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Improving An Estuarine Water Quality Ecosystem Model for Narragansett Bay 48 pp

User's Guide + Diskette for Mac Plus, SE or II with hard disk.

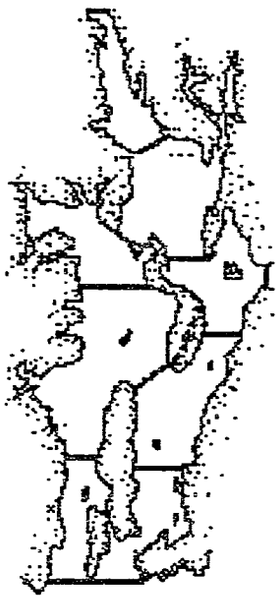
Kremer (USC)

Narragansett Bay Estuary Program

The Narragansett Bay Model

An Ecological Simulation of a Coastal Marine Ecosystem

Users' Guide

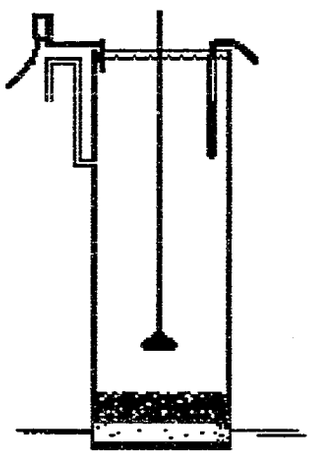


to

The Computer Model

&

The Bay Model Analyzer



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A QUICK "HI"

I know you don't want to wade through this manual. So let's make a quick foray into the model for an overview of what's in store for you if you invest the time to get to know the program!

1. Copy to your hard disk the Bay Model folder containing the Bay Model Analyzer, the model itself, and data files it uses. You need Hypercard (v. 1.2.2 or newer) and the Home stack if you don't have them. Always work on a copy, the original as a backup. (If you have a Mac II, see sec. "Using the Bay Model Analyzer" first.)
2. Open the folder and run the HyperCard stack "Bay Model Analyzer" by double clicking.

3. Click the button Help if you would like a brief explanation of the stack.
4. Click "Run the Model" to start a simulation run.
5. Hit the RETURN key repeatedly, passing the various queries that allow you to modify the default run. For now, you will run the standard simulation of a MERL control tank.
6. The real-time graph plots the progress of the run (while an output file is saved on disk):
   - P is the total phytoplankton stock (mgC/L); D is the portion that is diatoms and the difference in these two lines is the flagellates.
   - Z is the total copepod stock;
   - μ is the microzooplankton (both mgC/L).
   - N is total DIN in μM. (The printed value is real, but the plot is a tenth of it to fit better on the scale.)
   - fB is the fraction of the total water column filtered by benthic filter feeders.
   - ∂A is an error term indicating how well simulated total benthic flux of NH_4 agrees with the empirical flux equations. It is plotted on a log scale to the top right, and a perfect model would give a straight line of 1.0. (Good luck!)
7. Hit RETURN when the run finishes and you are finished looking at the graph. This should return to the Analyzer stack. If not, simply re-start the Analyzer yourself (click-click).
8. If you are not using Multifinder, the Analyzer should automatically ask to load the run's data file, to which you reply "OK" or hit return. If this does not happen, click "Load a previous run" and continue. You may need to direct HyperCard to the file in the folder "BayModel."
9. When the file has loaded, you will see the first of 3 pages of specifications defining the conditions of the run. Point to the word "PHYTO" click on it, and hold the mouse button down. Touching each of the coded words explains the meaning of the coefficients.
10. Click on the right-side buttons "P&Z", "Ben" and "I.C." and explore the range of variables that you may control in your own runs of the model.
11. Click on the right-side button "Jan" to see the state of the simulated MERL tank at the start of the run, simulated New Year's Day. This is a lot of detailed output, but don't be too intimidated. Explore each of the compartments by clicking & holding any of the keywords. Each value & related items are immediately explained.
12. Click the "Plots" button. Study the legend information. These are simple print-plots of all of the state variables (you'll be reminded of the line plots during the run, although these are weekly not daily values). Scroll up and down to see what temporal patterns resulted.
13. You may want to return to a given month to see what was going on during an interesting time in the plots. Just click on that month's button. Move around among months & plots.
14. When done, QUIT either from one of the data cards, or after returning to the top of the stack (by button "New," with which you may also try another run).

PREFACE

Why should you want to use this computer model anyway? Perhaps you are curious about what a simulation model of an estuary is, how it works, and what sort of things such a program does. This model will serve that purpose well; a lot of effort has gone into making it easy to use and somewhat self explanatory. But such use is limited. A more valuable use would be if studying the model could stimulate ongoing and future research, improve understanding of cause and effect in the estuary, reveal the logical and quantitative consequences of reasonable assumptions. These goals are lofty, and presumptuous. They may be obtained if, and only if, you the users take the time to understand the mechanisms and processes included in the model, *and* if these assumptions seem appropriate and interesting to you. *Only when you understand the formulations and see them as plausible generalizations of how the bay works can studying the model tell you anything you really want to know.* I hope that this guide makes this possible.

PURPOSE OF THIS USERS' GUIDE

This guide describes the new Narragansett Bay Model. The basic rationale and many of the biological assumptions are unchanged from the model presented in ***A Coastal Marine Ecosystem*** (Kremer and Nixon 1978). This Users' Guide presents a brief discussion of the conceptual model to help explain the assumptions of the model and the intended scope of the compartments and processes represented in the model. The use of the model is explained by presenting an annotated example of a model run, the normal output, and the various options that exist for changing the coefficients and conditions simulated by the program.

The program is complicated. A large variety of parameters must be specified to define all the conditions. Many of these, you will never choose to change, but the program attempts to put all these decisions in your hands. A careful reading of user-controlled parameters and the output produced by the model is perhaps the best description of the many assumptions of the model. The ***Bay Model Analyzer*** is a new addition that streamlines the use of the simulation program and puts help in understanding the coefficients and detailed output at your fingertips.

Changes to the original computer program were initiated in 1986 with two goals in mind. First, with the completion of the MERL Eutrophication Experiment, it was hoped that the model might help explore the extent to which conventional assumptions about bay ecology might be consistent with the MERL results. Second, The Narragansett Bay Project was interested in the predictions of the model toward our understanding of the processes relating to water quality in the upper reaches of Narragansett Bay, especially the Providence River. This work was supported by a sabbatical leave for J. Kremer from the **University of Southern California**, grants from the **URI Sea Grant Program**, from the **Marine Ecosystems Research Lab**, and from **the Narragansett Bay Project**. James McKenna provided substantial capable programming assistance in the development of the menu-driven feature for convenient modification of parameters and in the data reduction required to simulate the MERL header tank inputs. He provided information in the course of working on the benthic model for his Master's Thesis that proved useful in the development of the benthic model used here. Patricia Kremer helped to formulate the new microzooplankton model. I gratefully acknowledge all of this support.

A project like the Bay Model and the Users' Guide is never really "finished." I hope that early users of the program will provide suggestions for changes that will make the program more convenient to use, easier to understand and most importantly, more meaningful ecologically. The content and motivation for any revisions of the model and future editions of the Guide and ***Analyzer*** will be based on the feedback that results from this release.

Please contact me if you have questions or suggestions. My address and phone number are on the cover of this Guide. Copies of the source code are available, and I am willing to work with you to get the model up and running on your system. Thanks for your interest!

SYNOPSIS OF THE NEW MODEL

The basic structure of the model remains largely as explained in *A Coastal Marine Ecosystem* (Kremer and Nixon 1978). Serious users will want to refer to this reference for a complete description of the intent and scope of the overall project. Some changes have been made to almost all of the compartments of the model; they are outlined below. Several major additions were undertaken, specifically to enhance the utility of the model in the applications mentioned above, and in response to shortcomings discovered in working with the original model. The following paragraphs summarize the substantive changes that have been made. In the following section, the conceptual bases for the compartments are presented.

• **The Analyzer.** For the Macintosh, I have written a HyperCard stack that should substantially assist your work with the model. The Analyzer divides the standard output file generated by the model into convenient sections for display. You may navigate efficiently among the plots and the monthly tables of detailed results. Each page of the display (or "card" in HyperCard lingo) provides definitions and tips for each of the many coefficients and code words that punctuate the output. Simply click the mouse on the printed items.

• **User Interface.** The simulation program has been redesigned to be easy to use. Control of the program and selection of all coefficients are handled by menus and a dialog with the user. While the tabular output is extensive and detailed, this is essential since it is only by studying the rates of the detailed processes of the model that any insight can be gained. The program routinely produces modest time-series plots of variables at the end of the run. To facilitate more extensive analysis of results however, the program produces an optional output file that can be loaded into a personal computer spreadsheet program. This is presently implemented only for the Macintosh version which produces Excel files. Since my work with the program has been on the Macintosh, other versions are not yet available. Most of the program is written in standard FORTRAN and thus may be readily converted to run on other machines. The Analyzer however will only be available on the Mac. The software has been tested on Mac Plus, SE, and II models all with hard disks. I am not sure if it can be run without a hard disk, but I am fairly sure that you wouldn't want to!

• **Physics.** Three options exist. 1) The user may run the model for all of Narragansett Bay, simulating 8 vertically averaged and horizontally homogeneous spatial elements using the original TIDE mixing scheme. 2) The model can simulate the conditions of the MERL eutrophication experiment. And 3) the model can simulate a basin of arbitrary dimensions with a fixed average flushing rate.

• **Phytoplankton.** Minor changes were made in this compartment. Real emphasis was placed on implementing two functionally different "species groups." It was felt that nanoplankton were important especially in the summer, and that feeding preferences of zooplankton and the benthos might have important implications. Both phytoplankton groups are structurally identical, and the user specifies their differences via maximum growth rates, nutrient dependence, sinking rates, and potential utilization by various grazers. Sinking can now be specified as a function of the growth rate. In a small but important theoretical change, the growth rate is now computed as the maximum temperature-dependent growth rate times either the nutrient limitation or light limitation term, rather than the product of the two (see below).

• **Zooplankton.** A major change was made in the way that growth and reproduction are computed in the model. While conservation of mass still constrains the net yield after assimilation minus respiration, the *order of computation* has been modified. The model now defines the processes that are the most important to population dynamics and for which the most reliable data are available: egg production by adults and growth by juveniles. Formerly, egg production was determined by difference from estimated ingestion and respiration; now the maximum production as a function of temperature drives the calculation and a target ingestion is estimated from this plus estimated respiration. The realized ration is reduced by competition for available food. Finally, the respiration formulation was modified to include a non-feeding rate plus a portion dependent on the ingestion rate. Preferences, or efficiencies, for zooplankton feeding on the two algal groups, juvenile zooplankton, μzooplankton, and particulate carbon may be specified. Life history of copepods is simulated in detail, with daily cohorts of eggs followed independently through hatching and juvenile development until maturing into the reproductive adult compartment.

• **Microzooplankton.** This is a totally new compartment to the model. The basic physiological logic of this model is identical to that of the zooplankton: a maximum potential growth rate is diminished by food limitation. For μzooplankton however, growth is compounded directly into the single, biomass compartment, rather than tracking cohorts of eggs through hatching and juvenile development as with zooplankton. Similar to the zooplankton, feeding preferences may be specified but food is limited to the two algal groups and particulate carbon. Carbon-specific rates of respiration and maximum production are functions of temperature.

• **Benthos.** This is the second new compartment. The goal was to overcome the major shortcoming of the earlier model: the uncoupling of the chemical from the planktonic parts of the system. While there was a fair general concensus on what such a benthos compartment should include, detailed formulations and specification of the coefficients proved to be very difficult. For this reason, the benthic model permits three modes of increasing mechanistic detail.

1) Forcing the benthos: Fluxes of NH_4, O_2, PO_4 and Si are forced by empirical temperature-dependent regressions. Feeding by filter feeders is forced by a temperature dependent function of the specified biomass. This option is nearly the same as the benthic compartment of the original model. While coefficients of the flux equations may be modified, their empirical basis is very solid, and changes would be mainly for curiosity.

2) Mechanistic feeding, no growth: The initial biomass of macrofauna (filter feeders and deposit feeders) is specified, and ingestion and metabolism are fully simulated under the constraint that biomasses are not allowed to change. Microbial-meiofaunal decomposition of sedimentary carbon is specified as a temperature dependent first-order decay constant.

3) Fully mechanistic, including growth: Initial biomasses of the macrofauna are permitted to grow or decline based on the balance of ingestion and respiration. The maximum permissible growth is fixed by specifying a relative scope for growth. Microbial-meiofaunal decomposition of sedimentary carbon is again specified as a temperature dependent first-order decay constant.

In mechanistic modes 2 & 3, provision was made for a depression in macrofaunal respiration rate at low oxygen concentrations. Feeding preferences may be specified for the two algal groups, μzooplankton, and particulate carbon. Denitrification is specified as a fraction of the total organic nitrogen passing through the microbial-meiofaunal pathway. To help with the interpretation of these predicted rates, these modes provide a comparison of the simulated nutrient fluxes to those predicted by the empirical equations.

• **Nutrients.** The addition of oxygen as a state variable is the major change in this compartment. All metabolic fluxes in all compartments are related stoichiometrically to oxygen. For simplicity this assumes PQ=RQ=1.0 throughout, although this is not quite accurate for benthic microbial metabolism,. Air-sea diffusion is determined based on the saturation deficit and an average diffusion coefficient. The addition of nutrients from outside the system is allowed via direct input and with river flow (in the Bay case). In the MERL simulations, the inputs automatically reproduce the treatment gradient in the Eutrophication Experiment.

• **Integration scheme.** The original model used a unique exact analytical integral in a predictor corrector scheme over a 1 day interval. To handle the fast rates anticipated from the inclusion of nanophytoplankton and μzooplankton, a rectangular finite difference scheme with a variable time step was implemented. The DT varies automatically between 1 and 32 steps per day so as never to allow a change in any planktonic state variable of more than 50% in a time step. If any variable changes by more than 50% the DT is halved; if all variables changed less than 10% in any step, the DT is doubled. In practice, most runs are not qualitatively different if DT=1 throughout, and you may force this constraint to speed up trial runs.

DESCRIPTION OF THE CONCEPTUAL MODEL

PHYSICS

Bay Simulation.

The original subroutine TIDE mixes all dissolved and particulate constituents among the 8 spatial elements of the bay. While the dimensions of these elements could be changed, doing so would violate the assumptions of TIDE, and is not recommended! The user has no control over the mixing scheme as it is specifically designed to reproduce one year of daily tidal variations. River flow with appropriate nutrient loads may be specified, and variations in mixing exchanges will result. The TIDE routine was itself a statistical description of the time-dependent, vertically averaged fine-grid hydrodynamic model of the bay of Kurt Hess and Frank White (1974).

MERL Simulation.

The dimensions of MERL tanks are specified. Flushing of the tanks simulates the turnover of the eutrophication study (June 1981 - September 1983). The MERL data for the concentration in the source "header tank" of most state variables (Chlorophyll a, zooplankton adults and juveniles, NH4, PO4, Si) were analyzed and smoothed to provide daily values. A large sequential data file of these concentrations and the estimated volumes delivered to each tank during the experiment is used to deliver appropriate seed stocks into all tanks. Nutrient additions simulate the experimental gradient: Model element 1 is a control (no additions above the header inputs); element 2 is the MERL 1X treatment, elt. 3 is 2X, elt 4 is 4X, elt. 5 is 8X, elt. 6 is 16X and elt. 7 is 32X. The extinction coefficient for light used in the MERL case is dramatically different from the bay, as has been observed.

Basin Simulation

You must specify the volume and depth of this arbitrary generic basin. The only physical process is the daily flushing coefficient you specify. Each day when the mixing routine is called, all state variable are diluted assuming this daily instantaneous flushing rate. For example, a flushing rate of 0.95 would define a loss of -5% daily.

