their range, then an error message is written to the screen and the user is allowed to make corrections.

SUBROUTINE: **TEST_RESULTS**

PURPOSE: This routine is used only if the GEN_OUT or the GEN_CUT file is requested by the user. The simulations and gestation periods required for these files are tested and put in ascending order.

USAGE: **CALL TESTRESULTS (parameters)**

PARAMETERS: N, Results

NORMAL EXITS: The data are data type integer and within the respective ranges.

ERROR CONDITIONS: If the above condition is not true, then an error message is written to the screen and user is allowed to make corrections.

Variable	Description	Where used	Range/format	Reference
BASE	Intercept parameter for accelerated failure time model.	Used in the subroutine CALC. This is μ in Equation 3. Entered manually or via data file.	REAL RANGE (0.000 TO 100.000) FORMAT F11.5	Diamond et al. ,1989
CMALES	The maximum number of males contributing sperm per female when multiple insemination and sperm storage occurs.	Used in the subroutine SELECTGENO. Entered manually or via data file.	INTEGER RANGE (1 TO 5) FORMAT I5	
CNTLMT	Maximum number of females a male can inseminate during each gestation period.	Used in the subroutine SELECTGENO. Entered manually or via data file.	INTEGER RANGE (1 TO 1000) FORMAT I5	
CSLOPE	Slope coefficient for density and size-dependent mortality.	Used in the subroutine CANN. See Equation 10. Entered manually or via data file.	REAL RANGE (-1.000 TO 0.000) FORMAT F11.5	
DURATION1	Initial exposure duration (in hours).	Used in the subroutine CALC. This is t in Equation 5. Entered manually or via data file.	INTEGER RANGE (0 TO 1000 HOURS) FORMAT I5	
DURATION2	Final exposure duration (in hours).	Used in the subroutine CALC. This is t in Equation 5. Entered manually or via data file.	INTEGER RANGE (0 TO 1000 HOURS) FORMAT I5	
EXPOSE	Frequency of exposure (in gestation periods).	Used in the main program. Entered manually or via data file.	INTEGER RANGE (1 TO 5 GESTATION PERIODS) FORMAT I5	
FALLELE1	Probability of selection of first maternal allele (used with meiotic drive/gametic selection).	Used in the subroutine SELECTGENO. Entered manually or via data file.	REAL DIMENSION FALLELE1 (20, 6) RANGE (0.00 TO 1.00) FORMAT F11.5	
FALLELE2	Probability of selection of second maternal allele (used with meiotic drive/gametic selection).	Used in the subroutine SELECTGENO. Entered manually or via data file.	REAL DIMENSION FALLELE2 (20, 6) RANGE (0.00 TO 1.00) FORMAT F11.5	

Variable	Description	Where used	Range/format	Reference
FBETA	Female beta coefficient for natural mortality routine.	Used in the subroutines CREATE and MORTALITY. This is β in Equation 2. Entered manually or via data file.	REAL RANGE (0.000 TO 300.000) FORMAT F11.5	
FGRM	Mean female growth rate.	Used in the subroutine CREATE. Entered manually or via data file.	REAL RANGE (0.000 TO 1.000) FORMAT F11.5	Mulvey et al.
FGRSD	Standard deviation of female growth rate.	Used in the subroutine CREATE. Entered manually or via data file.	REAL RANGE (0.000 TO 1.000) FORMAT F11.5	Mulvey et al.
FINTERCEPT	Intercept parameter for maximum brood size relation with fecundity selection.	Used in the subroutine BROODSIZE. See Equation 8. Entered manually or via data file.	REAL DIMENSION FINTERCEPT (20, 6) RANGE (0.000 TO 100.000) FORMAT F11.5	Mulvey et al.
FLOWERWGT	Female's lower weight limit in mg (wet mass), for brood relation with fecundity selection.	Used in the subroutine BROODSIZE. Entered manually or via data file.	REAL DIMENSION FLOWERWGT(20,6) RANGE (5.000 TO 5000.000 OF WET MASS IN MG) FORMAT F11.5	Mulvey et al.
FMAX	Maximum weight in mg (wet mass), for a female.	Used in the subroutine GROWTH (within CREATEPOP) to assign an age to each individual. This is W_{max} in Equation 1. Entered manually or via data file.	REAL RANGE (0.001 TO 5000.000 MG) FORMAT F11.5	Mulvey et al.
FMAXBROOD	Maximum number of newborns per brood when fecundity selection is in effect.	Used in the subroutine BROODSIZE Calculated in Equation 7, then used in Equation 8.	INTEGER DIMENSION FMAXBROOD (20, 6) RANGE (0 TO 100)	Mulvey et al.
FMAXGEN	Maximum number of gestation periods a female can live.	Used in the subroutines CREATE and MORTALITY. Entered manually or via data file.	INTEGER RANGE (1 TO 30) FORMAT I5	Krumholz, 1948

Variable	Description	Where used	Range/format	Reference
FMEAN	Mean of underlying distribution of size of females.	Used in the subroutine WEIGHTS (within CREATEPOP) to assign a size to each individual. Entered manually or via data file.	REAL RANGE (0.001 TO 5.000) FORMAT F11.5	Mulvey et al.
FMIN	Minimum weight in mg (wet mass), for a female.	Used in the subroutine CREATE. Entered manually or via data file.	REAL RANGE (0.001 TO 5000.000 MG) FORMAT F11.5	Mulvey et al.
FORM	Indicates whether the fish weights and β_w have been log transformed.	Used in the subroutine CALC. Entered manually or via data file.	LOGICAL RANGE ('T' OR 'F') FORMAT L	
FSCALE	Female scale coefficient for natural mortality routine.	Used in the subroutines CREATE and MORTALITY. This is SCALE in Equation 2. Entered manually or via data file.	REAL RANGE (0.000 TO 200.000) FORMAT F11.5	
FSD	Standard deviation of underlying distribution of size of females.	Used in the subroutine WEIGHTS (within CREATEPOP) to assign a size to each individual. Entered manually or via data file.	REAL RANGE (0.001 TO 10.000) FORMAT F11.5	Mulvey et al.
FSELECTION	Indicates whether fecundity selection occurs.	Used in the subroutines MALELOC1 and BROODSIZE. Entered manually or via data file.	LOGICAL RANGE ('T' OR 'F') FORMAT L	
FSEXFREQ	Array of female sexual selection frequencies for each genotype.	Used in the subroutine MALELOC1 and BROODSIZE. Entered manually or via data file.	REAL DIMENSION FSEXFREQ (20, 6) RANGE (0.00 TO 1.00) FORMAT F11.5	
FSHAPE	Female shape parameter for growth routine.	Used in the subroutine CREATE. This is SHAPE in Equation 1. Entered manually or via data file.	REAL RANGE (0.00 TO 6.00) FORMAT F11.5	
FSLOPE	Slope coefficient for maximum brood size relation with fecundity selection.	Used in the subroutine BROODSIZE. See Equation 8. Entered manually or via data file.	REAL DIMENSION FSLOPE (20, 6) RANGE (0.000 TO 1.000) FORMAT F11.5	Mulvey et al.