BIOLOGY

Phytoplankton

The two subdivisions of the phytoplankton compartment represent primarily diatoms and nanoflagellates. Despite seemingly distinct differences between these types, it is not easy to document obvious coefficient choices to distinguish their functional responses. However, dramatic differences in simulated seasonal patterns result just from changing the feeding efficiencies of the consumers, so it is not clear that the physiological responses need be very different to account for seasonal differences in biomasses.

The conceptual model for the phytoplankton is only slightly different from the original. An exponential temperature function specifies a maximum growth rate. Nutrient limitation by a single most limiting factor is determined by Monod hyperbolae for N, P, and Si. (Although the integration scheme should avoid it, the model checks that the calculated uptake for the total phytoplankton stock does not exceed that available; if so, uptake is reduced to avoid a run-time computer error.) Light limitation is computed from Steele's P-I curve, which includes a single parameter, I_{opt}, that specifies the light level of optimum growth. While substantial attention has been given to other more accurate P-I formulations, once the instantaneous response is integrated over depth and time-of-day as is done in the model, the differences in these equations are generally small (for a complete discussion, see Kremer & Nixon 1978, Sec. 4.3, p.44-54). The Steele model assumes surface inhibition above the optimum. I_{opt} acclimates seasonally to the insolation at 1m depth; the earlier moving weighted average scheme for I_{opt} was eliminated as incompatible with the new integration method.

The net growth rate is the maximum rate times the most limiting of the light *or* nutrient factors. Realized growth is the integral of the net growth rate less sinking and grazing losses. Feeding efficiencies of zooplankton and benthic filter feeders, and algal sinking rates establish the transfers to other compartments. Sinking rate may be zero, constant, or a linear function of the nutrient limitation term reducing growth. Variable nutrient-to-carbon ratios are possible, but the present model does not include any formulations specifying how the composition might change with environmental or internal physiological factors. Thus, for the time being, the specification of upper-lower limits to C:N and C:P is superfluous. The one exception is Si. *If only one algal group is specified, the model imposes a seasonal variation on the C:Si ratio* in an attempt to represent the decreased dominance of diatoms in the summer. This forced cycle is crude, and the use of two algal groups with specific, fixed C:Si should be superior.

Zooplankton

The new model has two zooplankton compartments. The original one represents omnivorous calanoid copepods, with detailed treatment of their life history. The second compartment represents microzooplankton, and is modeled primarily based on recent literature on tintinnids (Capriulo 1982; Capriulo and Carpenter 1980; Gifford 1985; Heinbokel 1978; Stoecker and Sanders 1985; Verity 1985, 1986a,b). The conceptual foundation for both types of zooplankton in the model is similar.

Maximum production (egg production by adults or growth of juveniles and microzooplankton) is defined as a function of temperature. Food limitation may lower this rate using an Ivlev hyperbolic curve including a feeding threshold. Feeding efficiencies specify what fraction of the potential food groups are available as food. Respiration includes a temperature-dependent non-feeding rate plus a part linearly dependent on the projected growth rate. Growth plus respiration specifies a target or "preferred" ration. The preferred ration divided by the total available food defines an effective filtering rate. (For example, a target ration of 0.5 mgC $l^{-1}d^{-1}$ by the zooplankton with 1.0 mg C l^{-1} d^{-1} total food available suggests an instantaneous filtering rate of 0.5 d^{-1}.) However, when all other factors are considered (algal growth, pressure from other grazers) the realized ingestion will differ from the target ration. The actual ration resulting from the calculated feeding rate is then apportioned to respiration and production.

Growth of juvenile copepods proceeds over a development time dependent on temperature and available food. For each hatching cohort, its minimum development time is the average of the estimate for the temperature on the day of hatching and a second estimate for the temperature that many days in the future (which is known in advance in the model!). Day-to-day food availability via the Ivlev curve reduces the simulated development. Each cohort is tracked separately. The actual number of cohorts changes throughout the runs, and the model keeps track of how many are active.

Excretion is calculated from the elemental composition of the food and the animal tissue. The model calculates the nutrients available in the mixed diet ingested, assesses any nutrients available from the food used to meet respiratory demands, uses what is needed to grow new tissue of the proper composition (assimilating nutrients from the unassimilated food if necessary), and excretes the rest. Starving animals metabolize their body tissue, excreting any nutrients in proportion to their lost body tissue.

This plan is used for adult and juvenile zooplankton and µzooplankton, although coefficients may differ substantially. Thus the main conceptual difference is that zooplankton adults produce eggs and juveniles produce somatic biomass in cohorts, while the µzooplankton produce biomass in a single aggregated compartment.

Benthos

There are three modes of varying mechanistic detail that may be simulated. The indices FORCEB and BGROW select among the options.

Forced Mode. All functions of the benthic compartment are forced by temperature-dependent empirical equations. This includes NH_4, PO_4, and Si releases, O_2 consumption and grazing by filter feeders. Feeding efficiencies control the grazing pressure on the two algal groups, on µzooplankton, and on particulate carbon. This mode completely uncouples the benthic fluxes from the mass

constraints of the rest of the model (i.e. conservation of mass may be violated!). The output does report the net budget of the benthos for N, P, and Si.

Mechanistic mode, no growth. In this mode, biomasses of filter feeding and deposit feeding macrofauna are the bases for simulated grazing and excretion rates. Weight specific metabolic demands are temperature-dependent. Rates necessary for filter feeders to meet respiration are based on the available particulate food, subject to an arbitrary upper limit (see Vfilt0, QVfilt). Deposit feeders meet their demad from the pool of sedimentary carbon (Csed) accumulating from sinking phytoplankton, sinking zooplankton feces and unassimilated matter from filter feeders. If food is inadequate to meet demands, respiration rates are reduced to maintain the constant biomass. Nutrients (N, P, Si) are regenerated in proportion to the organic matter consumed and its simulated composition.

Mechanistic mode, with growth. Processes are similar to the no growth mode, except that the macrofauna compartments are allowed to change in biomass using a relative "scope for growth." The target ingestion includes respiration demands plus a maximum allowable daily growth increment, corrected for assimilation efficiency. The target ration may not be realized if competition from other grazers or if the filtering rate is inadequate. In such cases, growth will be less than the maximum, or starvation may occur. Changes in biomass may alter the relative regeneration of the three nutrients, maintaining the specified tissue composition.

In both of the mechanistic modes, microbial decomposition is modeled simply as a first order decay of particulate carbon accumulated in the sediments. Designed to represent crudely the composite activity of bacteria and meiofauna, this flux utilizes POC from sinking algal cells, plus unassimilated matter from zooplankton and filter feeder ingestion. Denitrification is assumed to be related to this DOC decomposition in a simple way. A constant fraction of the nitrogen in the decomposed sedimentary carbon is assumed to be lost; the rest is regenerated as part of the NH4 flux from the benthic community. Also, in both these modes, low oxygen concentrations may depress the respiration rate. In all cases, as in zooplankton feeding, nutrient conservation is maintained despite complex diets made up of components of different elemental composition.

Carnivores

These effects are unchanged from the original model. Biomasses of larval fish, ctenophores, and menhaden are forced seasonally throughout the regions of the bay. Partially mechanistic formulations estimate the grazing and excretion impact of the predators. The three stocks prey on all zooplankton and µzooplankton but not on algae. In the MERL simulation, no carnivores are present.

Particulate Carbon

This compartment awaits enough information to specify its source(s) in a useful way! The model continues to track this variable, and connections exist between it and all potential grazers. Its only use currently is to provide a food subsidy that seemed to be required in the original model to sustain adult zooplankton though the winter. Until hypotheses can suggest the origin of this material and until data are available to evaluate its simulated dynamics, little is served by including more detail here.

Chemistry

Most of the nutrient dynamics are specified by the processes in the other compartments discussed above. Pelagic nitrification is included. The temperature-dependent formulation appears consistent with recent work for the bay and was not modified. Oxygen diffusion with the atmosphere is driven by a saturation deficit and a simple diffusion coefficient. While reaeration certainly depends on wind speed at least, a constant average coefficient was used since wind is not specified in the model. Further, day-to-day variability in the wind speed and direction make the specification of any simple pattern invalid.

RUNNING THE PROGRAM

USING THE BAY MODEL ANALYZER

The HyperCard™ stack **Bay Model Analyzer** facilitates using the model. You need a Macintosh with a hard disk, the Apple application HyperCard 1.2.2 (or newer) and its Home stack to use it. If you haven't done so, copy the folder "Bay Model" to your hard disk.

If you have a Mac II, you need to rename the two model files in the folder to take advantage of the faster 68020 processor. Open the copy of the folder on your disk. Use the "Get Info" command to unlock the two BayMod files; notice that one is for the Mac II and the other for an SE or Plus. Close the Info windows. Rename the file "BayMod apl" to something different to save it, e.g. "BayMod apl for SE". Then shorten the name the file "BayMod apl for Mac II" to "BayMod apl" so that the **Analyzer** will find this one instead.

The **Analyzer** expects to find its files in a folder named "Bay Model" on your hard disk. If you keep all model related files in this folder, all should run smoothly. If the **Analyzer** can't find the files it needs, it will ask for help with a standard Mac file selection box. This is easy; just remember that the files are in the folder "Bay Model" -- the model application "BayMod apl" is there, and it puts its standard output file "BayModRun" there after every run.

Initial Options

Select and Open (or double-click) the Analyzer to begin. You have four options.

Run the model. Click on this button to transfer control the simulation model. When the run is done, the Mac will pass control back to the Analyzer to load & display the results.

Display current run. If a run is already loaded in the Analyzer from an earlier working session, you can return to it as long as you did not delete it when you Quit last time. Click to open the results display.

Load a previous run. Click to erase any earlier run from the work space, and to load a file to analyze. The Bay Model saves its results in a text file named "BayModelRun" but you can rename these run files to save them for later comparison. (Change file names the usual way by selecting the file on the Desktop and typing a new descriptive name.) The Analyzer will load the standard file unless you enter a new name to load. As the file loads, a message box displays the progress. When done, the screen dissolves to the output display.

Help. Click to get a brief explanation of the purpose and function of the Analyzer.

Quit. Click to exit the Analyzer. You may save the current file for later study, or you may delete it from the stack to save disk space.

Help! Displaying Coefficients, Results & Definitions

When a new file loads, or if you click "Display current run," you will see the first of three pages of coefficients and specifications that define the run. *Almost all of these are parameters you can change when you start a new run of the model.* The top three buttons in the right-side column labeled "P&Z", "Ben", and "I.C." let you switch among these specification cards (for Phytoplankton & Zooplankton, Benthos, and Initial Conditions, respectively.)

Each key word refers a parameter or initial value that is used by the model. These tables may be overwhelming at first! But you will soon learn to read the mnemonic codes that relate to their meaning. To assist you in this, the Analyzer provides an "on-line Help" feature. Simply point to the key word or its value, click, and hold the mouse button down. A pop-up window supplies a brief definition for the parameter. The help window will disappear when you release the button, unless you move the pointer off of the key word. If a window does not go away, click, hold and release on any button again.

The results of the model are in two forms: detailed tables of stocks and rates for each of the compartments, and plots. Use the rest of the buttons on the right margin to switch to each of the

months, to the plots, and back and forth. Simply click on the buttons to jump to any month, the coefficient cards, or the plots. As with the initial parameters, each of the variables in these tables of results will be explained if you simply point to the variable and click on the mouse button. Variables that are logically grouped are highlighted as a block with a single definition.

A typical session with the Analyzer

- Run the Model Click this button to initiate a simulation. See the section "Running the Default Run" below for an explanation of the input/output stream of the model. The program produces output on the screen during the run plus a standard output file named "BayModelRun," unless you cancel it. This is the file that is used by the Analyzer. (The model also offers the option of other very detailed output files that may be loaded into the spreadsheet Excel. These are independent and totally separate files.)
- RETURN At the end of the run, you must hit the return key once to clear the last of the model's output and return to the Analyzer. HyperCard should resume running the Analyzer automatically, asking your permission to load the run . If it does not, you will need to re-open the Analyzer and click "Load a previous run." When the data are loaded, the Analyzer dissolves to the first of three card specifying the conditions of the run. Note that button "P&Z" at the top of the row of buttons on the right side of the screen is now highlighted. This identifies this card as the phytoplankton and zooplankton coefficients.
- Click on a keyword You can see explanations of most of the keywords you see on screen by clicking *and holding* the mouse button on the word or its value. Confirm the run title and the coefficients. If you changed any coefficients or initial conditions, you can see that they were set properly. Browsing through the coefficients is a painless way to familiarize yourself with the coefficients that control the model. Note any values you would like to change in another run -- You may not change values from within the Analyzer; changes can only be made when running the model.
- Click, move & release If you move the mouse off the keyword before releasing, the definition field doesn't go away, giving time to read and think. Simply click & release on any button to clear the screen.
- Jump to the other Coefficient Cards Click on buttons "Ben" or "I.C." to see the variables in the benthic (and other compartments) and the initial conditions that were specified for this run. You may return to these specifications any time within the Analyzer by clicking on these three buttons.
- Jump to Plots Click on "Plots" to see the crude plots of state variables, fluxes, and rates. These are weekly values plotted in groups of up to 3 per plot sharing a common axis. There are a number of plots and that are stored back-to-back on this scrolling screen. You control them (see Menu 10 in the model's change parameters dialog). Read the pop-up information on how to view these plots, and click the "Help" button for an explanation of the plot's format.
- Jump to Results for January Click on button "Jan" and the screen displays a detailed tabular summary of all the rates and stocks on Jan. 1, the initial day of the simulation. As you did with the coefficients, you may get brief descriptions on each of these keywords by holding the mouse button down on the word. Related terms are explained together, so you will soon recognize the blocks of structure in the output. Near the bottom of the screen a line presents the external inputs (SWGAM, etc.). Click and read; note that these additions continue daily, though they are not printed in later months.
- Jump to other Months & Plots As you see features of interest in a plot, jump to the appropriate month to explore the underlying dynamics at that time. The monthly output may not correspond exactly to an event of interest, but remember that things change smoothly in the mode for the most part, and it is likely that the data from the nearest month will be helpful. (You can specify daily output in the model, but this will disagree with the Analyzer's monthly buttons. You may want to load the standard output file BayModelRun into a word processor in this case. Put the font into Monaco so it will align.)

- Jump to "New" Based on what you saw in the first run, you may now run another, modified run just as you did initially. *All changes in coefficients must be done while running the model!* The analyzer only reports results.

- Quit You may execute and study a number of simulations. Each run deletes and recreates the standard output file "BayModelRun." If you wish to save a run for later use, you must Quit the Analyzer (or just move to the Desktop with Multifinder) and rename it. You may then load this run by name into the Analyzer at a later time. When you Quit the Analyzer, you may leave the output results you were studying in the Analyzer stack. This means the stack takes up more space on the disk (not much), but it means you can return to look at it more quickly next time in you like. Even if you choose to delete the run when you Quit, you may reload it as a previous run as long as the standard file still exists.

Limitations of the Analyzer

The analyzer only displays results from certain variations of the standard run. The file must contain the coefficients and initial conditions, monthy output for a single spatial element or tank, and any number of plots. If you change the output intervals (i.e. simulating more than one MERL tank, or storing tabular results from more than one of the 8 bay spatial regions) the buttons may not match the printed output. For any given month, however, the keyword definitions should work OK. One exception is the output from the carnivores compartment in full bay runs, which are not explained by this version of the Analyzer. Refer to Kremer & Nixon (1978) p. 150 for explanations of the items listed under the section heading "CARN."

RUNNING THE DEFAULT RUN (A MERL RUN)

Follow along comparing this explanation with the screen on your computer.

- **When you first run the program, if you respond to *all queries* with a carriage return** (no entry) the program produces a run using the default conditions. The default output creates a file with the initial conditions and all coefficients of the run, and then the results, consistent with the Analyzer's requirements. The "Output Section" in this Guide explains what the run looks like and what sort of output you get. You may want to look ahead, but since the detailed results follow directly from the coefficients and formulations, it is logical to present here the steps required to run the model first.
- **The sample run is from a simulation of a single MERL tank.** Your run may differ in the specific values given, but the format of the menus and the flow of the dialog should agree. This default run is not a "best fit" run, nor is it especially noteworthy in any scientific way; it is only an example (indeed, the default run is constantly being revised). Running the full model for 8 spatial elements of the Bay rather than for one MERL tank is explained below.
- **Notice the format conventions** used in the descriptions below:
  - Text in this uniformly spaced type is output from the computer program.
  - **Bold type is commentary.** (Some sections are in normal type too.)
  - Outline type indicates user responses in the context of the dialog. Be sure to hit the return key after your entries (shown as ‹R›).
- With most queries in the dialog, **the default reply is shown in parentheses**; a reply of RETURN is the same as entering this default response.
- **Steps in doing a run are identified below as A-F.** In each case, the screen output is given followed by an explanation.