Variable	Description	Where used	Range/format	Reference
FUPPERWGT	Female's upper weight limit in mg (wet mass), for brood relation with fecundity selection.	Used in the subroutine BROODSIZE. Entered manually or via data file.	REAL DIMENSION FUPPERWGT (20, 6) RANGE (5.000 TO 5000.000 OF WET MASS IN MG) FORMAT F11.5	Mulvey et al.
FWBETA	Female beta coefficient for winter mortality routine.	Used in the subroutines CREATE and MORTALITY. This is β in Equation 2. Entered manually or via data file.	REAL RANGE (0.000 TO 300.000) FORMAT F11.5	
FWHICHLOCI	Indicates whether fecundity selection occurs at each specific locus.	Used in the subroutines MALELOCI and BROODSIZE. Entered manually or via data file.	LOGICAL DIMENSION FWHICHLOCI (20) RANGE ('T' OR 'F') FORMAT L	
FWSCALE	Female scale coefficient for winter mortality routine.	Used in the subroutines CREATE and MORTALITY. This is SCALE in Equation 2. Entered manually or via data file.	REAL RANGE (0.000 TO 200.000) FORMAT F11.5	
GENOBETAS	Array of betas for each genotype.	Used in the subroutine CALC. This is β_g in Equation 3. Entered manually or via data file.	REAL DIMENSION GENOBETAS (20,6) RANGE (0.000 TO 1.000) FORMAT F11.5	Diamond et al., 1989)
GENOFREQ	Array of frequencies of each genotype.	Used in the subroutine GETGENO (within CREATEPOP). Entered manually or via data file.	REAL DIMENSION GENOFREQ (20, 6) RANGE (-10.00 TO 10.00) FORMAT F11.5	Diamond et al., 1989 Hernandez-Martich and Smith, 1990 Newman et al., 1989
GENOTYPE*2	Array of labels for genotypes at each locus.	Used in the subroutines CREATE and CALC. Entered manually or via data file.	CHARACTER DIMENSION GENOTYPE (20, 6) EXAMPLE: '11' FORMAT A	
GPT	The gestation period in which the toxicant exposure duration changes.	Used in the main program. Entered manually or via data file.	INTEGER RANGE (1 TO 10000) FORMAT I5	
IMMPOP	Number of individuals migrating into the population each gestation period.	Used in the main program to simulate migration. Entered manually.	INTEGER RANGE (0 TO 10000)	

Variable	Description	Where used	Range/format	Reference
INITPOP	Number of individuals in the initial simulated population.	Used in the main program to set up the initial population. Entered manually.	INTEGER RANGE (2 TO 10000)	
INTERCEPT	Intercept parameter for maximum brood size relation.	Used in the subroutine BROODSIZE. See Equation 8. Entered manually or via data file.	REAL RANGE (0.000 TO 100.000) FORMAT F11.5	Mulvey et al.
K	The population carrying capacity.	Used in the subroutines SELECTGENO, BROODSIZE, MORTALITY, and CANN. See Equation 9. Entered manually or via data file.	INTEGER RANGE (1 TO 10000) FORMAT I5	
LENGEN	The number of days in one gestation period.	Used in the subroutines CREATE, MORTALITY, BROODSIZE, and GROWTH. Entered manually or via data file.	REAL RANGE (14.000 TO 42.000 DAYS) FORMAT F11.5	Krumholz, 1948
LOCILABEL*10	Array of names for each locus.	Used in output. Entered manually or via data file.	CHARACTER DIMENSION LOCILABEL (20) EXAMPLE: 'ICD-1' FORMAT A	
LONGEVITY	Parameter used in natural mortality calculation.	Used in the subroutine MORTALITY. See Equation 7. Entered manually or via data file.	REAL RANGE (0.0 TO 1.0) FORMAT F11.5	
LOWERWGT	Female's lower weight limit in mg (wet mass) for brood relation.	Used in the subroutine BROODSIZE. Entered manually or via data file.	REAL RANGE (5.000 TO 5000.000 OF WET MASS IN MG) FORMAT F11.5	Mulvey et al.
MALEFREQ	Array of probabilities of each possible number of males inseminating a female.	Used in the subroutine SELECTGENO. Entered manually or via data file.	REAL DIMENSION MALEFREQ (5) RANGE (0.000 TO 1.000) FORMAT F11.5	
MALLELE1	Probability of selection of first paternal allele (used with meiotic drive/gametic selection).	Used in the subroutine SELECTGENO. Entered manually or via data file.	REAL DIMENSION MALLELE1 (20, 6) RANGE (0.00 TO 1.00) FORMAT F11.5	

Variable	Description	Where used	Range/format	Reference
MALLELE2	Probability of selection of second paternal allele (used with meiotic drive/gametic selection).	Used in the subroutine SELECTGENO. Entered manually or via data file.	REAL DIMENSION MALLELE2 (20, 6) RANGE (0.00 TO 1.00) FORMAT F11.5	
MAXBROOD	Maximum number of newborns per brood.	Used in the subroutine BROODSIZE. Calculated in Equation 8, then used in Equation 9.	INTEGER RANGE (0 TO 100)	Mulvey et al.
MAXC	Maximum probability for density and size-dependent mortality.	Used in the subroutine CANN. See Equation 10. Entered manually or via data file.	REAL RANGE (0.000 TO 1.000) FORMAT F11.5	
MBETA	Male beta coefficient for natural mortality routine.	Used in the subroutines CREATE and MORTALITY. This is β in Equation 2. Entered manually or via data file.	REAL RANGE (0.000 TO 300.000) FORMAT F11.5	
MGRM	Mean male growth rate.	Used in the subroutine CREATE. Entered manually or via data file.	REAL RANGE (0.000 TO 1.000) FORMAT F11.5	Mulvey et al.
MGRSD	Standard deviation of male growth rate.	Used in the subroutine CREATE. Entered manually or via data file.	REAL RANGE (0.000 TO 1.000) FORMAT F11.5	Mulvey et al.
MMAX	Maximum weight in mg (wet mass), for a male.	Used in the subroutine GROWTH (within CREATEPOP) to assign an age to each individual. This is W_{max} in Equation 1. Entered manually or via data file.	REAL RANGE (0.001 TO 5000.000 MG) FORMAT F11.5	Mulvey et al.
MMAXGEN	Maximum number of gestation periods a male can live.	Used in the subroutines CREATE and MORTALITY. Entered manually or via data file.	INTEGER RANGE (1 TO 30) FORMAT I5	Krumholz, 1948
MMEAN	Mean of underlying distribution of size of males.	Used in the subroutine WEIGHTS (within CREATEPOP) to assign a size to each individual. Entered manually or via data file.	REAL RANGE (0.001 TO 5.000) FORMAT F11.5	Mulvey et al.

Variable	Description	Where used	Range/format	Reference
MMIN	Minimum weight in mg (wet mass), for a male.	Used in the subroutine CREATE. Entered manually or via data file.	REAL RANGE (0.001 TO 5000.000 MG) FORMAT F11.5	Mulvey et al.
MSCALE	Male scale coefficient for natural mortality routine.	Used in the subroutines CREATE and MORTALITY. This is SCALE in Equation 2. Entered manually or via data file.	REAL RANGE (0.000 TO 200.000) FORMAT F11.5	
MSD	Standard deviation of underlying distribution of size of males.	Used in the subroutine WEIGHTS (within CREATEPOP) to assign a size to each individual. Entered manually or via data file.	REAL RANGE (0.001 TO 10.000) FORMAT F11.5	Mulvey et al.
MSELECTION	Indicates whether male weight limit selection occurs.	Used in the subroutines MALELOCI . Entered manually or via data file.	LOGICAL RANGE ('T' OR 'F') FORMAT L	
MSEXFREQ	Array of male sexual selection frequencies for each genotype.	Used in the subroutine MALELOCI. Entered manually or via data file.	REAL DIMENSION MSEXFREQ (20, 6) RANGE (0.00 TO 1.00) FORMAT F11.5	
MSHAPE	Male shape factor for growth routine.	Used in the subroutine CREATE. This is SHAPE in Equation 1. Entered manually or via data file.	REAL RANGE (0.00 TO 6.00) FORMAT F11.5	
MULTI	Indicates whether multiple insemination and sperm storage occur.	Used in the main program. Entered manually or via data file.	LOGICAL RANGE ('T' OR 'F') FORMAT L	
MWBETA	Male beta coefficient for winter mortality routine.	Used in the subroutines CREATE and MORTALITY. This is β in Equation 2. Entered manually or via data file.	REAL RANGE (0.000 TO 300.000) FORMAT F11.5	
MWGTLMT	Array of male weight limits for each genotype (used with male weight limit selection).	Used in the subroutine MALELOCI. Entered manually or via data file.	REAL DIMENSION MWGTLMT (20, 6) RANGE (0.001 TO 5000.000) FORMAT F11.5	

Variable	Description	Where used	Range/format	Reference
MWHICHLOCI	Indicates whether weight limit selection occurs at each particular male locus.	Used in the subroutines MALELOCI . Entered manually or via data file.	LOGICAL DIMENSION MWHICHLOCI (20) RANGE ('T' OR 'F') FORMAT L	
MWSCALE	Male scale coefficient for winter mortality routine.	Used in the subroutines CREATE and MORTALITY. This is SCALE in Equation 2. Entered manually or via data file.	REAL RANGE (0.000 TO 200.000) FORMAT F11.5	
NUMGEN	The number of gestation periods per simulation	Used in the main program gestation period loop. Entered manually.	INTEGER RANGE (1 TO 10000)	
NUMGENO	The number of genotypes per locus.	Used in the subroutine CREATE. Entered manually or via data file. Also used as a delimiter throughout the program routines.	INTEGER DIMENSION NUMGENO (20) RANGE (3 OR 6) FORMAT I5	
NUMLOCI	The number of loci.	Used in the subroutine CREATE. Entered manually or via data file. Also used as a delimiter throughout the program routines.	INTEGER RANGE (0 TO 20) FORMAT I5	
NUMSIM	The number of simulations to be processed.	Used in the main program simulation loop. Entered manually.	INTEGER RANGE (1 TO 10000)	
PDF	Indicates whether fish weights are normally distributed.	Used in the subroutine CREATE. Entered manually or via data file.	LOGICAL RANGE ('T' OR 'F') FORMAT L	
REFGENO*2	Array of reference genotypes for each locus.	Used in the subroutines CREATE and CALC. Entered manually or via data file.	CHARACTER DIMENSION REFGENO (20) EXAMPLE: '11' FORMAT A	
REFSEX	Indicates the reference sex.	Used in the subroutines CREATE and CALC. Entered manually or via data file.	CHARACTER RANGE ('F' OR 'M') FORMAT A	
SCALE	Scale coefficient for accelerated failure time model.	Used in the subroutine CALC. This is σ in Equation 3. Entered manually or via data file.	REAL RANGE (0.000 TO 100.000) FORMAT F11.5	Diamond et al., 1989FSELECTION

Variable	Description	Where used	Range/format	Reference
SELECTION	Indicates whether meiotic drive/gametic selection occurs.	Used in the subroutines SELECTGENO. Entered manually or via data file.	LOGICAL RANGE ('T' OR 'F') FORMAT L	FSELECTION
SEXBETA	Beta coefficient for sex.	Used in the subroutine CALC in the calculation of XBETA. See β_s below Equation 3. Entered manually or via data file.	REAL RANGE (-10.00 TO 10.00) FORMAT F11.5	Diamond et al., 1989
SEXCHAR	Indicates whether sexual selection occurs at each locus for male /female/both.	Used in the subroutines MALELOCI and BROODSIZE. Entered manually or via data file.	CHARACTER DIMENSION SEXCHAR (20) RANGE (M/F/B) FORMAT A	
SEXRATIO	Percentage of individuals of the reference sex in the population.	Used in the subroutine ASSIGNSEX (within CREATEPOP). Entered manually or via data file.	REAL RANGE (0.00 TO 1.00) FORMAT F11.5	
SHIFT	The median shift: $\exp(\epsilon)$ in Equation 3; 0.693147 for Weibull distribution.	Used in the subroutine CALC. Entered manually or via data file.	REAL RANGE (-10.000 TO 10.000) FORMAT F11.5	
SIZEBETA	Beta coefficient for size.	Used in the subroutine CALC in the calculation of XBETA. See β_w below Equation 3. Entered manually or via data file.	REAL RANGE (0.00 TO 100.00) FORMAT F11.5	Diamond et al., 1989
SLOPE	Slope coefficient for maximum brood size relation.	Used in the subroutine BROODSIZE. See Equation 8. Entered manually or via data file.	REAL RANGE (0.000 TO 1.000) FORMAT F11.5	
SSELECTION	Indicates whether sexual selection occurs.	Used in the subroutines MALELOCI and BROODSIZE. Entered manually or via data file.	LOGICAL RANGE ('T' OR 'F') FORMAT L	
UPPERWGT	Female upper weight limit in mg (wet mass), for brood relation.	Used in the subroutine BROODSIZE. Entered manually or via data file.	REAL RANGE (5.000 TO 5000.000 OF WET MASS IN MG) FORMAT F11.5	
WD	Duration of winter (in gestation periods).	Used in the main program. Entered manually or via data file.	INTEGER RANGE (0 TO 15) FORMAT I5	