A.

```
Enter maximum STEPS/Day for DT; only use 4,8,16,32, etc. (8):‹R›
Integration DT will vary between      .1250    and    1 day.
   STD MERL RUN FROM BLOCKDATA
INITIAL CONDITIONS IN THE 1 REGIONS:
==================================
PTOT     ugCHL/L      1.000
DIAT    fraction       .900
ZTOT    MG. DW/L       .010
UZoo     mg. C/L       .001
NH4      ug-AT/L      4.000
NO2NO3  ug-AT/L       7.000
PHOS     ug-AT/L      1.600
SI        ug-AT/L    22.000
O2           mg/L    11.000
FFB       gm C/M2    10.000
DFB       gm C/M2    10.000
SEDC     mM C/M2        .000
SEDN     mM N/M2        .000
SEDP     mM P/M2        .000
SEDSI   mM Si/M2        .000
POC      mg. C/L        .000
```

First, you are given the option of changing the minimum time step for integration of the model. Hitting the "RETURN" key (‹R›) accepts the default of 8 steps per day shown in parentheses. (Remember that the model increases its computation from 1 per day when rapid rates require it. The default of 8 STEPS per day will be adequate for most cases, but you may want to increase it to 16 or 32 if zero oxygen or nutrient concentrations are occurring, or decrease it to 2 or even 1 to allow faster runs for initial testing.)

Next the output to the screen specifies the run title and initial conditions of all state variables in the defined units.

B.

```
Running:   1 years, starting month   1 (day     1);
Daily output starting month   0 for   0 days;
 4 Plot(s).

Enter 1 (Run) or 2 (Change parameters) (Default=1):<R>
Enter a FILENAME to run from saved file:(none)<R>
```

The model displays the run length, whether you have specified daily output, and how many plots have been specified. You are then given two RUN OPTIONS; 1 is the default and 2 is explained below in the section "Modifying the Default Parameters." Enter "<R>" to continue the default run. You must hit the RETURN key after your entries.

C.

```
Running 1 tanks, with output intervals (months):   1;
OK? or enter new MAX TANKS (& specify intervals):<R>
```

Next, in the MERL option, you may change the number of tanks to be simulated, and the frequency of printed output. (This part of the dialog differs when the 8-element bay model is run.) Specifying MAX TANKS > 1 in response to the "OK?" question line runs other treatments in the Eutrophication Experiment. Tank 1 is the control, 2 is the 1X treatment, 3 is 2X, 4 is 4X, 5 is 8X, etc., up to a maximum of seven. The model automatically specifies the nominal levels of added nutrients, as well as simulating the header tank inputs specific to each tank.

NOTE that in the default case, 1 tank is run, with output every 1 month. If you type a number instead of RETURN, you will be asked to supply the output interval in months for each of the tanks to be simulated -- they need not be the same. Except with the full bay version, output intervals of "0" keeps the tank from being simulated, so it is possible to run only the control and 4X tank, for example. See the section "Running the 8 Element Bay Version" for examples of specifying different output elements and intervals.

D.

```
Would you like output to the CRT rather than a standard file? (N)<R>
Would you like a 32 day test run? (N)<R>
Write COEFS & INITIAL CONDITIONS?(Y)<R>
Beginning run:    Diatom Fraction reduced to 0.5

RUNNING   1 YEARS STARTING MONTH   1     4 PLOTS   OUTPUT UNIT   14
```

Replying "Y" to any of these three questions can 1) re-direct the numerical output to the screen, 2) shorten the run to a brief 1 month for testing, and 3) eliminate the list of the coefficient values from the output.

Normally, the run will generate a plot on-screen during the run. Numerical output is sent to a standard file named "BayModelRun" that then may be analyzed in the Analyzer stack, viewed with a text editor, or printed. This output includes a list of all coefficients and conditions for this run. You may want to suppress this output to the screen, but always allow these coefficients to be printed with the file output. The additional pages of output are your only confirmation that the run is what you intended. And, you cannot use the Bay Model Analyzer except on standard output files.

E. Writing disk files of detailed output in EXCEL format,
for these elts/tanks:
1, Enter one ELT# for only 1, -1 for all, or RETURN (NONE)

This option creates an additional file that may be loaded into the spreadsheet Excel™ for further statistical analysis and plotting. If you are running multiple tanks or bay elements, you may choose this detailed output for any single one by entering its number. Entering "-1" should create a file for each simulated tank or bay element. (This has not been fully tested for more than one tank's output...)

F. Run time MAC screen plotting?(Y)

The last option can suppress the run-time plot of the simulation. This would be desirable if you routed the numerical output to the CRT (in D above).

At last, the endless stream of queries are done, and you may sit back and let the computer go to work.

RUNNING THE 8 ELEMENT BAY VERSION

A standard data file on the disk allows the full model of the bay to be run. Physiological coefficients are largely the same, but the outside input of nutrients and the seasonal presence of carnivores substantially differ. All 8 elements must be simulated, and mixing occurs by the TIDE subroutine, so bay runs take longer than MERL runs of a single tank. To run the full bay model, load the file BAY8.NBM in response to the "Change Parameters" query after entering the simulation program. This is Option 2 in section B of the run dialog:

```
B .     Running:   1 years, starting month   1 (day    1);
        Daily output starting month   0 for   0 days;
         4 Plot(s).

        Enter 1 (Run) or 2 (Change parameters) (Default=1):2<R>
        Enter a FILENAME to run from saved file:(none)BAY8.NBM<R>
```

When the file loads, you will want to look at Menu 1 (Init. Specs.) and 6 (Nutr.) to confirm that MIXOPT=1 and that nutrient inputs are appropriate.

Running the BAY8 version raises the possibility of specifying plots and detailed results for more than one region. You control the variable and the element when specifying plots using Menu 10 (PLOTS). Monthly output is controlled with the array ELTOUT that can be changed either in Menu 1 (Init. Specs.) or with the question that arises as the run begins after leaving the Change Parameters section. Section "C" in the run dialog changes, and now indicates the output interval for the the 8 elements:

```
C .     Output every ( 0, 0, 0, 1, 0, 0, 0, 0)  months for 8 elements.
        You may enter new Output Freq. (months) for up to 8 elements
        (Zeros OK if some tanks not to have output):3,0,0,1,0,0,0,0<R>
```

You must enter 8 numbers separated by commas. This example reply would generate detailed output every 3 months for element 1 (Prov. R.), every month for element 4 (mid west passage), and none for the other regions. Plotting is independent of the tabular output, and you may find that plots of many regions and tabular output of a single one allow for adequate evaluation. The Analyzer will only work properly with monthly output tables from a single tank or bay element. After you have familiarized yourself with the output, the standard output file can be studied with any text word processor if the Analyzer gets confused!

RUNNING THE BASIN VERSION

You can define a basin of any depth, volume and flushing rate by changing MIXOPT, XF, etc. in the "Initial Specifications" menu. Additionally, you would want to specify all initial conditions, nutrient inputs, and perhaps other variables. However, the most practical way to run the Basin version is to load either the default MERL or BAY8.NBM files, make changes to MIXOPT, the dilution factor XF and any other conditions or coefficients. This defines one or more basins with the characteristics of a MERL tank, or one of the original bay elements, but treats them independently using the simple flushing scheme. In this way, for example, you might run a basin quite similar to mid-West passage element of BAY8 without the computer time to simulate the other seven regions. Saving the parameter file after you make these changes (Menu 12, below) can provide a standard for a new series of basin runs.

MODIFYING THE DEFAULT PARAMETERS

After the model displays the run length, whether you have specified daily output, and how many plots have been specified, you are given two RUN OPTIONS. Choosing OPTION 2 transfers to the Change Parameter section. There, you are given the chance to load a previously saved file of run specifications. If you enter a file name, the file is loaded, its name and ID are reported to you, and you are given the opportunity to make further changes to these specifications. If you do not enter a file name, you may proceed to change the default parameters.

Upon reaching section "B" of the run dialog, choose Option 2 (enter "2<R>") and no saved file (<R>).

B.

```
Enter 1 (Run) or 2 (Change parameters) (Default=1):2<R>
Enter a FILENAME to run from saved file:(none)<R>

 You may change values in the following groups:
*************************************************
* 1. INITIAL SPECIFICATIONS 2. PHYTO. Coeffs.   *
*                                               *
* 3. ZOO. Coeffs.            4. uZOOPL. Coeffs. *
*                                               *
* 5. BENTHIC Coeffs.         6. NUTRIENT Coeffs.*
*                                               *
* 7. CARNIV. Coeffs.         8. PARTICULATE C   *
*                                               *
* 9. RIVER FLOW Coeffs.     10. PLOTS           *
*                                               *
*11. INITIAL STOCKS         12. SAVE NEW PARAMETERS*
*                                               *
*13. RUN MODEL                                  *
*************************************************
ENTER YOUR CHOICE:(CR=13, Run)1<R>
```

• Entering numbers 1-11 allow you to change conditions and parameters of the model. Choice 12 will save your choices in a file for later uses; 13 initiates the run.

• In each sub-menu, you may change the various parameters by entering first the index of the number to be changed, and then the new value. Entering "-99" will refresh the sub-menu, and "0" or <R> will return to the main menu. *After entering a new value, you must confirm the change -- if you type anything but a return <R> the change will be aborted.* "Done." confirms the change, and you are given a chance to make another change in the same sub-menu.

```
Enter 99 to REFRESH menu and 0 for Main Menu;
Enter INDEX * of parameter and NEW VALUE:25,.6<R>
Hit RETURN to change .700000 to .600000   OK?<R>
Done.
Enter 99 to REFRESH menu and 0 for Main Menu;
Enter INDEX * of parameter and NEW VALUE:
```

• In some cases, values are needed for each of the tanks or elements to be simulated (based on the current value of MAXELT). These are indicated by "()" and are to be entered as separate items, one-by-one.

```
Variables followed by () are arrays,
and only the value for array element 1 is shown.
```

The following menus appear for the first 11 choices. Try them out. You can always return to this main menu with no changes just by hitting RETURN.

Menu 1: INITIAL SPECIFICATIONS.

```
Variables followed by () are arrays;only element 1 is shown.
INITIAL  SPECIFICATIONS:
    ********************************************************************
    *      1-8  VOL();        9-16 DEPTH();     17-24 EXCOEFF();   25   ATMEX; *
    *        13.10E+00             5.00              .30               .70   *
    *       26 Avg. Temp;     27 T amplitude;   28 Jday of T-min.            *
    *            11.50             8.50              40.                     *
    *       29   XF             30   MIXOPT (1=BAY;2=MERL;3=BASIN)          *
    *           .980                2                                        *
    *   31-38 ELTOUT();       39   MAXELT;        40 YEARS;         41 MONTH;  *
    *                  1              1                 1                 1   *
    *       42     LAG;          43 Mon for daily 44 for * days;  45 INSOL.   *
    *                 0              0                 0                 0    *
    *       46   FixT() (±∂T for 12 months x 8 elements)                      *
    *       .0    .0    .0    .0    .0    .0    .0    .0    .0    .0    .0   *
    ********************************************************************
```

1-8. **VOL()**: Volume of the tank or bay element in cubic meters.

9-16. **DEPTH()**: Depth of the tank or bay element in meters.

17-24 **EXCOEFF()**: The background diffuse attenuation coefficient for visible light in seawater (m^{-1}). The total extinction coefficient is simulated as the sum of this constant background plus a term dependent on the Chl. a concentration (see PHYTO menu).

25. **ATMEX**: The atmospheric extinction coefficient (fractional reduction). Based on INSOL (item 40) Solar radiation is interpolated from a theoretical, clear sky maximum for the latitude of Narragansett Bay, then reduced by this empirical fraction plus a cloudiness term. Modifying ATMEX will systematically reduce the light reaching the surface, but will usually have small effects because the phytoplankton are assumed to acclimate to 1m light levels down to a threshold. (See PHYTO: REQIAV)

26-28. **Avg. Temp, T amplitude, Jday of T-min.**: Define the seasonal temperature pattern, a sinusoid varying around the average with its minimum on a specific Julian day. The default equation specifies 11.5°C ± 8.5, reaching the minimum of 3.0°C on February 9 (Jday 40). **FixT** (#46 below) allows each of the spatial elements or MERL tanks to be different.

29-30. **XF, MIXOPT**: Select among three options for physical mixing.

MIXOPT=1 runs the tidal mixing routine for the 8 spatial elements of the bay. Tidal mixing driven by daily tidal heights at Newport for 1974 occurs automatically. River flow and inputs are controlled under River Flow (menu 9 below).

MIXOPT=2 runs the MERL scheme with daily additions approximating the actual additions of the Eutrophication Experiment. (You begin the run June 1st, or you may start January 1st, in which case the data from June-December 1973 are passed, and input begins 1/1/74.

MIXOPT=3 runs a simple basin flushing model assuming a constant daily flushing rate of XF. A value of 0.98 for XF results in a 2% net loss by exchange and dilution daily. You may load either MERL or 8-element bay data files, then change MIXOPT to 3 to run either case with the simple flushing scheme.

31-38. **ELTOUT()**: Specifies the frequency in months for detailed tabular output. MAXELT values (up to 8) are required, one for each simulated tanks or elements.

Example: ELTOUT():1,0,3,0,6 would result in monthly output for tank 1, every 3 months for tank 3, every 6 months for tank 5, and no output for tanks 2 and 4. Tanks greater than the highest non-zero ELTOUT are not simulated; Bay model elements are always all simulated.

39. **MAXELT**: The maximum number of entities to be simulated. This is tanks in the MERL case, and may often be less than the maximum of 7 tanks (treatments) of the eutrophication experiment. For the Bay model, all 8 spatial elements *must* be simulated. This is an important choice, as it determines the runtime of the simulation! Fewer run faster, and you can use Basin physics to estimate for one part of the bay (see "Running the Basin Version").

40. **YEARS**: Duration of the run. This is usually 1 year, but may be longer. (See Lag.)

41. **MONTH**: The starting point of the run, 1=Jan, 2=Feb, etc. Specifying a starting month other than January results in a run of YEARS plus the remainder of the partial year. Thus a start MONTH of 6 would run from June for 1.5 years (MONTH=6 and YEARS=2 is the choice to simulate the total MERL experiment, but remember that this long a run would not load properly into the present version of the Analyzer.)

42. **LAG**: If you specify MONTH≠1, you may want to suppress output until Jan. 1 of the new year. LAG>0 will cause this, and is useful to allow the model to "spin up" to avoid transients associated with unrealistic initial zooplankton age structure, etc. This has been rarely used. Winter is generally inactive, and January is a good ecological starting time. Also, the model does not simulate the winter period well for reasons that still need investigation (in the field as well as the model!), so LAG-ed runs, and multiple year runs have not been used much. Month=6, YEARS=1,LAG=1 would run 1.5 years, but print results only for a full year after a 6 month spin-up. Since only one year is saved, this run would load properly in the Analyzer.

43. **Mon for daily**: Specify the MONTH (1-12) when you would like to initiate DAILY OUTPUT of the detailed tabular summaries.

44. **for # days**: Specify the number of consecutive days of DAILY OUTPUT that are desired. For example, changes "43,2" and "44,10" would add 10 days of detailed output starting the first of February to the output file.

45. **INSOL**: Formerly there were three options for specifying solar insolation. (INSOL<0 to read 365 day's of real light data; INSOL=0 to interpolate cloud cover daily given long term monthly averages for Narragansett Bay (Green Airport); INSOL>0 to use a stochastic cloudiness generator.) Because phytoplankton I_{opt} acclimates daily to insolation, the model has proved to be insensitive to these three options. Use of the default INSOL=0 is likely to be satisfactory; only it is implemented in this version. (See ATMEX above and REQIAV in PHYTO.)