Variable	Description	Where used	Range/format	Reference
WGTLMT	Lower weight limit in mg (wet mass), for a breeding male.	Used in the subroutine SELECTGENO. Entered manually or via data file.	REAL RANGE (0.001 TO 5000.000 MG) (FOR SELECTGENO) FORMAT F11.5	
WHICHLOCI	Indicates whether sexual selection occurs at each particular locus.	Used in the subroutines MALELOCI and BROODSIZE. Entered manually or via data file.	LOGICAL DIMENSION WHICHLOCI (20) RANGE ('T' OR 'F') FORMAT L	
WIMMPOP	Number of individuals migrating into the population each winter gestation period.	Used in the main program to simulate migration during winter. Entered manually.	INTEGER RANGE (0 TO 10000)	
WW	Frequency of winter (in gestation periods).	Used in the main program. Entered manually or via data file.	INTEGER RANGE (0 TO 15) FORMAT I5	

Input Data File Format :

NumLoci I5	Selection L	SSelection L	FSelection L	MSelection L	
LociLabel A*10	NumGeno I5	RefGeno A*2			
WhichLoci L	FWhichLoci L	MWhichLoci L			
SexChar A					
GenoType A*2	GenoFreq F11.5	GenoBeta F11.5			
MAllele1 F11.5	FAllele1 F11.5	MAllele2 F11.5	FAllele2 F11.5		
MSexFreq F11.5	FSexFreq F11.5				
FUpperWgt F11.5	FLowerWgt F11.5	FSlope F11.5	FIntercept F11.5		
MWgtLmt F11.5					
MBeta F11.5	FBeta F11.5	MScale F11.5	FScale F11.5		
Longevity F11.5	MMaxGen I5	FMaxGen I5			
MWBeta F11.5	FWBeta F11.5	MWScale F11.5	FWScale F11.5	WW I5	WD I5
MMean F11.5	FMean F11.5	MSD F11.5	FSD F11.5	PDF L	
MMax F11.5	FMax F11.5	MMin F11.5	FMin F11.5		
MGRM F11.5	FGRM F11.5	MGRSD F11.5	FGRSD F11.5		
MShape F11.5	FShape F11.5	Base F11.5	Scale F11.5	Duration1 I5	Duration2 I5
GPt I5	Shift F11.5	SizeBeta F11.5	SexBeta F11.5	Form L	Expose I5
K I5	WgtLmt F11.5	CntLmt I5			
UpperWgt F11.5	LowerWgt F11.5	Slope F11.5	Intercept F11.5		
MaxC F11.5	CSlope F11.5				

Multi L	CMales I5				
MaleFreq F11.5					
RefSex A	SexRatio F11.5	LenGen F11.5			

Additional Input Data File Format for Batch Routine:

InitPop I5	ImmPop I5	WImmPop I5			
NumSim I5	NumGen I5				
GO L	GC L	MO L	MC L	PS L	
NumOut I5	SelectOut I5				
SimNum I5	GenNum I5				

Fish and NewFish arrays :

	Id #	
1	Sex	based on the sex ratio entered by the user
2	Size	weight in mg (wet mass), initially selected randomly, based on the mean, standard deviation, and the pdf entered by the user; then is incremented based on the growth rate, #7
3	Cumulative Survival	calculated and assigned every gestation period, using the sex beta, size beta, form of size beta, the median shift, and the hazard model slope and intercept entered by the user
4	Median Time-to-death	calculated and assigned every gestation period, using the sex beta, size beta, form of size beta, the median shift, and the hazard model slope and intercept entered by the user
5	Age	based on size, and incremented every gestation period by the length of a gestation period entered by the user
6	Natural Time-to-death	time-to-death by natural cause assigned at birth, based on the betas and scale factors entered by the user
7	Growth Rate	selected randomly, based on the mean and standard deviation entered by the user
8	Winter Time-to-death	time-to-death by natural cause during winter gestation periods assigned at birth, based on the betas and scale factors entered by the user

EXAMPLE:

The following example contains one locus of six genotypes with selection. However, there is no meiotic drive/gametic selection, fecundity selection, sexual selection, or male weight selection occurring. The program ran for two simulations of 50 gestation periods each. The initial population was 750 individuals with no migration. There was no winter specified in this example and the number of hours of toxicant exposure was zero. All possible output files were requested. However, only a sample of Gen_Out.dat and Gen_Cut.dat were listed in this example.

The following file, STRS.dat, is the initial input file for the batch routines. This file can easily be modified to run with the interactive routines by deleting the last five lines of data which specify the initial population, migrating population, migrating population during winter, number of simulations, number of gestation periods, and outputs requested by the user.

```
1 F F F F
GPI-2 633
33 0.03330 0.00000
23 0.07860 0.32353
13 0.14050 0.35505
22 0.16190 0.37370
11 0.25450 0.35713
12 0.33570 0.45437
2.00000 2.00000 100.00000 150.00000
0.50000 7 7
1.00000 1.00000 1.00000 1.00000 0 0
30.00000 160.00000 100.00000 1000.00000 T
300.00000 3500.00000 10.00000 10.00000
0.06000 0.06000 0.02500 0.02500
1.00000 1.00000 5.71908 0.50822 0 0
1 0.69315 0.38060 1.29707 T 1
3000 150.00000 50
3000.00000 750.00000 0.03000 6.00000
0.30000 -0.00060
T 3
0.20000
0.50000
0.30000
M 0.50000 28.00000
750 0 0
2 50
T T T T T
4 1
1 50
```

INIT OUT.DAT

INITIAL INFORMATION

NAME OF DATA FILE USED :	STRS.DAT
NUMBER OF SIMULATIONS :	2
NUMBER OF GESTATION PERIODS :	50
INITIAL POPULATION :	750
IMMIGRANT POPULATION :	0
WINTER IMMIGRANT POPULATION :	0
REFERENCE SEX :	MALE
SEX RATIO :	0.50000
LENGTH OF GESTATION PERIOD :	28.00000

LOCUS CHARACTERISTICS

NUMBER OF LOCI :	1				
NUMBER	REFERENCE	GENOTYPE	GENOTYPE	GENOTYPE	
LOCI LABEL	GENOTYPES	GENOTYPE	LABEL	FREQUENCY	BETAS
GPI-2	6	33	33	0.03330	0.00000
			23	0.07860	0.32353
			13	0.14050	0.35505
			22	0.16190	0.37370
			11	0.25450	0.35713
			12	0.33570	0.45437

NO MEIOTIC DRIVE/GAMETIC SELECTION

NO SEXUAL SELECTION

NO FECUNDITY

NATURAL MORTALITY FACTORS

MALE BETA :	2.00000	FEMALE BETA :	2.00000
MALE SCALE :	100.00000	FEMALE SCALE :	150.00000
MALE MAXIMUM PERIODS OF		FEMALE MAXIMUM PERIODS OF	
GESTATION :	7	GESTATION :	7
PROPORTIONAL			
LONGEVITY :	0.50000		

WINTER MORTALITY FACTORS

MALE BETA :	1.00000	FEMALE BETA :	1.00000
MALE SCALE :	1.00000	FEMALE SCALE :	1.00000
WINTER FREQUENCY : ..	0	WINTER DURATION :	0

GROWTH AND SIZE FACTORS

MALE MAXIMUM		FEMALE MAXIMUM	
WEIGHT :	300.00000	WEIGHT :	3500.00000
MALE MINIMUM		FEMALE MINIMUM	
WEIGHT :	10.00000	WEIGHT :	10.00000
MALE GROWTH RATE		FEMALE GROWTH RATE	
MEAN :	0.06000	MEAN :	0.06000
MALE GROWTH RATE		FEMALE GROWTH RATE	
MALE MEAN WEIGHT : ..	30.00000	FEMALE MEAN WEIGHT : ..	160.00000
MALE STANDARD DEVIATION		FEMALE STANDARD DEVIATION	
WEIGHT :	100.00000	WEIGHT :	1000.00000
PROBILITY DENSITY			
FUNCTION :	LOGNORMAL		

EXPOSURE COEFFICIENTS

FREQUENCY OF EXPOSURE		HAZARD MODEL	
(GESTATIONS) :	1	INTERCEPT :	5.71908
HAZARD MODEL SCALE		DURATION OF EXPOSURE 1	
PARAMETER :	0.50822	(HOURS) :	0
DURATION OF EXPOSURE 2		CHANGE DURATION AT	
(HOURS) :	0	GESTATION PERIOD : ..	1
SIZE BETA :	1.29707	SEX BETA :	0.38060
SIZE TRANSFORMED : ..	LOGNORMAL	MEDIAN SHIFT :	0.69315

CANNIBALISM COEFFICIENTS

MAXIMUM :	0.30000	SLOPE :	-0.00060
-----------------	---------	---------------	----------

BREEDING AND BROOD RELATION COEFFICIENTS

MINIMUM WEIGHT FOR A	MAXIMUM NUMBER OF FEMALES
MALE TO BREED : . . 150.00000	PER MALE : 50
UPPER WEIGHT LIMIT : . 3000.00000	LOWER WEIGHT LIMIT : . 750.00000
SLOPE : 0.03000	INTERCEPT : 6.00000
CARRYING CAPACITY : . . 3000	MAXIMUM BROOD SIZE : . 96

MULTIPLE INSEMINATION AND SPERM STORAGE OCCURS
POSSIBLE 3 MALES CONTRIBUTING.

NUMBER	FREQUENCY
1	.20000
2	.50000
3	.30000

PT SN.DAT

SIMULATION # 1 0 HOURS OF EXPOSURE

SIM	GES	TOTAL	MALES	FEMALES	MTTD
1	1 B	750	375	375	103.835
1	2 B	1381	667	714	56.425
1	3 B	2324	1106	1218	66.949
1	4 B	1832	775	1057	111.672
1	5 B	3006	1327	1679	70.118
1	6 B	1395	491	904	130.588
1	7 B	5394	2500	2894	58.535
1	8 B	2729	1026	1703	125.055
1	9 B	2148	726	1422	161.388
1	10 B	5824	2588	3236	56.905
1	11 B	2455	884	1571	128.710
1	12 B	3073	1165	1908	87.904
1	13 B	1355	427	928	146.014
1	14 B	9729	4556	5173	51.574
1	15 B	4310	1646	2664	120.873
1	16 B	2045	521	1524	264.108
1	17 B	10100	4572	5528	55.804
1	18 B	4200	1535	2665	124.634

I	19	B	1913	462	1451	277.925
I	20	B	11151	5062	6089	54.295
I	21	B	4748	1809	2939	121.468
I	22	B	2231	556	1675	265.584
I	23	B	8524	3756	4768	57.585
I	24	B	3438	1279	2159	127.945
I	25	B	1571	404	1167	291.697
I	26	B	12345	5763	6582	54.724
I	27	B	5302	2028	3274	121.982
I	28	B	2444	595	1849	259.425
I	29	B	5808	2375	3433	59.558
I	30	B	2896	1113	1783	120.949
I	31	B	1612	518	1094	182.037
I	32	B	9552	4428	5124	55.770
I	33	B	3939	1470	2469	128.880
I	34	B	1778	430	1348	277.896
I	35	B	11244	5157	6087	56.266
I	36	B	4626	1672	2954	129.938
I	37	B	2103	480	1623	297.526
I	38	B	9801	4366	5435	55.778
I	39	B	4117	1501	2616	126.829
I	40	B	1903	453	1450	277.739
I	41	B	11186	5105	6081	55.939

I	42	B	4681	1778	2903	125.384
I	43	B	2155	550	1605	273.715
I	44	B	9196	4110	5086	57.109
I	45	B	3820	1417	2403	128.856
I	46	B	1715	420	1295	275.430
I	47	B	11481	5307	6174	54.176
I	48	B	4871	1849	3022	122.201
I	49	B	2200	559	1641	256.377
I	50	B	8017	3456	4561	59.160
I	50	F	3255	1195	2060	131.287