46. **FixT()**: Correction factors allowing spatial and temporal variation from the average temperature equation (above). You may specify monthly factors that differ by spatial region in the bay (or by MERL tank). The computed average temperature each day is adjusted by these factors In the MERL standard run, default values of FixT are 0.0; in the full bay version (BAY8.NBM) representative spatial variation is included (see Kremer & Nixon p. 24). The dialog to change the values of FixT asks you to enter the correction in degrees (+ or −) for 12 months for each of the spatial regions or tanks to be simulated:

```
Enter INDEX * of parameter and NEW VALUE:4<R>          to change FixT
Accepting 12 ±∂T shifts; for which element?1<R>        Tank #1
Enter the new value for * 1(-1 exits):                 i.e., For January
4.<R>                                                  T will be Tavg+4
Hit RETURN to change        .000 to        4.000  OK?<R>  Anything else cancels.
Done.
```

Etc., for all remaining months for this region or tank. Menu will confirm updated values.

Menu 2: PHYTO. Coeffs.

This compartment represents 2 species-groups of phytoplankton. "P1" & "P2" are designed to be diatoms and nanoflagellates; in fact, they are whatever is defined by the coefficients below.

```
PHYTO.  COEFFICIENTS:
        ****************************************************************
      * 1-2    C:N (P1)    ; 3-4     C:N (P2)                           *
      *        7.00  7.00          7.00  7.00                          *
      * 5-6    C:P (P1)    ; 7-8     C:P (P2)                           *
      *       85.00 85.00         85.00 85.00                          *
      * 9-10   C:SI(P1)    ; 11-12   C:SI(P2)                           *
      *       5.00 5.00         15.0015.00                             *
      * 13      C:DWP1       ; 14       C:DWP2 ; 15 C:CHL1             *
      *           .300                 .300  30.00                      *
      * 16   C:CHL2          ; 17       KNP1    ; 18    KNP2           *
      *         30.00                 1.50     .75                      *
      * 19     KPP1          ; 20       KPP2    ; 21   KSIP1           *
      *           .05                  .05     .50                      *
      * 22     KSIP2         ; 23       SIOP1   ; 24   SIOP2           *
      *           .05                  .00     .00                      *
      * 25    REQIAV         ; 26-27 ChlK, ChlK2                       *
      *       40.00                  .0090 .0000                       *
      * 28-31   P1GMX0, P1GMXT ;   P2GMX0, P2GMXT                       *
      *             .5900     .0633     .5000     .0500                 *
      * 32-35     P1S0,   P1SLM ;     P2S0,   P2SLM                    *
      *             .2000     .0000     .0000     .0000                 *
        ****************************************************************
```

1-14. **C:N, C:P, C:SI, C:DW:** Elemental atomic ratios (µg-at C/µg-at N) specify the composition of the 2 P-groups, P1 & P2. Min and max values must be specified for each, but for now they are identical since no scheme is included to control the mechanism. This would be easy -- any suggestions? The carbon-dry weights are not used in this version of the model.

NOTE: When P2=0, C:Si varies seasonally, and it is important that items 9&10 be changed to 15 & 5 to allow the major annual changes in diatom dominance to be crudely represented. See Kremer and Nixon 1978, p. 133.

15-16. **C:CHL (mg C/mg Chl):** Chlorophyll content is not simulated. These forced values are used to convert initial P1 & P2 stocks to carbon, to compute their contribution to extinction coefficient, and to print out an estimate of simulated carbon stocks as chlorophyll.

17-24. **KN, KP, KSI, SI0 (µg-at/L):** Half saturation coefficients for growth for both P-groups and the 3 nutrients. SI0 is a threshold that may be used to cause zero growth as a finite [Si]. G/Gmx = N/(K + N) or G/Gmx = (SI-SI0)/(KSI + Si-SI0).

25. **REQIAV (ly/day water column average):** Lower limit to light acclimation. Iopt, for the Steele P-I formulation. The value of 40 is based on Riley's 1967 estimate for long Island Sound. (Kremer and Nixon 1978, sec. 4.3 & p.134.)

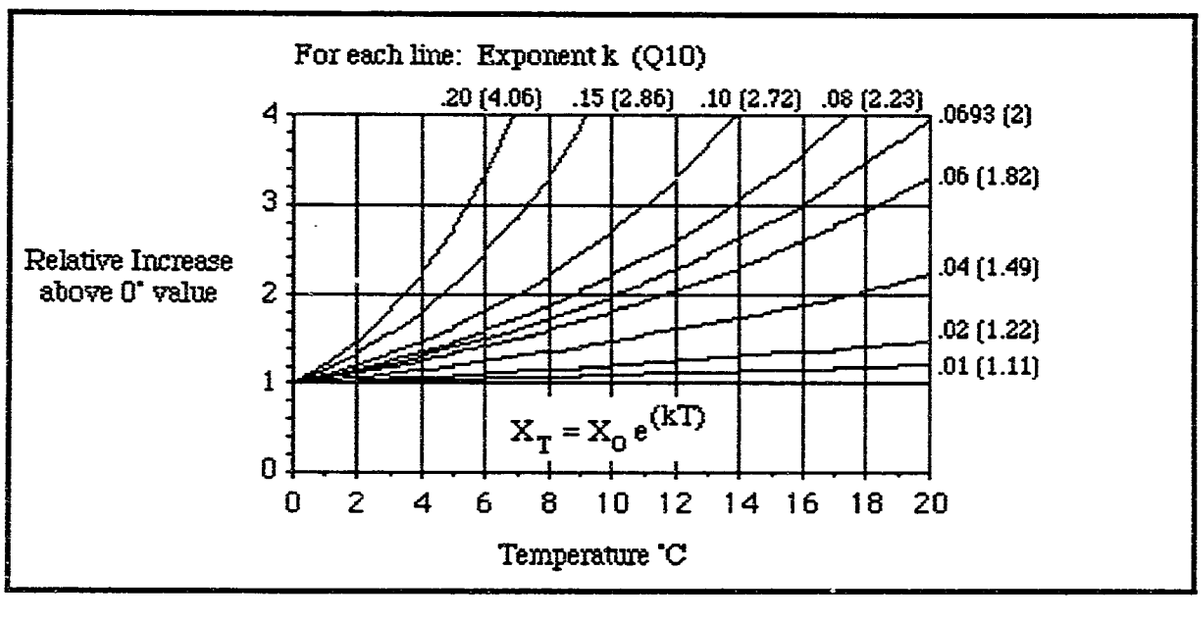
26-27. ChlK, ChlK2: The Chl-K eqn. defines the extinction coefficient (per m) as a function of background absorbance and the stock of chlorophyll (µg/L). k_O is the constant background, non-Chl term (see EXCOEFF); coeffs. ChlK and ChlK2 set the Chl-dept. contribution. Common choices are a linear eqn. based on MERL data (set CHLK2=0) and Riley's 1956 quadratic model.

$$k=k_O + (ChlK)*C + (ChlK2)^{2/3}$$

Riley:	0.0088	0.054
MERL:	0.009	0.0

28-31. Growth: GMX0 (d^{-1}), GMXT ($°C^{-1}$): The max continuous growth rate (per day, base e) is an exponential function of Temp., starting at GMXO at 0°C. For each of the P-groups: $G_{mx} = G_{mx_0} * \exp(G_{mx_T}*T)$.

Refer to the following chart in selecting the exponent; both the instantaneous exponent and the equivalent Q_{10}'s are indicated. This chart will be helpful for many other parameters.



32-35 S0(m/d), SLM (unitless): Specify the sinking rate S (m/d) as a linear function of nutrient limitation for the 2 P-groups. Using LIM, the unitless hyperbolic term for the most limiting nutrient, the sinking rate S = S0 + SLM * LIM.

NOTE: SLM should usually be negative, since S=S0 when LIM=0, and S is reduced as NLIM increases to 1.0. Sinking phyto. carbon is passed directly to the benthic SEDC compartment.

Menu 3: ZOO. Coeffs.

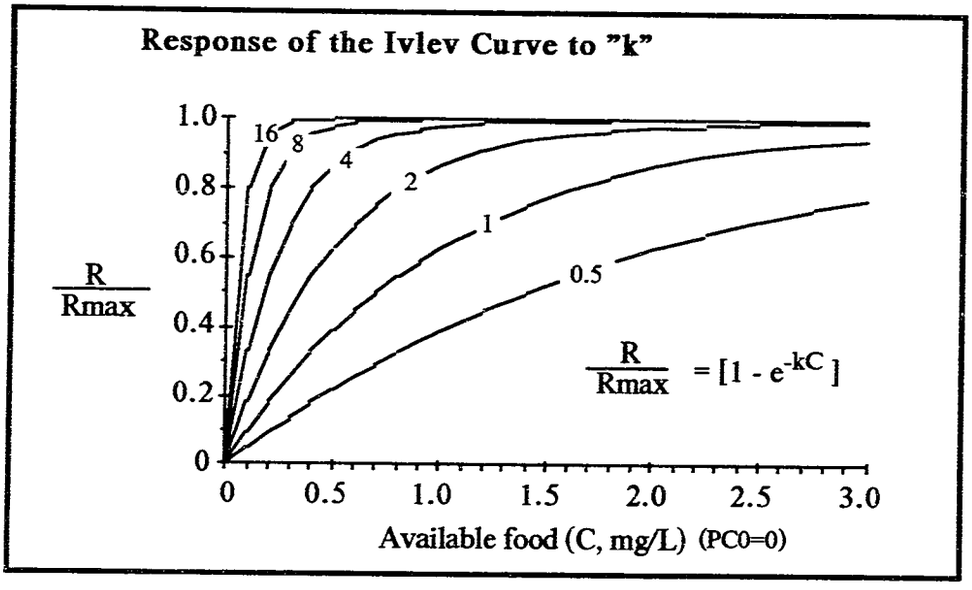
This compartment represents copepods. Often considered herbivores, they are omnivores in the model, feeding cannibalistically and on µzoo and POC depending on the feeding efficiencies (see ZFExx). Adults produce eggs, which hatch and develop as juvenile cohorts.

ZOOPLANKTON COEFFICIENTS

1. IvlevK	2. PC0	3. RmxO	4. Q10Rmx)	5. XRspO	6. Q10Rsp
7.00	.000	.000	1.00	.100	2.00
7. XRP	8. ZEP0	9. ZEPT	10. CxN Z	11. CxP Z	12. CxDW Z
.250	.200	0.600E-01	5.00	85.0	.350
13. XAssim	14. ZJGmxO	15. ZJGmxT	16. RJxRA	17. SAFE	
.800	0.300E-01	.100	1.44	.200	
18. ZFE P1	19. ZFE P2	20. ZFE PC	21. ZFE ZJ	22. ZFE UZ	23. JZmax
1.00	1.00	1.00	1.00	1.00	150

1. **IvlevK (l/mgC)**: The curvature term for the hyperbolic food limitation effect. Based on the total particulate carbon available as food (PCMG), the ration is reduced by a fraction (FLIM) dependent on this term: $FLIM + 1 - e^{(IVLEVK*PCMG)}$. (The "foodlim" effect is applied in the model by reducing both the metabolic demands that contribute to estimating the ration: respiration and egg production/growth.) The total available food depends on the ambient stocks, the feeding efficiencies (ZFEP1, etc.), and the threshold (PC0). For adult zooplankton, the potential food includes: both algal groups, eggs and juveniles not SAFE from cannibalism, µzooplankton, and particulate carbon if present. For juveniles, potential food includes only the 2 algal groups and particulate carbon, assuming that they are not carnivorous.

   The chart below shows the Ivlev limitation factor for values of IvlevK from 0.5 - 16.



2. **PC0 (mgC/l)**: Threshold for feeding of zooplankton. If the total available food (the sum of the potential food groups times their respective feeding efficiencies) is less than PC0, the estimated ration is zero. This rarely happens, since the food groups are lumped. At the present time, it is not possible to specify different thresholds for feeding on the various potential foods.

(3, 4) Rmx0 (d^{-1}), Q10Rmx (unitless): No longer used in this version of the model.

5. **XRsp0 (d^{-1}):** The specific respiratory rate at 0°C without growth or egg production. Based on the Q_{10}, this basal rate is adjusted for the ambient temperature.

6. **Q10Rsp (unitless):** The temperature effect on respiration, Q_{10}. With Q_{10} = 2.0, respiration will double with a 10°C raise in temperature. (In the model, this Q_{10} is converted to the appropriate exponent.) Refer to the chart with G_{mxT} in the Phyto Menu in selecting the exponent.

Coefficients 7, 8 & 9 are used together to specify the specific egg production of adults (SEP). A similar formulation is used for juvenile growth (GRO) based on coefs. 14, 15 & 7.

7. **XRP (unitless):** A fraction specifying the respiratory cost of secondary production. Part of the total respiration is related to the specific production rate. For adults, the amount of assimilated ration needed to produce a certain specific egg production (SEP) is thus SEP*(1+XRP), and the SEP possible given available assimilate is AVAIL/(1+XRP).

8. **ZEP0 (d^{-1}):** Specific egg production rate at 0°C, for adults.

9. **ZEPT ($°C^{-1}$):** Slope of the specific egg production rate (SEP) vs. T(°C), for adults. It is calculated as SEP = ZEP0 + $e^{(ZEPT*T)}$. Refer to the chart with GmxT in the Phyto Menu in selecting the exponent.

10-11. **CxN, CxP Z (µg-at C/µg-at N or P):** Atomic C:N and C:P ratio for all zooplankton. Since the content of food varies, growth maintains the proper tissue composition before releasing any N or P by excretion.

12. **CxDW Z (mgC/mg DW):** C:dry weight ratio for all zooplankton. This is only used to convert the initial condition (d.w.) into carbon.

13. **XAssim (fraction):** Assimilation efficiency. This fraction applies for adults and juveniles and all foods.

14. **ZJGmx0 (d^{-1}):** Maximum juvenile specific growth rate at 0°C.

15. **ZJGmxT ($°C^{-1}$):** Slope of the maximum specific growth rate vs. T(°C), for juveniles. Gmx is calculated as ZJGmx = ZJGmx0 + $e^{(ZJGmxT*T)}$. The temperature dependence of development time uses the same exponent, thus insuring that the biomass of juveniles at maturity is the uniform throughout the year. Refer to the chart with GmxT in the Phyto Menu in selecting the exponent.

16. **RJxRA (unitless):** Allometric conversion factor to correct for higher juvenile weight-specific respiration rate. The final calculated juv. resp. differs from the adult rate as it takes into account growth, foodlim and temp, but the RJXRA term essentially increases Juv. rate to Adult resp. * RJXRA. (See Kremer and Nixon 1978, sec. 5.4, p. 76)

17. **SAFE (unitless):** The fraction of juvenile development time that they are safe from adult cannibalism. SAFE = 0.8 means predation occurs for the first 80% of development. SAFE=1.0 means no adult cannibalism.

18-22. **ZFE P1, P2, PC, ZJ, UZ (unitless):** Feeding efficiencies of zooplankton on algal group P1 (diatoms), group P2 (flagellates), non-living particulate carbon, zoo. juveniles, and µzoo, respectively. Use these terms to specify all or part of the food group as unavailable.

ZFEP1=1 allows complete feeding; ZFEP1=0 excludes feeding on this food source. ZFE ZJ and UZ apply to adults feeing on juveniles (see SAFE) and eggs as well as µzoo.

23. **JZmax (days, or cohorts):** The development time for hatching eggs depends on temperature assuming the exponent -ZJGMXT. JZmax is the theoretical intercept for 0 C. For each hatching cohort, D is the average of D1 for the temp. on the day of hatching and D2 for the temp. that many days in the future (which is known in advance in the model!). Day-to-day food availability may further change the simulated development. Each cohort is tracked separately. The actual number of cohorts changes throughout the runs, and the model keeps track of how many are active.

Menu 4: uZOOPL. Coeffs.