SIMULATION # 2 0 HOURS OF EXPOSURE

SIM	GES	TOTAL	MALES	FEMALES	MTTD
2	1 B	750	375	375	106.820
2	2 B	1940	961	979	61.851
2	3 B	1896	838	1058	96.142
2	4 B	2310	1018	1292	84.262
2	5 B	2967	1307	1660	74.523
2	6 B	1462	523	939	142.015
2	7 B	5855	2719	3136	59.043
2	8 B	2955	1162	1793	122.384
2	9 B	1412	393	1019	222.893
2	10 B	10279	4833	5446	54.596
2	11 B	4415	1709	2706	123.328

2	12	B	2069	522	1547	273.808
2	13	B	9429	4199	5230	56.218
2	14	B	3843	1431	2412	126.102
2	15	B	1793	411	1382	292.734
2	16	B	12066	5504	6562	55.166
2	17	B	5138	1919	3219	126.395
2	18	B	2395	618	1777	275.257
2	19	B	6361	2674	3687	59.634
2	20	B	2537	903	1634	131.279
2	21	B	3050	1136	1914	94.725
2	22	B	1310	402	908	157.316
2	23	B	8972	4228	4744	55.420
2	24	B	3798	1420	2378	126.651
2	25	B	1748	425	1323	274.639
2	26	B	11850	5490	6360	55.390
2	27	B	5033	1862	3171	126.210
2	28	B	2296	575	1721	266.030
2	29	B	7271	3110	4161	59.979
2	30	B	2937	1043	1894	131.876
2	31	B	1610	449	1161	215.347
2	32	B	11562	5430	6132	55.604
2	33	B	4982	1868	3114	124.653
2	34	B	2294	577	1717	269.572

2	35	B	7550	3256	4294	57.582
2	36	B	3080	1155	1925	128.448
2	37	B	1328	330	998	284.498
2	38	B	11232	5271	5961	55.329
2	39	B	4835	1875	2960	126.381
2	40	B	2191	570	1621	270.942
2	41	B	8773	3860	4913	57.146
2	42	B	3628	1326	2302	126.688
2	43	B	1625	375	1250	293.173
2	44	B	11807	5465	6342	54.419
2	45	B	5151	1965	3186	125.916
2	46	B	2337	598	1739	268.977
2	47	B	6755	2875	3880	60.073
2	48	B	2711	969	1742	130.419
2	49	B	2433	850	1583	144.139
2	50	B	4042	1704	2338	63.904
2	50	F	1990	727	1263	129.627

..... PROGRAM RUN COMPLETE.

MTTD OUT.DAT**MEDIAN TIME TO DEATH**

SIMULATION : 1

GESTATION	POPULATION	MTTD 25%	MTTD 50%	MTTD 75%
1 BEFORE	750	55.8394	103.8354	197.6312
2 BEFORE	1381	41.0152	56.4249	98.7818
3 BEFORE	2324	45.5073	66.9488	114.5941
4 BEFORE	1832	68.0203	111.6724	182.4610
5 BEFORE	3006	45.3835	70.1179	170.5849
6 BEFORE	1395	82.7165	130.5884	229.2500
7 BEFORE	5394	42.5551	58.5348	99.2569
8 BEFORE	2729	84.4783	125.0550	195.1087
9 BEFORE	2148	66.0207	161.3879	394.3001
10 BEFORE	5824	42.0160	56.9048	99.8174
11 BEFORE	2455	86.0721	128.7102	222.1350
12 BEFORE	3073	49.2842	87.9039	302.1966
13 BEFORE	1355	91.8123	146.0142	348.6466
14 BEFORE	9729	39.8495	51.5738	75.3638
15 BEFORE	4310	81.5424	120.8734	195.3799

16 BEFORE	2045	148.0736	264.1085	562.8987
17 BEFORE	10100	41.9207	55.8042	88.6062
18 BEFORE	4200	85.0089	124.6341	202.9312
19 BEFORE	1913	157.5053	277.9254	552.6414
20 BEFORE	11151	41.1047	54.2946	83.3606
21 BEFORE	4748	81.8303	121.4678	195.4674
22 BEFORE	2231	148.9612	265.5838	556.8875
23 BEFORE	8524	42.7203	57.5851	94.9057
24 BEFORE	3438	84.8305	127.9451	205.2758
25 BEFORE	1571	153.3463	291.6966	567.9891
26 BEFORE	12345	41.6587	54.7238	79.9644
27 BEFORE	5302	84.5721	121.9825	192.1638
28 BEFORE	2444	151.9784	259.4246	557.7822
29 BEFORE	5808	43.2139	59.5585	133.9016
30 BEFORE	2896	83.0387	120.9491	197.9897
31 BEFORE	1612	111.4936	182.0366	454.5093
32 BEFORE	9552	42.4791	55.7702	83.7519
33 BEFORE	3939	86.8559	128.8802	203.1264
34 BEFORE	1778	159.9235	277.8959	557.8219
35 BEFORE	11244	42.8576	56.2662	85.4687
36 BEFORE	4626	87.0710	129.9383	209.2869
37 BEFORE	2103	162.7050	297.5257	565.3935
38 BEFORE	9801	42.5120	55.7779	88.3340

39 BEFORE	4117	85.3329	126.8287	204.0603
40 BEFORE	1903	160.5086	277.7392	572.9948
41 BEFORE	11186	41.8401	55.9386	86.5609
42 BEFORE	4681	83.6589	125.3841	201.0934
43 BEFORE	2155	156.5854	273.7150	563.9034
44 BEFORE	9196	42.7970	57.1086	92.8943
45 BEFORE	3820	85.2455	128.8559	212.9800
46 BEFORE	1715	155.3486	275.4304	544.6885
47 BEFORE	11481	41.5833	54.1758	82.1525
48 BEFORE	4871	83.9785	122.2014	190.9807
49 BEFORE	2200	154.8475	256.3771	533.5867
50 BEFORE	8017	43.4013	59.1604	102.3287
50 FINAL	3255	86.7761	131.2868	221.3599

SIMULATION : 2

GESTATION	POPULATION	MTTD 25%	MTTD 50%	MTTD 75%
1 BEFORE	750	59.8300	106.8197	235.2341
2 BEFORE	1940	46.2597	61.8511	94.7795
3 BEFORE	1896	56.2043	96.1417	167.2811
4 BEFORE	2310	50.8351	84.2619	177.2092
5 BEFORE	2967	48.0208	74.5230	144.1667
6 BEFORE	1462	86.5192	142.0154	258.9432
7 BEFORE	5855	44.1129	59.0429	99.3165
8 BEFORE	2955	82.9463	122.3841	190.2633

9 BEFORE	1412	142.2506	222.8929	514.1082
10 BEFORE	10279	41.6207	54.5965	80.0004
11 BEFORE	4415	82.4774	123.3280	193.4029
12 BEFORE	2069	154.5059	273.8084	551.6699
13 BEFORE	9429	42.3868	56.2176	92.1136
14 BEFORE	3843	85.2245	126.1015	207.8440
15 BEFORE	1793	156.3165	292.7345	591.0576
16 BEFORE	12066	41.9767	55.1660	82.4105
17 BEFORE	5138	84.4020	126.3951	198.6854
18 BEFORE	2395	155.0889	275.2566	549.0350
19 BEFORE	6361	43.2692	59.6345	120.7706
20 BEFORE	2537	87.4162	131.2789	219.7211
21 BEFORE	3050	53.5517	94.7253	305.1295
22 BEFORE	1310	98.1192	157.3159	365.2402
23 BEFORE	8972	42.5951	55.4196	82.3556
24 BEFORE	3798	85.7326	126.6508	199.8373
25 BEFORE	1748	157.2906	274.6386	567.9128
26 BEFORE	11850	41.8804	55.3898	84.5170
27 BEFORE	5033	83.6622	126.2102	198.4177
28 BEFORE	2296	155.5609	266.0305	550.0037
29 BEFORE	7271	43.8776	59.9785	105.5946
30 BEFORE	2937	87.4350	131.8761	218.5056
31 BEFORE	1610	124.8226	215.3469	534.9467

32 BEFORE	11562	42.1734	55.6041	82.0475
33 BEFORE	4982	84.6663	124.6530	197.5867
34 BEFORE	2294	154.1063	269.5715	557.3779
35 BEFORE	7550	42.8526	57.5816	100.5354
36 BEFORE	3080	84.2837	128.4477	215.2456
37 BEFORE	1328	155.4617	284.4980	550.5299
38 BEFORE	11232	42.5191	55.3287	81.7490
39 BEFORE	4835	84.8717	126.3813	202.0520
40 BEFORE	2191	154.2947	270.9424	568.7601
41 BEFORE	8773	42.9952	57.1461	95.1977
42 BEFORE	3628	86.8830	126.6876	204.8461
43 BEFORE	1625	158.6203	293.1734	560.4737
44 BEFORE	11807	41.6371	54.4188	80.9102
45 BEFORE	5151	85.4060	125.9157	196.4492
46 BEFORE	2337	156.9981	268.9773	549.1364
47 BEFORE	6755	44.3988	60.0734	114.4737
48 BEFORE	2711	89.2976	130.4189	226.9448
49 BEFORE	2433	61.0281	144.1389	395.4994
50 BEFORE	4042	45.1158	63.9042	135.3406
50 FINAL	1990	86.7195	129.6270	213.3209

MTTD CUT.DAT

I	1 B	750	56	104	198
I	2 B	1381	41	56	99
I	3 B	2324	46	67	115
I	4 B	1832	68	112	182
I	5 B	3006	45	70	171
I	6 B	1395	83	131	229
I	7 B	5394	43	59	99
I	8 B	2729	84	125	195
I	9 B	2148	66	161	394
I	10 B	5824	42	57	100
I	11 B	2455	86	129	222
I	12 B	3073	49	88	302
I	13 B	1355	92	146	349
I	14 B	9729	40	52	75
I	15 B	4310	82	121	195
I	16 B	2045	148	264	563
I	17 B	10100	42	56	89
I	18 B	4200	85	125	203
I	19 B	1913	158	278	553
I	20 B	11151	41	54	83
I	21 B	4748	82	121	195
I	22 B	2231	149	266	557
I	23 B	8524	43	58	95
I	24 B	3438	85	128	205
I	25 B	1571	153	292	568
I	26 B	12345	42	55	80
I	27 B	5302	85	122	192
I	28 B	2444	152	259	558
I	29 B	5808	43	60	134
I	30 B	2896	83	121	198
I	31 B	1612	111	182	455
I	32 B	9552	42	56	84
I	33 B	3939	87	129	203
I	34 B	1778	160	278	558
I	35 B	11244	43	56	85
I	36 B	4626	87	130	209
I	37 B	2103	163	298	565
I	38 B	9801	43	56	88
I	39 B	4117	85	127	204
I	40 B	1903	161	278	573

1	41 B	11186	42	56	87
1	42 B	4681	84	125	201
1	43 B	2155	157	274	564
1	44 B	9196	43	57	93
1	45 B	3820	85	129	213
1	46 B	1715	155	275	545
1	47 B	11481	42	54	82
1	48 B	4871	84	122	191
1	49 B	2200	155	256	534
1	50 B	8017	43	59	102
1	50 F	3255	87	131	221
2	1 B	750	60	107	235
2	2 B	1940	46	62	95
2	3 B	1896	56	96	167
2	4 B	2310	51	84	177
2	5 B	2967	48	75	144
2	6 B	1462	87	142	259
2	7 B	5855	44	59	99
2	8 B	2955	83	122	190
2	9 B	1412	142	223	514
2	10 B	10279	42	55	80
2	11 B	4415	82	123	193
2	12 B	2069	155	274	552
2	13 B	9429	42	56	92
2	14 B	3843	85	126	208
2	15 B	1793	156	293	591
2	16 B	12066	42	55	82
2	17 B	5138	84	126	199
2	18 B	2395	155	275	549
2	19 B	6361	43	60	121
2	20 B	2537	87	131	220
2	21 B	3050	54	95	305
2	22 B	1310	98	157	365
2	23 B	8972	43	55	82
2	24 B	3798	86	127	200
2	25 B	1748	157	275	568
2	26 B	11850	42	55	85
2	27 B	5033	84	126	198
2	28 B	2296	156	266	550
2	29 B	7271	44	60	106
2	30 B	2937	87	132	219
2	31 B	1610	125	215	535
2	32 B	11562	42	56	82
2	33 B	4982	85	125	198
2	34 B	2294	154	270	557

2	35 B	7550	43	58	101
2	36 B	3080	84	128	215
2	37 B	1328	155	284	551
2	38 B	11232	43	55	82
2	39 B	4835	85	126	202
2	40 B	2191	154	271	569
2	41 B	8773	43	57	95
2	42 B	3628	87	127	205
2	43 B	1625	159	293	560
2	44 B	11807	42	54	81
2	45 B	5151	85	126	196
2	46 B	2337	157	269	549
2	47 B	6755	44	60	114
2	48 B	2711	89	130	227
2	49 B	2433	61	144	395
2	50 B	4042	45	64	135
2	50 F	1990	87	130	213