This compartment is based on recent literature for tintinnids, especially in Narragansett Bay. Every attempt has been made to make the formulations general, however. The meaning of the µZooplankton coefficients are essentially identical to those in the copepod compartment, except that all secondary production goes directly into a single compartment with no life history variations.

```
u-ZOOPLANKTON  COEFFICIENTS
*************************************************************************
*  1. uZ IvK    2. uZGmx0    3. uZGmxT    4. uZRsp0    5. uZRspT         *
*     1.00         .250          0.600E-01    .100         0.693E-01      *
*  6. uZ CxN    7. uZ CxP    8. uZFEP1    9. uZFEP2   10. uZFEPC          *
*     5.00        85.0          1.00         1.00         1.00            *
* 11. uZ PC0   12. uZ AE    13. uZ XRG                                    *
*     .000         .800          .100                                     *
*************************************************************************
```

1. **uZ IvK (l/mgC):** The curvature term for the hyperbolic food limitation effect. Based on the total particulate carbon available as food (PCMG), the ration is reduced by a fraction (FLIM) dependent on this term: $FLIM = 1 - e^{(IVLEVK*PCMG)}$. (The foodlim effect is applied in the model by reducing both the metabolic demands that contribute to estimating the ration: respiration and growth.) The total available food depends on the ambient stocks, the feeding efficiencies (uZFEP1, etc.), and the threshold (uZPC0). For µzooplankton, the potential food includes: both algal groups and particulate carbon. Refer to the chart with IvlevK under the Zooplankton Menu in selecting values.

Coefficients 2-4 & 13 are used together to specify the specific growth rate (GRO).

2-3. **uZGmx0(d^{-1}), uZGmxT($°C^{-1}$):** Define the maximum specific rate as an exponential function of temperature. This rate may be reduced due to insufficient food according to the Ivlev equation (see IvK). Ingestion is based on growth and total respiration.

4. **uZRsp0 (d^{-1}):** The specific respiratory rate at 0°C without growth. Based on the temperature exponent, this basal rate is adjusted for the ambient temperature.

5. **uZRspT ($°C^{-1}$):** The temperature exponent for respiration. This term is used directly in the exponential equation, but has the same effect as the Q10 used for zooplankton. Here, uZRspT=.0693 is a Q_{10} of 2.0. The equation is $XRESP = uZRsp0 * e^{(uZRspT*T)}$. Refer to the chart with GmxT in the Phyto Menu in selecting the exponent.

6-7. **uZ CxN, CxP (µg-atC/µg-at N or P):** Elemental composition for µzoo. biomass. Since the content of food varies, growth maintains the proper tissue composition before releasing any N or P by excretion.

8-10. **uZFEP1, P2, PC (unitless):** Feeding efficiency of µzooplankton on algal group P1 (diatoms), group P2 (flagellates), and non-living particulate carbon. Use these terms to specify all or part of the food group as unavailable. uZFEP1=1 allows complete feeding; uZFEP1=0 excludes feeding on this food source.

11. **uZ PC0 (mgC/l):** Threshold for feeding of µzooplankton. If the total available food (the sum of the potential food groups times their respective feeding efficiencies) is less than PC0, the estimated ration is zero.

12. **uZ AE (unitless fraction):** Assimilation efficiency for all µzoo ingestion.

13. **uZ XRG (unitless):** A fraction specifying the respiratory cost of secondary production. Part of the total respiration is related to the specific production rate. The amount of assimilated ration needed to produce a certain specific growth (GRO) is thus GRO*(1+XRP), and the GRO possible given available assimilate is AVAIL/(1+XRP).

Menu 5: BENTHIC Coeffs.

This compartment offers 3 options: 1) Force the nutrient fluxes and filtering rates; 2) Model the benthos without allowing growth of macrofauna; 3) Model the benthos with growth. Because of these options, not all the menu terms are active in any given run.

BENTHIC COEFFICIENTS

1.ForceB(1/0)	2.BGrow(1/0)	3. VfiltO	4. QVfilt	5. FlxAmO	6. FlxAmT
T	F	0.600E-02	5.00	.142	.160
7. XDenit	8. FlxPO	9. FlxPT	10. FlxSiO	11. FlxSiT	12. Flx02O
.300	0.180E-01	.130	.554	.120	.378
13. Flx02T	14. OxLslp	15. BRO	16. QBR	17. C:N B	18. C:P B
0.870E-01	.250	0.100E-02	4.00	5.00	85.0
19. FF AE	20. FF EP1	21. FF EP2	22. FF EPM	23. FF EuZ	24. Fscope
.800	1.00	.000	1.00	.000	1.00
25. BBmin	26. Dscope	27. Bac RO	28. Q BacR		
1.00	1.00	0.800E-01	2.00		

1. **ForceB (logical: T or F):** Specifies whether the benthic processes are to be forced or not. When ForceB is True (you enter a 1, but it is shown at "T"), nutrient and oxygen fluxes are forced by the empirical temperature dependent equations below. F (you enter "0") allows benthic processes to be fully simulated.

2. **B Grow (logical: T or F):** Specifies whether benthic macrofauna are to be allowed to grow; BGROW is only active if ForceB=F, and the growth is then based on the scope for growth specified for filter and deposit feeders below. (You enter "1" for True, "0" for False.)

3, 4. **Vfilt0 (m^3/day/mgC), QVfilt (unitless):** Set the max stock-specific filtering rate of benthic filter feeders vs. temperature. The rate at 0°C increases with the specified Q_{10}. With Q_{10} = 2.0, the rate will double with a 10°C rise in temperature. (In the model, this Q10 is converted to the appropriate exponent.) If FORCEB=T: this eqn. forces the filtering rate. If

FORCEB=F: the eqn. sets an arbitrary upper limit to control the estimated rate based on the ration and available food. Refer to the chart with G_{mxT} in the Phyto Menu in selecting the exponent.

Terms 5-12 deal with the nutrient fluxes. When ForceB=True, these equations drive the fluxes. When ForceB=False, simulated fluxes are compared to these equations to help interpret the results. In the bay version, the equations for N, P, and Si are based on Nixon's recent revision of these flux equations. For the MERL version, MERL equations are used.

5. **FlxAm0 (mg-at. NH_4-N·$m^{-2}d^{-1}$)**: The 0°C intercept of the equation for the empirical flux of ammonium.

6. **FlxAmT ($°C^{-1}$)**: The temperature exponent for the ammonium flux equation.

7. **XDenit (unitless fraction)**: If FORCEB=F, this is the fraction of the total ammonium flux generated by the benthos that is assumed to be lost from the system as N2 gas. When ForceB=T this has no effect.

8. **FlxP0 (mg-at. PO_4-P·$m^{-2}d^{-1}$)**: The 0°C intercept of the equation for the empirical flux of phosphate.

9. **FlxPT ($°C^{-1}$)**: The temperature exponent for the phosphate flux equation.

10. **FlxSi0 (mg-at. Si·$m^{-2}d^{-1}$)**: The 0°C intercept of the equation for the empirical flux of silicon.

11. **FlxSiT ($°C^{-1}$)**: The temperature exponent for the silicon flux equation.

12. **FlxO20 (gm O_2·$m^{-2}d^{-1}$)**: The 0°C intercept of the equation for the empirical uptake of oxygen.

13. **FlxO2T ($°C^{-1}$)**: The temperature exponent for the oxygen uptake equation.

14. **OxLslp (liters·mgO_2^{-1})**: The slope of an equation to reduce benthic respiration at low oxygen levels. The equation has no intercept and produces OXLIM that is multiplied by the BRESP from terms 15 & 16. OXLIM = OxLslp * OX (OX in mg/L)

15. **BR0 (d^{-1})**: The specific respiratory rate at 0°C of benthic macrofauna. Based on the Q_{10}, this basal rate is adjusted for the ambient temperature. (See QBR & OXLIM)

16. **QBR (unitless)**: The temperature effect on respiration, Q_{10}. With Q_{10} = 2.0, respiration will double with a 10°C rise in temperature. (In the model, this Q_{10} is converted to the appropriate exponent.) The specific respiration rate (mgC.mgC-1 d-1) specified here is used for filter and deposit feeders. Refer to the chart with G_{mxT} in the Phyto Menu in selecting the exponent.

17-18. **C:N, C:P B (µg-at C/µg-at N)**: Atomic C:N and C:P ratio for all benthic macrofauna.

19. **FF AE (unitless)**: Assimilation efficiency of filter feeders.

20-23. **FF EP1, P2, PM, uZ (unitless)**: Feeding efficiency of filter feeders on algal group P1 (diatoms), group P2 (flagellates), non-living particulate matter, and µzoo, respectively. Use this term to specify all or part of the food group as unavailable. FFEP1=1 allows complete feeding; FFEP1=0 excludes feeding on this food source.

24. **Fscope (unitless)**: Scope for growth of filter feeders at 0°C, defined here as a stock-specific fraction. When ForceB=False and Bgrow=True, this specifies the maximum daily growth increment allowed (i.e. Fscope=0.1 allows a maximum growth of 10% daily). The target feeding rate is calculated to provide respiration plus this scope after assimilation. If food is limiting, the actual ration may be less. Since this term is used with respiration, any temperature effect on respiration also affects the scope.

25. **BBmin ($gmC \cdot m^{-2}$)**: Arbitrary lower limit to benthic biomass, used for both filter feeders and deposit feeders.

26. **Dscope (unitless)**: Scope for growth of deposit feeders 0°C, defined here as a stock-specific fraction. When ForceB=False and Bgrow=True, this specifies the maximum daily growth increment allowed. The target feeding rate is calculated to provide respiration plus this scope after assimilation. If food is limiting, the actual ration may be less. Since this term is used with respiration, any temperature effect on resp. also affects the scope.

27. **Bac R0 (d^{-1})**: The bacterial decomposition rate at 0°C. Based on the Q_{10}, this basal rate is adjusted for the ambient temperature. Designed to represent microbial and meiofaunal metabolism, a single equation determines an instantaneous first order decay of sedimentary carbon. (see Q BacR)

28. **Q BacR (unitless)**: The temperature effect on bacterial decomposition; a Q_{10}. With Q_{10} = 2.0, decomposition will double with a 10°C raise in temperature. (In the program, this Q_{10} is converted to the appropriate exponent.) Refer to the chart with G_{mxT} in the Phyto Menu in selecting the exponent.

Menu 6: NUTRIENT Coeffs.

This compartment includes the concentrations of dissolved inorganic N, P, Si, and O_2. Fluxes in the model mostly are defined through connections with other compartments, so few additional coefficients need specification.

```
NUTRIENT  COEFFICIENTS
      ********************************************************************
      * 1      K20          ; 2       THETA                               *
      *      0.680E-01              1.19                                  *
      * 3-10   SWGAM()      ; 11-18   SWGON()                             *
      *        .000                  .000                                  *
      * 19-26  SWGP()          ; 27-34   SWGSIL();       35-42 Diff K()    *
      *        .000                  .000                  .700            *
      ********************************************************************
```

1, 2. **K20 (hr^{-1}), THETA(unitless):** Empirical constants defining the rate of pelagic nitrification vs. temp., based on a value specified at 20°C.

$$K_t = K20\ \theta^{(T-20)}$$
$$NO_2{+}NO_3 = NH_4\ e^{(k_t * dt)}$$

Items 3-34 define daily exogenous nutrient inputs for up to eight spatial elements, tanks, or basins. Runs using the Bay values use rates estimated from sewage samples in 1972 (see K & N '78 sec. 6.4, esp. Table 11, p. 102). For MERL runs, default inputs represent the treatments in the Eutrophication experiment, with model tank 1 the control (no inputs except through the header tank, tank 2 the 1X treatment, tank 3 the 2X, etc.

3-10. **SWGAM (µg-at NH_4-N per day):** The total external input of ammonium into each spatial element of the model. This is an array with different values for each tank or bay region.

11-18. **SWGON (µg-at $NO_2{+}NO_4$-N per day):** The total external input of nitrate plus nitrite into each spatial element of the model. This is an array with different values for each tank or bay region.

19-26. **SWGP (µg-at PO_4-P per day):** The total external input of phosphate into each spatial element of the model. This is an array with different values for each tank or bay region.

27-34. **SWGSIL (µg-at Si per day):** The total external input of reactive silicon into each spatial element of the model. This is an array with different values for each tank or bay region.

35-42. **Diff K (cm/hr):** Diffusion coefficient driving the air-sea exchange of oxygen. No provision for diel or seasonal variations are presently included, so a single average value must be used. The default value is based on direct measurements in the MERL system. In the model, K is multiplied times the saturation deficit SD, and converted to give the rate of diffusion D in mg/L averaged throughout the depth, Z. The concentration of O_2 at saturation, SAT, is estimated from temperature assuming a constant salinity of 30‰. The equations are:

$SAT = 14.161-0.3942*T+7.714E-3*T^2-6.46E-5*T^3-30.*(0.0841-2.56E-3*T+3.7E-5*T^2)$
$SD = SAT - OX$
$D = SD * K * 0.24 / Z$
or with units: $D(mg/L/d) = SD(mg/L) * K(cm/hr) * 24(hr/d) * .01\ (m/cm) / Z\ (m)$

Menu 7: CARNIV. Coeffs.

This compartment is unchanged from the original model (see Kremer and Nixon 1978, secs. 6.1 & 6.2, p. 91ff.) The first order effects of ctenophores, larval fish, and menhaden schools are considered based on forced schedules of monthly abundance. Subroutine CARNIV is not used unless stocks are supplied. These are presently only available in the full model of the Bay, not in the MERL or basin models. (Adding or changing these stock schedules is not possible using the normal dialog menus of the program, but is not difficult. I would be happy to assist anyone who is interested in doing this -- J. Kremer.)

```
CARNIVORE  COEFFICIENTS
*************************************************************************
*  1. FRMXO     2. QFRMX     3. IVFSH     4. CTFLT.    5. CTEXNO    6. CTEXNT  *
*   0.750E-01     2.00         30.0         .100         0.142E-02     .130      *
*  7. IVMENH    8. THRESH    9. RMXMEN                                          *
*    33.0         0.300E-01    500.                                             *
*************************************************************************
```

1-3. **FRMX0 (mgC/fish/d), QFRMX (unitless Q10), IVFSH (L/mgC):** Specify the maximum ration of larval fish as a function of temperature and the Ivlev hyperbolic reduction due to available food concentration.

4-6. **CTFLT(L/mgDW/d), CTEXN0(ug-at/mgDW/d at 0°C), CTEXNT (per °C):** Specify the weight-specific constant filtering rate of ctenophores on copepods, and their temp.-dept. excretion rate.

7-9. **IVMENH (per mgC), THRESH (mgC/L), RMXMEN (mg C/lb. wet wt./d):** Specify the maximum daily ration of menhaden feeding on zooplankton, including Ivlev food limitation and a feeding threshold.

Menu 8: PARTICULATE C.

This compartment represents non-living particulate carbon. Although the model tracks this stock faithfully, no definitive formulations of the source(s) and rates have yet been included, so the compartment is not very useful. It may be used to provide an additional food source to copepods, µzoo, and benthic filter feeders however.

```
PARTICULATE  CARBON  COEFFICIENTS
      ***************************************************************
      * 1      CXNPC      ; 2       CXPPC     ; 3  CXSIPC             *
      *           6.0             100.0           5.0                *
      ***************************************************************
```

1-3. **CXN, CXP, CXSI PC (µg-at C/µg-at N, P, Si):** C:N ratio by atoms for particulate carbon.

Menu 9: RIVER FLOW Coeffs.

The coefficients for this compartment are only used when the full bay model is being run (see MIXOPT in INITIAL SPECIFICATIONS). The Bay version includes river flows, nutrient inputs, and tidal exchanges (see Kremer and Nixon 1978, sec. 3.3-3.5, p. 27ff.).

```
RIVER  FLOW  COEFFICIENTS
       ********************************************************************
       * 1. RIVAM     2. RIVON     3. RIVP      4. RIVSI                   *
       *     .000         .000         .000         .000                   *
       * 5. QBAR      6. QAMP      7. QMIN      8. XTAUNT                  *
       *    41.00E+05    41.00E+05    17.00E+05     .260                    *
       ********************************************************************
```

1. **RIVAM (µg-at NH_4-N)** The concentration of ammonium in river water.

2. **RIVON (µg-at NO_2+NO_4-N)**: The total external input of nitrate plus nitrite in river water.

3. **RIVP (µg-at PO_4-P)**: The total external input of phosphate in river water.

4. **RIVSI (µg-at Si)**: The total external input of reactive silicon in river water.

   NOTE: While nutrient concentrations of river water have been extensively measured, runs with the model have assumed zero; realistic values caused the earlier version of the model to reach unacceptably high levels of all nutrients. We speculated that chemical and biotic processes in the Providence River section were poorly understood and not well modeled, so that nutrients were somehow trapped in this region. This is a serious shortcoming of the model that needs serious study.

5. **QBAR (m^3d^{-1})**: The mean combined river flow of the Providence and Taunton Rivers.

6. **QAMP (m^3d^{-1})**: The amplitude of the annual cycle of river flow around the mean. Peak flow is on day 60 (Feb 1) and equals the total of QBAR + QAMP.

7. **QMIN (m^3d^{-1})**: Empirical minimum river flow. The annual sinusoidal cycle is truncated in the summer months at this value. The equation for total river flow is:

$$Q = Q_{bar} + Q_{amp} * \cos [2\pi (day-60) / 365]$$

8. **XTAUNT (unitless)**: A fraction specifying what part of the total river flow calculated above enters bay element 6 from Mt. Hope Bay; the remainder enters into element 1, the Providence River.

Menu 10: PLOTS.

First this option reminds you of the present plot choices, then gives you the chance to change them. To add more plots to this set of four, you would answer "5" as the 1st new entry. Entering 1, 2, or 3 would begin the additions at that point, keeping the preceding plots.

```
Presently set for  4 plot(s):
     1. ( P1 for elt 1)    ( P2 for elt 1)    (PTOTfor elt 1)
     2. ( ZJ for elt 1)    (ZTOTfor elt 1)    (  UZfor elt 1)
     3. (NH4 for elt 1)    (NO23for elt 1)    (PO4 for elt 1)
     4. (  O2for elt 1)    ( SI for elt 1)    (
You may replace these with new plots, or add more.
Specify the * at which new plots are to be added,
deleting the rest. (Entering "1" will replace all.)
ENTER the * of the 1st NEW entry (0 cancels):5<R>
```

In this example, we entered "5" to add another plot. Upon receiving this answer, the plot code options are listed:

```
ID*  + 1       2       3       4       5       6       7       8       9       10
 0   TEMP    DAYRAD  PHOTPD  K       DEPTH   UANZ    UAPZ    UASIZ   EGGTOT  P1MGC
10   P2MGC   PTOT    ZTOT    ZAMGC   ZJTOT   NTOT    NH4     NO2NO3  PO4     SI
20   POC     O2      UZ      FFB     DFB     CSED    NSED    PSED    SISED   GP1
30   GP2     FCARN   RLFZA   RLFZJ   RLFUZ   RLFBEN  SINKC   SRP1    SRP2    ZRESP
40   uZResp  DNH4    NXCP1   NXCP2   PXCP1   PXCP2   SIXCP1  SIXCP2  DELP1   DELP2
50   DN      DP      DSI     TOTRP1  TOTRP2  TOCARN  EXCN    EXCP    CTEXN   CGAIN
60   FLUXAM  FLUXP   FLUXSI  FLUXO2  TRACER

Now enter: *N lines/plot;&for each [ID* (e.g. PTOT=12) & Elt*], & axis limits
Specify plot:   [*N,(ID*,Elt*,1-N),Max,Min](0 ends):
3,33,1,34,1,35,1,0,0
OK, this plot frame will contain F ZA  F ZJ  F UZ
Enter 3 plot symbol(s)<RET> AND a LABEL<RET>:ZJU
Comparison of Adult, Juvenile & uZoo grazing rates
```

For each plot frame, you specify the number of lines on the plot (1 to 3), for each of these the plot code and tank or spatial element, and finally the max and min for the axis. In the above example, we specify a plot of 3 lines, which are RLFZA (code 33, tank 1), RLFZJ (code 34, tank 1), and RLFUZ (code 35, tank 1). Entering max & min = 0, forces the plot to auto-scale from the highest to lowest value. Or, you may fix the plot axes by specifying real values here.

In this way you may plot any of the variables above for any tank or element. The same plot frame may compare different variables for one region, or the same variable for different tanks or regions. This input cycle repeats until you answer 0 to "Specify plot."

Menu 11: INITIAL STOCKS.

Initial standing stocks and other specifications for the run. NOTE that phytoplankton (PTOT) and copepod (ZTOT) stocks are converted to carbon from values of Chl. and dry wt. Changing initial stocks requires you to specify a new value for each of the 8 elements to be simulated. For example, we might change the division of Chl. from 90% diatoms to 50% as follows:

```
STOCK INITIAL CONDITIONS IN THE 1 ELEMENTS:
 1 PTOT    ugChl/L 1.00
 2 DIAT   fraction .900
 3 ZTOT   mg. DW/L .010
 4 UZoo    mg. C/L .001
 5 NH4     ug-AT/L 4.000
 6 NO2NO3 ug-AT/L 7.000
 7 PHOA    ug-AT/L 1.600
 8 SI      ug-AT/L 22.000
 9 Part C mg. C/L .000
10 O2         mg/L 11.000
11 FFB     gm C/M2 10.000
12 DFB     gm C/m2 10.000
13 SEDC    mM C/M2 .000
14 SEDN    mM N/M2 .000
15 SEDP    mM P/m2 .000
16 SEDSI mM Si/M2 .000
Enter 99 to REFRESH menu and 0 for Main Menu;
Enter INDEX * of STOCKs to change:2<R>
Enter the new value for * 1(-1 exits):.5<R>
Hit RETURN to change       .900 to      .500    OK?<R>
Done.
Enter 99 to REFRESH menu and 0 for Main Menu;
Enter INDEX * of STOCKs to change:<R>
```

The cycle repeats for each tank or element (MAXELT). You must confirm the change by hitting RETURN (the echo "Done" confirms the change was made). Any entry other than RETURN aborts the change. Entering a value -1 exits the change cycle and returns to the menu.

Menu 12. SAVE NEW PARAMETERS.

You may save the set of options as modified in a file to run or to base more changes on later. The saved file uses a name you specify, and includes a descriptive ID phrase you enter. You may want to use a standard file extension to help identify Narr. Bay Model input files, e.g. NAME.NBM

```
Run title is now:STD RUN MERL RUN FROM BLOCKDATA
Enter a new title to change it:Diatom Fraction reduced to 0.5
Enter a FILE NAME:dDFRAC.NBM
```

NOTE: When you are running a number of runs in succession to try a range of coefficients, it is convenient to use a quick file name, like "LAST," over and over. When you get a run you like, you may then save the file with a more descriptive name, as above.

Menu 13. RUN MODEL.

This is the default choice, so hitting RETURN will select option 13. This returns to the main program and runs the model with the modified parameters.

```
ENTER YOUR CHOICE:(CR=13, Run)«R»
```

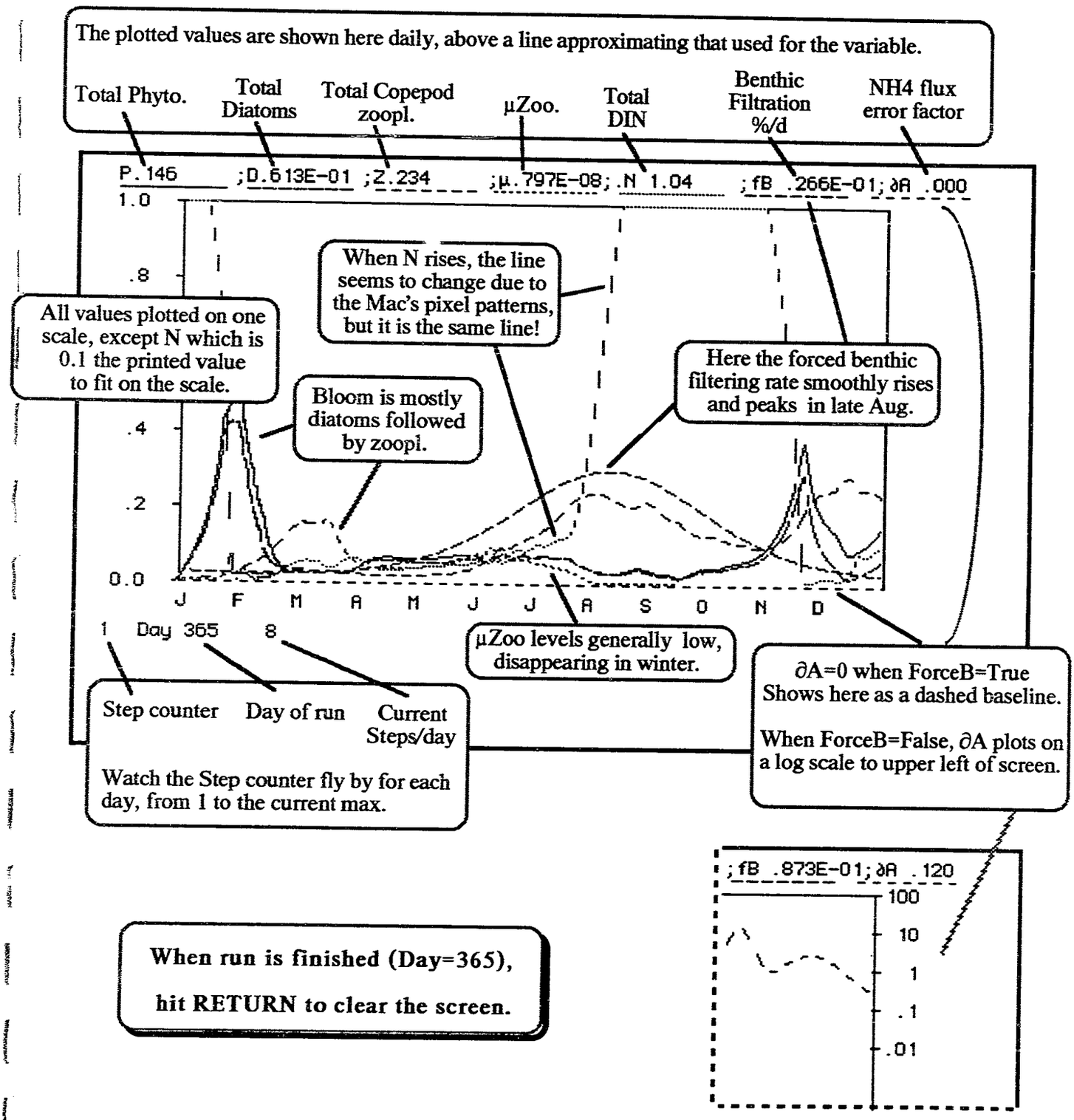
Upon leaving the section for changing parameters, the run continues with the other standard dialog options. You get another chance to type a new run title, in case you did not save the parameter file after making some changes; here just type RETURN to continue.

```
Run title is now:  Diatom Fraction reduced to 0.5
Enter a new title to change it:«»
```

OUTPUT SECTION

THE RUN-TIME PLOT

This figure explains the plot of state variables and rates that you see during the run. The plot shows trends, but the constant scale is not designed for detailed study.



INITIAL SPECIFICATIONS FOR THE RUN.

The first page of numerical output documents the run conditions. The date and time, the run title and the coefficients and initial conditions are printed. All the coefficients are defined earlier in this Guide.

```
Run on   6/ 6/89   at   16: 32
Beginning run:     STD MERL RUN FROM BLOCKDATA
COEFFICIENTS BY COMPARTMENTS
============================
PHYTO:
Growth: P1GMX0=     .59   P1GMXT =   .063 ;   P2GMX0 =     .50    P2GMXT =     .05
        C:N  RANGES    P1:   7.00 TO   7.00 ;   P2:   7.00 TO   7.00
        C:P  RANGES    P1:  85.00 TO  85.00 ;   P2:  85.00 TO  85.00
        C:SI RANGES    P1:   5.00 TO   5.00 ;   P2:  15.00 TO  15.00
        C:DWP1 =     .30    C:DWP2 =     .30 ;  C:CHL1 = 30.00    C:CHL2 = 30.00
       KNP1    =  1.50    KNP2    =     .75 ;  KPP1    =    .05    KPP2    =    .05
       KSIP1   =    .50   KSIP2   =     .05 ;  SIOP1   =    .00    SIOP2   =    .00
       REQIRV = 40.00
Chl-K eqn:   K = Ko(i)        .0090*Chl +   .0000*Chl^.667
   Sinking: P1S0=     .20   P1SLM=     .00; P2S0 =     .00   P2SLM=     .00
-------------------------------------------------------------------------------
ZOOPLANKTON  COEFFICIENTS
*  1. IvlevK    2. PC0        3. RmxO       4. Q10Rmx    5. XRspO      6. Q10Rsp  *
*     7.00          .000          .000          1.00          .100          2.00    *
*  7. XRP       8. ZEP0       9. ZEPT      10. CxN Z    11. CxP Z     12. CxDW Z  *
*     .250          .200        0.600E-01      5.00          85.0          .350    *
* 13. XAssim   14. ZJGmxO   15. ZJGmxT   16. RJxRA    17. SAFE                    *
*     .800        0.300E-01     .100          1.44          .200                  *
* 18. ZFE P1   19. ZFE P2   20. ZFE PC   21. ZFE ZJ   22. ZFE UZ   23. JZmax    *
*     1.00          1.00          1.00          1.00          1.00          150    *
-------------------------------------------------------------------------------
u-ZOOPLANKTON  COEFFICIENTS
*  1. uZ IvK    2. uZGmxO    3. uZGmxT    4. uZRspO   5. uZRspT    6. uZ CxN    *
*     5.00          .500        0.600E-01     .100        0.600E-01     5.00      *
*  7. uZ CxP   8. uZFEP1   9. uZFEP2                                             *
*     85.0          .500          1.00                                          *
* 10. uZFEPC  11. uZ PC0   12. uZ AE    13. uZ XRG                               *
*     .000          .000          .900          .100                            *
-------------------------------------------------------------------------------
BENTHIC  COEFFICIENTS
*  1. ForceB    2. B Grow    3. VfiltO    4. QVfilt    5. FlxAmO    6. FlxAmT  *
*           T             F    0.600E-02     5.00          .142          .160    *
*  7. XDenit    8. FlxPO     9. FlxPT    10. FlxSiO   11. FlxSiT   12. Flx02O  *
*     .300        0.180E-01     .130          .554          .120          .378    *
* 13. Flx02T   14. OxLsip   15. BRO      16. QBR      17. C:N B    18. C:P B    *
*    0.870E-01     .250        0.100E-02     4.00          5.00          85.0    *
* 19. FF AE    20. FF EP1   21. FF EP2   22. FF EPC   23. FF EuZ   24. Fscope  *
*     .800          1.00          .000          1.00          .000          1.00    *
* 25. BBmin    26. Dscope   27. Bac RO   28. Q BacR                              *
*     1.00          1.00        0.800E-01     2.00                              *
-------------------------------------------------------------------------------
NUTRN:
       K20 =    .0680    THETA =  1.1880
       RIVAM =    .00    RIVON =    .00    RIVP =    .00    RIVSI =    .00
       SWGAM:   .00
       SWGON:   .00
       SWGP:    .00
       SWGSi:   .00
-------------------------------------------------------------------------------
```

```
CARNIV:
       FRMXO  =     .07500    QFRMX  =    2.00000    IVFSH  =   30.00000
       CTFLT  =     .10000    CTEXNO =     .00142    CTEXNT =     .13000
       IVMENH =   33.00000    THRESH =     .03000    RMXMEN = 500.00000
-------------------------------------------------------------------------
PARTIC:
       C:NPC =    6.00    C:PPC = 100.00    C:SIPC =    5.00
-------------------------------------------------------------------------
PHYSICS:   STD MERL TANKS WITH HEADER TANK INFLOW.
             Volumes & concentrations from Eutrophication Experiment.



-------------------------------------------------------------------------
TEMPERATURE:   Tavg = 11.50 +/-  8.50 with min on Julian day    40.
-------------------------------------------------------------------------
INITIAL CONDITIONS IN THE 1 TANKS:
==================================
(PTOT & ZTOT units have been converted)
PTOT    mg. C/L       .030
DIAT   fraction       .900
ZTOT    mg. C/L       .005
UZoo    mg. C/L       .001
NH4     ug-AT/L      4.000
NO2NO3  ug-AT/L      7.000
PHOS    ug-AT/L      1.600
SI      ug-AT/L     22.000
O2          mg/L    11.000
FFB     gm C/M2     10.000
DFB     gm C/M2     10.000
SEDC    mM C/M2       .000
SEDN    mM N/M2       .000
SEDP    mM P/M2       .000
SEDSI  mM Si/M2       .000
POC     mg. C/L       .000
EXCOEFF     1/M       .300
DEPTH         M      5.000
VOLUME       M3    13.1E+0
O2 Dif K cm/Hr        .700
ATMOSPHERIC EXTINCTION =       .70 ;    CLOUD COVER, INSOL. =       0
-------------------------------------------------------------------------
Running:   1 years, starting month   1 (day    1);
 Daily output starting month   0 for   0 days;
  4 Plot(s).
    CODES, ELT:  10 1   11 1   12 1   14 1   15 1   23 1   16 1   17 1   19 1   22 1
                 20 1
```

MONTHLY OUTPUT IN DETAIL

The most important product of the model are the plots and the detailed monthly output. While it is tempting to interpret what is going on when you look at the plots, you must be cautious doing so! The results are caused by the equations of the model which may not agree with your conceptual model. Looking at the detailed output is the best way to be sure that you understand what is going on in the model. The output is complicated; it takes some practice to learn the codes and to be able to understand it.