SAMPLE PORTION OF GEN OUT.DAT

GEN_OUT.DAT

PAGE 1

SIMULATION : 1

GESTATION PERIODS : 1

BEFORE EXPOSURE

POPULATION : 750

NUMBER OF FEMALES : 375

ID	SEX	SIZE	CUMSURV	MTTD	AGE	NAT. TTD	GROWTH	WINTER LOCI:	
1	1.0	1008.0023	0.0000	530.040	112.0000	183.6124	0.0575	1.0653	13
					ASSIGNED MALE LOCI 1 :				22
2	1.0	46.8695	0.0000	95.886	28.0000	180.6916	0.0777	0.0407	22
3	1.0	135.7124	0.0000	171.299	112.0000	211.0235	0.0284	0.8480	13
4	1.0	188.6855	0.0000	210.123	84.0000	125.3141	0.0540	0.2810	22
5	1.0	1495.7668	0.0000	674.467	56.0000	158.2039	0.1062	0.0814	22
					ASSIGNED MALE LOCI 1 :				13
					ASSIGNED MALE LOCI 2 :				11
6	1.0	555.3567	0.0000	378.856	56.0000	80.6220	0.1049	1.2291	13
7	1.0	96.8266	0.0000	141.926	56.0000	226.6267	0.0743	2.2145	11
8	1.0	458.0734	0.0000	340.615	84.0000	117.9343	0.0651	0.9482	11
9	1.0	126.6021	0.0000	165.066	84.0000	41.4864	0.0438	0.3646	11
10	1.0	185.0586	0.0000	204.423	84.0000	163.8846	0.0470	1.7051	11
11	1.0	623.9852	0.0000	405.398	168.0000	195.7305	0.0309	0.2683	11
12	1.0	18.6198	0.0000	56.069	28.0000	215.7376	0.0797	0.7730	11
13	1.0	754.9127	0.0000	497.406	84.0000	107.6284	0.0561	0.3047	12
					ASSIGNED MALE LOCI 1 :				12
					ASSIGNED MALE LOCI 2 :				13

•
•
•

GEN_OUT.DAT

PAGE 32

ID	SEX	SIZE	CUMSURV	MTTD	AGE	NAT. TTD	GROWTH	WINTER LOC:
739	0.0	33.9370	0.0000	54.636	56.0000	159.6893	0.0382	2.4642 22
740	0.0	208.4662	0.0000	151.905	84.0000	120.8164	0.0516	0.1338 22
741	0.0	52.5339	0.0000	69.884	28.0000	81.2287	0.0682	2.3726 22
742	0.0	10.2058	0.0000	27.311	28.0000	100.2792	0.0654	3.3394 11
743	0.0	215.7213	0.0000	151.999	56.0000	86.8918	0.0964	0.0585 13
744	0.0	161.6347	0.0000	129.458	840.0000	107.2479	0.0205	0.4804 11
745	0.0	78.0425	0.0000	87.338	56.0000	72.7606	0.0456	2.2230 22
746	0.0	217.0473	0.0000	152.842	84.0000	80.6204	0.0647	0.0738 11
747	0.0	14.6476	0.0000	33.476	28.0000	104.4454	0.0386	0.0910 11
748	0.0	149.7896	0.0000	126.097	112.0000	47.6575	0.0398	1.1166 22
749	0.0	19.8708	0.0000	39.750	28.0000	129.5409	0.1265	1.1478 11
750	0.0	26.4521	0.0000	46.701	28.0000	96.7412	0.0502	1.2797 11

SUMMARY OF ABOVE POPULATION

TOTAL POPULATION :	750
NUMBER OF FEMALES :	375
NUMBER OF MALES :	375

MEDIAN WEIGHTS (MG) :	
FEMALES :	170.97896
MALES :	53.85256

25% AND 75% QUANTILES OF WEIGHTS (MG) :	
FEMALES :	33.38180 TO 663.24640
MALES :	22.07749 TO 141.72086

GENOTYPES AND FREQUENCIES :

LOCUS : GPI-2

33 0.03333

23 0.07867

13 0.14000

22 0.16000

11 0.25333

12 0.33467

SAMPLE PORTION OF GEN CUT.DAT

I	I	B	750	11	1008	530	112	184	113
I	I	B	750	21	47	96	28	181	022
I	I	B	750	31	136	171	112	211	113
I	I	B	750	41	189	210	84	125	022
I	I	B	750	51	1496	674	56	158	022
I	I	B	750	61	555	379	56	81	113
I	I	B	750	71	97	142	56	227	211
I	I	B	750	81	458	341	84	118	111
I	I	B	750	91	127	165	84	41	011
I	I	B	750	101	185	204	84	164	211
I	I	B	750	111	624	405	168	196	011
I	I	B	750	121	19	56	28	216	111
I	I	B	750	131	229	231	56	60	111
I	I	B	750	141	755	497	84	108	012
I	I	B	750	151	445	369	140	69	012
I	I	B	750	161	102	161	56	69	012
I	I	B	750	171	30	71	28	157	123
I	I	B	750	181	1143	570	112	220	011
I	I	B	750	191	175	218	84	148	112
I	I	B	750	201	155	204	56	29	012
I	I	B	750	211	15	54	28	43	012
I	I	B	750	221	46	103	56	186	012
I	I	B	750	231	35	89	84	139	012
I	I	B	750	241	180	201	56	58	313
I	I	B	750	251	85	132	56	105	013

•
•
•

I	I	B	750	7260	28	49	28	26	022
I	I	B	750	7270	299	183	112	146	213
I	I	B	750	7280	170	135	56	48	122
I	I	B	750	7290	14	32	28	34	011
I	I	B	750	7300	48	65	56	73	513
I	I	B	750	7310	279	176	56	25	713
I	I	B	750	7320	206	148	140	69	111
I	I	B	750	7330	242	179	56	96	112
I	I	B	750	7340	237	177	84	123	112
I	I	B	750	7350	153	138	84	112	312

I	I B	750	736 0	38	63	28	58	0 12
I	I B	750	737 0	47	71	56	27	1 12
I	I B	750	738 0	47	64	28	44	0 13
I	I B	750	739 0	34	55	56	160	2 22
I	I B	750	740 0	208	152	84	121	0 22
I	I B	750	741 0	53	70	28	81	2 22
I	I B	750	742 0	10	27	28	100	3 11
I	I B	750	743 0	216	152	56	87	0 13
I	I B	750	744 0	162	129	840	107	0 11
I	I B	750	745 0	78	87	56	73	2 22
I	I B	750	746 0	217	153	84	81	0 11
I	I B	750	747 0	15	33	28	104	0 11
I	I B	750	748 0	150	126	112	48	1 22
I	I B	750	749 0	20	40	28	130	1 11
I	I B	750	750 0	26	47	28	97	1 11