Output is in sections by ecological compartment. Much of the monthly output is the same as the original model. Refer to K&N '78 Ch. 9 for a discussion of these compartments and the output.

Section 1. General

```
DAY    1   MO   1   ELT   1 DT/d=    1            TEMP =     4.8429   QM3/D=0.6263E+07
                            DAYLT=      .3772  CVRAV=     5.5500   RADAV=   131.0545
```

DAY, MO & ELT: Julian day, month, & the region (element of the Bay or MERL Tank) for which this output applies. DAY 1 output is Initial Conditions; MO 12 occurs twice, on the 1st of Dec and the 31st, the End of the run.

DT/d: Integration time step (STEPS/d) for the day of this output. The model adjusts DT dynamically (2, 4, 8,16, etc. steps/d), with more steps during active times.

TEMP: the temperature (Celcius) on this day; Average temp. is based on a sine function, to which a specified increment may be added or subtracted each month.

QM3/D: Total river flow (m^3/d); only used with simulations of the bay (See coef. MIXOPT=1).

DAYLT, CVRAV & RADAV: define Insolation: Length of the day (unitless, 0.5=12L:12D); the average Cloud cover (1.0=100%), & resulting total Ly/d received.

Section 2. Phytoplankton output

```
PPL  K     = .3090       IOPT = 96.22       LTLIM= .2776       (   0   0   0)
      DLQN =  0.13E+03   DLQP =  0.23E+03   DLQSI=  0.20E+03   Csink=0.1162E-02
      P1mgC=0.3120E-01   P1GMX= .8017       GP1  = .2225       DELP1=0.6464E-02
      NLIM1= .8800       PLIM1= .9697       SILM1= .9778       S1 m/d= .2000
      CHLµg= 1.040       C:N1 = 7.000       C:P1 = 85.00       C:Si1= 5.000
      P2mgC=0.3530E-02   P2GMX= .6370       GP2  = .1768       DELP2=0.5760E-03
      NLIM2= .9362       PLIM2= .9697       SILM2= .9977       S2 m/d= .0000
      CHLµg= .1177       C:N2 = 7.000       C:P2 = 85.00       C:Si2= 15.00
```

PPL K (1/m): Starting the Phytoplankton section, K is the extinction coefficient, including background plus CHL-dept. contributions (See coefs. CHLK & CHLK2).

IOPT (Ly/d): The optimum light for growth calculated as the avg. at 1 m depth. A "*" after the number means that acclimation was blocked by the lower limit (See coef. LOIOPT).

LTLIM: Growth Limitation by light (unitless fraction), from the Steele curve integrated over 24-hr & surface-to-bottom; same for P1 & P2.. Growth is limited by the minimum of LTLIM vs. nutrient-LIM (where P1 & P2 may differ).

(0 0 0) 3 Counters (for N, P & Si respectively) indicating how often PPL growth rates were adjusted to avoid exceeding the supply available. This can usually be ignored, but indicate minor

integration errors, or you may change the number of allowable steps in the variable integration scheme.

DLQN, P, SI: "Demand-to-Limitation Quotients" for total N, P, & Si. These unitless ratios relate supply to demand; DLQ>1 for an excess, DLQ<1 for shortfall.

Csink: Rate of loss by sinking from the water column (mgC/L/d). (See BEN:Cfall for the total C reaching the benthos.)

P1MGC: Stock of 1st phyto. group (mgC/L). P1 usually represents diatoms, depending on specific coefficients.

P1GMX: Maximum T-dept. net growth rate for P1 (1/d), based on an exponential. equation (like Eppley's): P1GMX=P1GMX0 *exp(P1GMXT*T).

GP1: Realized net growth rate (1/d), taking into account TEMP(P1GMX) & the most limiting of LIGHT(LTLIM) & NUTRIENTS (NLIM, P, or Si).

DELP1: Actual change in stock of P1 (mgC/L/d) for this time step, i.e. the real net growth before sinking & grazing losses.

NLIM1, PLIM1, SILM1: Monod-limitation terms for total DIN, PO4, and Si (unitless fractions).

S1 m/d: Sinking rate of P1 (m/d) as determined by the linear equation relating S1 to nutrient limitation (by N, P or Si): S1=P1S0+P1SLM*NLIM

CHLμg: Estimated concentration of CHL (μg/L), simply based on the C:Chl ratio for P1.

C:N1, C:P1, C:Si1: The carbon-to-element ratio by atoms for N, P, & Si, respectively, in P1. Though the model can handle variable ratios, no scheme is presently included, so these ratios stay fixed at their initial values.

P2MGC: Stock of 2nd phyto. group (mgC/L). P2 usually represents μflagellates, depending on the specified coefficients.

P2GMX: Maximum T-dept. net growth rate for P1 (1/d), based on an exponential. equation (like Eppley's): P2GMX=P2GMX0 *exp(P2GMXT*T).

GP2: Realized net growth rate (1/d), taking into account TEMP(P1GMX) & the most limiting of LIGHT(LTLIM) & NUTRIENTS (NLIM, P, or Si).

DELP2: Actual change in stock of P2 (mgC/L/d) for this time step, i.e. the real net growth before grazing losses, and sinking if it occurs for this group.

NLIM2, PLIM2, SILM2: Monod-limitation terms for growth by total DIN, PO4, and Si (unitless fractions).

S2 m/d: Sinking rate of P2 (m/d) as determined by the linear equation relating S1 to nutrient limitation (by N, P or Si): S2=P2S0+P2SLM*NLIM

CHLμg: Estimated concentration of CHL (μg/L), simply based on the C:Chl ratio for P2.

C:N2, C:P2, C:Si2: The carbon-to-element ratio by atoms for N, P, & Si, respectively, in P2. Though the model can handle variable ratios, no scheme is presently included, so these ratios stay fixed at their initial values.

Section 3. Microzooplankton

```
UZOO  uZmgC=0.9368E-03   GROMX= .6686          Flim =0.7919E-01   XRESP= .1283
       RLF   =0.4635E-02   XRTN =0.8242E-01   ChgR = 1.078        SpGRO=-.5413E-01
       GGE   =-.6568        Net G= .9368        EXC N=0.1785E-02   EXC P=0.1258E-03
       C:Nex= 5.989        C:Pex= 85.00        N/Pex= 14.19       %N ex= 11.43
       %P ex= 13.70         =>ZOO=0.9026E-05 =>CARN= .0000        =>BEN= .0000
```

uZmgC: Stock of µzooplankton (mg C/L). Note that although there are 3 compartments of zooplankton -- adult & juvenile copepods, plus µzoo. -- the basic formations are identical, and their outputs are directly comparable.

GROMX: Maximum C-specific growth rate (1/d) as an exponential function of TEMP.: GROMX=UZGM0 * exp(UZGMXT*TEMP)

Flim: Food-limitation factor (unitless) by which growth is reduced from GROMX. This is based on an Ivlev function (see UZIVK) of total available food above the specific threshold (UZPC0); total food is the potential foods (P1, P2 and POC) as modified by their respective feeding efficiencies (see UZFEP1, etc.).

XRESP: Fraction of the body C respired daily (1/d). Specific respiration includes a temp. dependent basal rate plus a contribution dependent on the growth rate (UZXRG*GRO).

RLF: "Ration-Liters Filtered" for µZoo population, the effective volume swept clear (L/d). RLF is the feeding rate required to achieve the target ration given the available food concentration. No explicit constraints are placed on RLF, so it could reach very high rates when available food is low if Flim does not reduce the target ration.

XRTN, ChgR: The C-specific ration (1/d). This realized rate does not exactly equal the target calculated from temp, available food, etc. Rather, the program specifies the RLF, and the yield resulting from this feeding rate is returned to the µzoo population. ChgR is fraction expressing the change in the realized from the target, with 1.0 meaning they are equal.

SpGRO: The realized specific growth rate (1/d).

GGE: The Gross Growth Efficiency (unitless fraction), calculated as the realized growth rate divided by the daily ration.

Net G: The net change in the µzoo stock (unitless fraction) resulting from growth minus predation.

EXC N, EXC P: Excreted N and P by the µzoo stock (µg-at/L/d). This is based on the respiration rate, but varies depending on differing C:N and C:P ratios of the food and the µzoo. [The message "ALL INGESTED N REQURED BY UZ" means that there was not enough N in the food to make the required µzoo biomass; this usually occurs in extreme cases, or with unreasonable combinations of elemental composition.]

C:Nex, C:Pex, N/Pex, %N ex: Details on the excretion by µzoo: Ratios (by atoms) of respired C to excreted N and P, the excreted N:P, and the N excretion as a percent of total body N.

%P ex: The P excretion as a percent of total body P.

=>CAR, ZOO, BEN: Predation losses (mg C/L/d) of µzoo to three potential predators -- "Carnivores" include fish larvae, ctenophores, & menhaden and are assumed to feed equally well on µzoo as on larger zoopl. & eggs. ZOOplankton (the copepod compartment), and the filter feeding BENthos feed on µzoo with a specifed feeding efficiency (see ZFEUZ, FFEUZ).

Section 4. Zooplankton

```
ZOO   ZTOT =0.3500E-02   %Diet P1: 87; P2: 10; ZJ:  0; PC:  0; uZ:  3.
       ZAMGC=0.3500E-02   EPmax= .2674        Flim = .1951        XRESP=0.2576E-01
       RLFZA=0.9588E-02   XRTN =0.9108E-01   ChgRTN 1.072        SpEP =0.4710E-01
      EGGS =0.1649E-03   H & D=     7     0
      ZJTOT= .0000        GROMX= .0000        FlimJ= .0000        XRSPJ= .0000
      RLFZJ= .0000        XJRTN= .0000        ChgRJ= .0000        SpGRO= .0000
      GGE  = .0000          NetJG= .0000        EXC N=0.3229E-03   EXC P=0.8841E-04
      C:Nex= 23.27        C:Pex= 85.00        N:Pex= 3.652        %N ex= .5535
      %P ex= 2.576        ZJTMP= .0000        +ADLT= .0000       =>CARN= .0000
```

ZTOT: Total stock of zooplankton (mg C/L) including adults and juveniles. [Note that although there are 3 compartments of zooplankton -- adult & juvenile copepods, plus µzoo. -- the basic formations are identical, and their outputs are directly comparable.]

%Diet: P1 50; P2 30; ZJ 0; PC 0; uZ 10: % Composition of the realized adult ration among potential foods, including the 2 phyto groups (P1, P2), eligible copepod juveniles (ZJ, see SAFE), non-living particulate C (PC), and µzoo (uZ). The diet mix is determined by availability the respective feeding efficiencies for each food source (see ZFEP1, ZFEP2, ZFEZJ, ZFEPC & ZFEUZ).

ZAMGC: Stock of adult zooplankton (mg C/L).

EPmax: Maximum specific egg production rate (1/d) as a function of TEMP for adult copepods. EPMAX=ZEP0 * exp(ZEPT*TEMP)

Flim: Food-limitation factor (unitless) by which egg production is reduced from the maximum. This is based on an Ivlev function (see IVLEVK) of total available food above the specific threshold (PC0); total food is the potential foods (P1, P2, zoopl. juveniles not SAFE from cannibalism, µzoo and POC) as modified by their respective feeding efficiencies (see ZFEP1, etc.).

XRESP: Fraction of the body C respired daily (1/d). Specific respiration includes a temp. dependent basal rate plus a contribution dependent on the specific production rate (ZXRP*SEP).

RLFZA: "Ration-Liters Filtered" for adult zoopl. population, the effective volume swept clear (L/d). RLF is the feeding rate required to achieve the target ration given the available food concentration. No explicit constraints are placed on RLF, so it could reach very high rates when available food is low if Flim does not reduce the target ration.

XRTN, ChgRTN: The C-specific ration (1/d). This realized rate does not exactly equal the target calculated from temp, available food, etc. Rather, the program specifies the RLF, and the yield resulting from this feeding rate is returned to the zoopl. adults. ChgR is fraction expressing the change in the realized from the target, with 1.0 meaning they are equal.

SpEP: The specific egg production rate of adult copepods (1/d for Carbon).

EGGS, H & D: Egg production by the copepod population (mg C/L/d), plus the Hatching time and target Development time (in days) for this cohort of eggs. Real development after hatching is slowed by food limitation.

ZJTOT: Stock of juvenile copepods (mg C/L). Individual cohorts are tracked until they become adults, each responding to ambient food and TEMP, and predation. Younger juveniles may be subject to cannibalistic predation, with older ones not (see SAFE, the portion of the development time juveniles are not cannibalized). All other predation is equal on all juveniles.

GROMX: Maximum C-specific growth rate (1/d) as an exponential function of TEMP.: GROMX=UZGM0 * exp(UZGMXT*TEMP)

FlimJ: Food-limitation factor (unitless) by which growth is reduced from the maximum. This is based on an Ivlev function (see IVLEVK) of total available food above the specific threshold (PC0); total food is the potential foods (P1, P2, µzoo and POC) as modified by their respective feeding efficiencies (see ZFEP1, etc.).

XRSPJ: Fraction of the body C respired daily (1/d). Specific respiration includes a temp. dependent basal rate plus a contribution dependent on the specific growth rate (XRP*GRO).

RLFZJ: "Ration-Liters Filtered" for juvenile copepods, the effective volume swept clear (L/d). RLF is the feeding rate required to achieve the target ration given the available food concentration. No explicit constraints are placed on RLF, so it could reach very high rates when available food is low if Flim does not reduce the target ration.

XJRTN, ChgRJ: The C-specific ration (1/d). This realized rate does not exactly equal the target calculated from temp, available food, etc. Rather, the program specifies the RLF, and the yield resulting from this feeding rate is returned to the zoopl. adults. ChgR is fraction expressing the change in the realized from the target, with 1.0 meaning they are equal.

SpGRO: The realized specific growth rate (1/d) for juvenile copepods.

GGE: The Gross Growth Efficiency (unitless fraction), calculated as the realized growth rate divided by the daily ration.

NetJG: The net change in the juvenile copepod stock (unitless fraction) resulting from growth minus predation.

EXC N, EXC P: Excreted N and P by the µzoo stock (µg-at/L/d). This is based on the respiration rate, but varies depending on differing C:N and C:P ratios of the food and the µzoo. [The message "ALL INGESTED N REQURED BY UZ" means that there was not enough N in the food to make the required µzoo biomass; this usually occurs in extreme cases, or with unreasonable combinations of elemental composition.]

C:Nex, C:Pex, N:Pex, %N ex: Details on the excretion by copepod zoopl.: Ratios (by atoms) of respired C to excreted N and P, the excreted N:P, and the N excretion as a percent of total body N.

%P ex: The P excretion as a percent of total body P.

ZJTMP, +ADLT: Cohort information: ZJTMP are the hatching eggs forming today's youngest juveniles; +ADLT are the maturing juveniles joining adult ranks (both in mg C/L).

=>CAR: Predation losses (mg C/L/d) of zoopl to "CARnivores" include fish larvae, ctenophores, & menhaden. (CAR stocks are forced seasonally, and are zero in the standard MERL runs.)

Section 5. Benthos

```
BEN   Cfall=0.5969E-02   Cfilt=0.3800E-02   GSRm/d    .2494        GSRreq   5.516
      %Diet   P1: 39; P2:   0; uZ:   0; PC:   0;   S: 59; ZF:   2.   RLF= 0.262E-01
      Csed = -.210         Nsed =. -.330        Psed =-0.279E-01   Sised= -.870
      02g/m2   .5761       NmM/m2   .3082       PmM/m2 0.3378E-1  SimM/m2   .9906

      ErrO2= 0.3256E-1   ErrAM=   .1902       ErrP =   .2041       ErrSi=   .1400
      DFB gC   10.00       FFB gC   10.00       Bgrth=   .0000       Fm3/d=   .131      *
      BacR =   .112        %Bact=   .000        Denit= 0.2512E-1   OxLim=   1.00
```

Cfall, Cfilt: The BENTHOS compartment. The carbon (gm C/m2/d) passing to the benthos by 2 paths -- Cfall: the sinking of phytoplankton and unassimilated matter from copepods; and Cfilt: active filtering by the biomass of filter feeders (see FFB)

GSRm/d, GSRreq: "Gross Sedimentation Rate" expressing the effective transfer of Carbon to the benthos as a sinking rate (m/d) removing all particulate matter. GSRreq is the GSR required to meet the total demand of actual benthic oxygen metabolism assuming the empirical temperature-dependent function (see FLXO20 AND FLZO2T).

%Diet: P1 80; P2 11; uZ 0; PC 0; S 8; ZF 1.: Source by % of the carbon reaching the benthos, including the 2 phyto groups (P1, P2), µzoo (uZ), non-living particulate C (PC), passive phyto. sinking and copepod unassimilated feces (ZF). The mix is determined by availability the

respective feeding efficiencies of filter feeders for each food source (see FFEP1, FFEP2, FFEPC & FFEUZ).

Csed, Nsed, Psed, Sised: Balance of non-living C, N, P and Si accumulated in the sediments (mg-at/m2). With FORCEB=True, this is a simple Input/Output balance indicating if supply is adequate to meet the forced fluxes. When FORCEB=False, these stocks are fully simulated as the resource for deposit feeders and bacterial metabolism.

O2g/m2, NmM/m2, PmM/m2, SimM/m2: Benthic fluxes of O2 (g/m2/d), N, P and Si (mM/m2/d). When FORCEB=True, these are the forced empirical fluxes. When FORCEB=False, these fluxes are simulated as the sum of metabolic contributions of filter and deposit feeding benthic macrofauna plus bacterial metabolism.

The remaining BENTHIC output only appears if ForceB = False.

ErrO2, Am, P, Si: When FORCEB=False, and benthic fluxes are fully simulated, these error terms compare the modeled flux to that expected from the empirical temp-dependent equations for O2, NH4, PO4 and SiO4. A value of 1.0 is exact agreement; 0.8 means the prediction was 80% of the expected; 5.0 would mean the model predicted 5 times the expected flux.

DFB, FFB: When FORCEB=False, these are the standing stocks of deposit feeder and filter feeder biomass in the benthos (g C/m2). Unless GROW=True, these biomasses will stay constant at the initial values. (You may set a lower limit to these stocks, see BBMIN.)

F m3/d, RLF /d: The simulated filtering rate of filter feeders (m3/m2/d), is calculated as a Ration-Liters Filtered, "RLF," based on respiration (see BR0,QBR), assimilation efficiency (see FFAE), and the scope for growth (see FSCOPE). The estimated filtering rate must be less than the maximum rate as a function of temperature (see VFILT0, QVFILT, VFMAX). OXMIN may reduce respiration at low [O2] thus affecting the ration & filtering estimates.

Bgrth: The growth of benthic biomass, deposit & filter feeders combined (gm C/m2/d). Only when GROW=True will this be > 0.

%Bact: The % of the benthic oxygen demand due to bacterial decomposition. The remainder is respiration by the deposit and filter feeders.

Denit: Denitrification by the benthos (mg-at/m2/d)

OxLim: Oxygen limitation of benthic respiration (see OXSLP). Designed to evaluate the effect of low O2 on changing benthic metabolism, this will usually be 1.0, no effect. If OxLim<1.0, benthic respiratory demand is reduced by this fraction in the calculation of benthic ration & filtering rate.

Section 6. Nutrients

```
NUT   NH4  =     3.9583  NO2/3=     7.0198  PO4  =     1.5999  Si   =    22.0872
        O2  =    10.8765  dOP1 =      .0173  dOP2 =      .0015 dOZoo =      .0002
      dOu2  =      .0003 dONitn=      .0013 dOBen =      .1152 Dmg/LD=     -.0253
     -[O2] =       0 times.
>> Daily: SWGAM=       .0000 SWGNO=       .0000 SWGP =       .0000 SWGSI=       .0000
```

NH4, NO2/3, PO4, Si: NUTRIENT compartment, the ambient concentrations (µM) of the 4 major nutrients simulated by the model

O2, dOP1, dOP2, dOZoo, dOuZ, dONitn, dOBen, Dmg/LD: the Oxygen concentration (mg/L) and terms in the budget (all mg/L/d); production by 2 phyto. groups, respiration by copepod zoopl, by µzoo, pelagic nitrification, benthic respiration, and air-sea diffusion.

-[O2]: Programming output -- How many times did the oxygen budget try to go negative since the last output. Ideally this doesn't happen, but in some simulations it may. The model simply resets ambient [O2] to zero without adjusting any rates, thus mass is not conserved. This is likely a minor error compared to the ones that draw O2 down so low to start with!

>> **Daily: SWGAM, SWGNO, SWGP, SWGSI:** Inputs of nutrients into the spatial elements of the bay or the MERL tanks (ug-at/L added each L of total volume). Since the default MERL run is for the control tank, there are no added nutrients; MAXELT>1 will simulate the other treatments.

NOTE: These amounts are added daily, but this line of output only given once at the start of the run.

Section 7. Carnivores

CARN output is suppressed unless carnivores are present. Carnivore stocks are only provided for runs of the full 8-element bay model. Even then, carnivores are not present throughout the year. Further, menhaden are never assumed to be feeding in the lower bay in significant numbers (see Sec. 6.2 and 10.5 in K&N '78). The presence of menhaden in the upper bay is documented along with the output for element 4, since results for this mid-West Passage region are often printed out. This output block is not explained in the Analyzer.

```
CARN CTENS=       .0060   CTFLT=       .0006   FISH =      6.0000   FPREF=0.1102E-02
      RTN   =0.1230E-02   FCARN=       .0049   CTEXN=       .0001
       MENH  =0.1000E-04    M RTN=0.4998E-02    FMENH=0.1885E-01    IN ELEMENT 2
```

CTENS, CTFLT, CTEXN: Biomass (mg DW/L), instantaneous filtering rate (per day), and NH4 excretion rate (µg-at N/L/day) for ctenophores.

FISH, FPREF: Biomass (no./m3) and preferred daily ration (mg C/L) for larval fish.

RTN, FCARN: Total net consumption of zooplankton (mg C/L) and the combined total grazing rate (per day) by all carnivores.

MENH, M RTN, FMENH: Biomass of menhaden (pounds wet wt./L), their preferred ration (mg C/L) and their grazing rate (per day). When menhaden are present in the upper bay, these values for element 2 are printed. Since default output is only for element 4 in the BAY8 case, this allows you to tell when menhaden are active.

Section 8. Net Changes

```
NET %:   P1=   13.45 P2=   15.01 ZA=      .00 ZJ=      .00 AN=   -1.05 ON=      .28
          PH=    0.00 SI=      .39 O2=   -1.14 UZ=   -6.74
```

These final 2 lines of output each month are net daily % changes for the main standing stocks throughout the run.

NET %: P1, P2, ZA, ZJ, AN, ON, PH, SI, O2, UZ: Net day-to-day changes in the simulated stocks (before physical mixing) -- 2 Phyto. groups, Copepod zoopl. adults & juveniles, ammonium & NO2+NO3, PO4, SiO4, O2, and µzoo, respectively. ["******" means a large number; usually from a very small stock with a large change.]

FINAL OUTPUT

Section 10. Plotted output

The specified plots conclude the normal output. Here 4 plots were specified, only one is shown here.

- **The top line records the title of the run.**
- **Next, the program reports the variable codes and the spatial element (tank) for each plotted item in the plot frame; this protects you from specifying the wrong code by mistake -- what is plotted is what is reported here.**
- **The third line identifies the data columns with their plot symbol. The upper and lower limits to the plot scale are given. The first character of the minimum and the last character of the maximum mark the printed columns of the plotted symbols.**
- **Each line of data presents the date, the simulated values, and then the plotted points. The date is given as month+day, e.g. 108 is January 8th, and 1029 is October 29th.**
- **Symbols are plotted in order, so that successive symbols may obscure each other if the values plot together. If you can't see a symbol, it was hidden by another one. If you specify minimum and maximum values for the scale, points that fall outside the range will be plotted at the margin with the symbol "<" or ">".**

RUN: STD MERL RUN FROM BLOCKDATA
VARIABLES, ELEMENTS: P1 1 P2 1 PTOT 1

MO	1	2	T	0.10310E-03	0.50365E+00
101	0.31196E-01	0.35297E-02	0.34726E-01	21T	
108	0.88895E-01	0.11289E-01	0.10018E+00	2 1T	
115	0.20145E+00	0.28844E-01	0.23030E+00	2 1 T	
122	0.43531E+00	0.68343E-01	0.50365E+00	2 1 T	
129	0.21535E+00	0.16728E-01	0.23207E+00	2 1T	
205	0.55380E-02	0.10310E-03	0.56411E-02	T	
212	0.74358E-02	0.35120E-03	0.77870E-02	T	
219	0.21682E-01	0.12404E-02	0.22922E-01	2T	
226	0.58633E-01	0.34051E-02	0.62038E-01	2 T	
305	0.12618E+00	0.63443E-02	0.13253E+00	2 1T	
312	0.13376E+00	0.43317E-02	0.13809E+00	2 T	
319	0.24847E-01	0.88566E-03	0.25733E-01	2T	
326	0.22773E-01	0.12532E-02	0.24027E-01	2T	
402	0.40154E-01	0.25239E-02	0.42678E-01	2 T	
409	0.56589E-01	0.47943E-02	0.61383E-01	2 T	
416	0.58752E-01	0.67884E-02	0.65540E-01	2 1T	
423	0.56334E-01	0.82000E-02	0.64534E-01	2 T	
430	0.53618E-01	0.95064E-02	0.63124E-01	2 T	
507	0.53208E-01	0.11122E-01	0.64330E-01	2 T	
514	0.53048E-01	0.12315E-01	0.65364E-01	2 1T	
521	0.58302E-01	0.12429E-01	0.70732E-01	2 1T	
528	0.63313E-01	0.88848E-02	0.72198E-01	2 1T	
604	0.61671E-01	0.47968E-02	0.66468E-01	2 1T	
611	0.69084E-01	0.21905E-02	0.71275E-01	2 T	
618	0.68895E-01	0.34809E-02	0.72376E-01	2 T	
625	0.72390E-01	0.25935E-02	0.74983E-01	2 T	
702	0.66499E-01	0.17968E-02	0.68296E-01	2 T	
709	0.70017E-01	0.14485E-02	0.71466E-01	2 T	
716	0.69008E-01	0.12804E-02	0.70288E-01	2 T	
723	0.60175E-01	0.11670E-02	0.61342E-01	2 T	
730	0.42191E-01	0.12189E-02	0.43410E-01	2 T	
806	0.31355E-01	0.14543E-02	0.32809E-01	21T	
813	0.28764E-01	0.21899E-02	0.30954E-01	2T	
820	0.32585E-01	0.34327E-02	0.36018E-01	21T	
827	0.34978E-01	0.46431E-02	0.39622E-01	2 T	
903	0.25039E-01	0.38455E-02	0.28884E-01	2T	
910	0.26635E-01	0.42298E-02	0.30865E-01	2T	
917	0.18993E-01	0.34399E-02	0.22432E-01	2T	
924	0.32363E-01	0.51300E-02	0.37493E-01	21T	
1001	0.37479E-01	0.62483E-02	0.43727E-01	2 T	
1008	0.40377E-01	0.68066E-02	0.47183E-01	2 T	
1015	0.50548E-01	0.85000E-02	0.59048E-01	2 T	
1022	0.58746E-01	0.10753E-01	0.69499E-01	2 1T	
1029	0.80475E-01	0.16239E-01	0.96715E-01	2 1T	
1105	0.12698E+00	0.28532E-01	0.15552E+00	2 1 T	
1112	0.21643E+00	0.54966E-01	0.27139E+00	2 1 T	
1119	0.19289E+00	0.80863E-01	0.27375E+00	2 1 T	
1126	0.85767E-01	0.84895E-01	0.17066E+00	2 T	
1203	0.52307E-01	0.95163E-01	0.14747E+00	1 2 T	
1210	0.25380E-01	0.88118E-01	0.11350E+00	1 2T	
1217	0.17549E-01	0.68854E-01	0.86403E-01	1 2T	
1224	0.35010E-01	0.75123E-01	0.11013E+00	1 2 T	
1231	0.57623E-01	0.90227E-01	0.14785E+00	1 2 T	

SECTION 9. ERROR MESSAGES

Occasionally an error pops up. There are a few diagnostic messages designed to help in the development of the program. If these tips don't help, you may have found a bug! Please contact Jim Kremer to help exterminate it.

The first two types are nutrient demand errors, suggesting minor integration problems. These effects are not serious, and are unlikely to change the patterns of a run. There is little you can do, except increase the maximum number of STEPS per day in reply to the very first question of the run.

```
ERROR -- DAY, ELT   27    1,   N DEMAND EXCEEDS SUPPLY BY   -.024945
ERROR -- DAY, ELT   27    1,   P DEMAND EXCEEDS SUPPLY BY   -.024945
ERROR -- DAY, ELT   27    1,   SI DEMAND EXCEEDS SUPPLY BY   -.024945

PHYTO DEMAND ERROR:DAY,ELT,GP1,GP2:   83    1         0.000000 0.000000
```

The third type of error results when the elemental composition of the zooplankton cannot be maintained on the available food. This is usually a correctable "user error." Check that the combinations of zooplankton and phytoplankton C:N and C:P ratios are reasonable and that assimilation efficiency is low enough to give animals a chance to make up the needed deficit.

```
ALL  INGESTED N REQUIRED BY Z,  UANZ=     -.01427
ALL  INGESTED P REQUIRED BY Z,  UAPZ=     -.01427

ALL  INGESTED N REQUIRED BY UZ, UANUZ=    -.01427
ALL  INGESTED P REQUIRED BY UZ, UAPUZ=    -.01427
```

HyperCard occasionally generates an error. Try quitting and rerunning the Analyzer from scratch. If it still fails, delete the Analyzer file and copy a clean version from your backup floppy diskette. (You always keep a backup, right?)

The HyperCard Analyzer should find the file it needs, or ask you to help it locate it the first time you run it. Should it be totally confused, it may produce an error.

HyperCard can't find file _____
File error -34
or File error -45

Be sure that the data files it needs (run results stored in file BayModelRun, or any others you have renamed to save) are placed within the folder "Bay Model". That should correct these errors.

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