
Simulation Experiments Comparing Alternative Process Formulations Using a Factorial Design

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ABSTRACT

This paper reviews methods for exploring the differences between alternative equations in complex ecosystem models. A factorial design is proposed as a method for exposing possible interactions between equation forms in their effect on model output as well as to clarify differences between the main candidate equations. A number of display methods arising from statistical analysis are used including normal Q-Q plots, linear rank plots and interaction diagrams. The methods were illustrated using a complex ecosystem model of Lake Ontario. We found the methods effective at illustrating major differences between equations although several difficulties arose due to the complexity of the models and the diffuse nature of the data supporting model validation. Questions of the method for standardization of equation forms so that the compared equations are in some way analogous are important. These methods are probably most useful in cases where the data are of sufficient quality to indicate not only how different equations effect model output but also which forms are to be preferred.

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1 Introduction

Simulation models have seen wide application: in prediction; as an aide in understanding ecosystems; in directing future research; and as a management decision making aid. Since ecological models consist of a collection of mathematically posed hypotheses about how process rates are affected by state and environmental conditions the question frequently arises as to how good the specific hypotheses used in the models are in representing the processes at hand. A number of researchers have discussed this issue (Swartzman et al., 1980, Swartzman 1979, Caswell 1976, Noble 1975) and specifically the importance of choosing the best among a number of alternative mathematical representations. This paper presents and illustrates methods for comparing alternative formulations using designed simulation experiments with an eye to how alternative equation formulations affect model output. If two alternatives do not result in significantly different model output then the choice between them should be based on other criteria such as which is simpler.

The most obvious way to examine the effect of alternative process equation formulation is to conduct simulations with the alternatives replacing each other. This method, patterned after the method used most commonly in sensitivity analysis of changing parameters singly, has several difficulties, as does sensitivity analysis done in this way. The major problem is that if alternatives are considered for different processes (e.g. alternative photosynthesis formulations and alternative feeding formulations) there may be an interaction between them in the way they affect model output. This problem has been addressed for sensitivity analysis by Steinhorst (1979), McKay et al. (1979) and Rose and Swartzman (1981). Among the methods suggested is using an analysis of variance (ANOVA) model and conducting a factorial design experiment. Whereas in sensitivity analysis there are usually too many parameters to conduct a full factorial design and fractional factorial designs are indicated, in the case of alternative hypotheses for processes the number of alternatives is usually small enough that a full factorial design is possible. With this design all interaction effects are considered. If an interaction is seen as significant this implies that all further consideration of the appropriateness of any of the processes having the significant interaction must consider its relationship with the other process(es) as well.

Once an experimental design has been set up, and the simulations conducted, various methods can be used to analyse the results. Since the ordinary statistical assumption of normally distributed errors does not pertain to a simulation experiment on a deterministic simulation model the conventional 'F' tests do not apply. Among the methods explored here are ranking effects, linear rank plots, normal G-G plots and plots of th percent variability explained by the various alternative hypotheses. These methods are regarded as exploratory rather than statistical in nature.

What we really want to do with this analysis is to help decide which alternative equation formulation are most appropriate for the ecosystem under consideration. This of course depends upon the objectives of the model and upon what is considered to be acceptable behavior. For purposes of illustration of the methods in a large

ecosystem model we have used a model of part of Lake Ontario in the northeastern United States. This model, LAKONT, was built to examine the effect of power plant operation on fish and plankton in the neighborhood of the Nine Mile Point nuclear power station. The primary effects are through increase in water temperature (thermal loading) and entrainment of fish in the power plant cooling waters. A complete documentation for this model is found in Kaluzny et al (1983) and only a brief description is provided below.

2 Example Ecosystem Model

We have developed an ecosystem simulation model (LAKONT) for a 385 square kilometer area surrounding the Nine Mile Point Power Station at the southeast end of Lake Ontario. Four separate regions are considered within this area; a littoral zone near the plant, a littoral zone downcurrent from the plant, a pelagic region and benthic region. There are 6 fish groups, 4 zooplankton groups, 3 phytoplankton groups and 2 benthos groups (see Exhibit 1). Each fish and zooplankton group is divided into size classes to represent size structure in the population. Recruitment between these size classes is based on the dynamic pool concept (see Kaluzny et al., 1983). Fish movement among the regions is represented by having the fraction of the day spent in each region as parameters. The plankton and benthos remain within a region.

The model is an energetics based system of differential equations for the change in weight and numbers of organisms. These equations are solved using an Euler approximation with a time step of one day. The usual run time is one year. Water temperature and nitrogen and phosphorus concentrations are read in daily as driving variables.

Flows between model compartments are shown in Exhibit 1. Phytoplankton biomass is increased due to growth and decreased due to predation and sinking. (Since phytoplankton have a constant weight any change in their biomass is equivalent to a change in number). Growth is a function of temperature, light and nutrient availability.

The two groups of benthic organisms (amphipods and seasonal benthos) in the model provide an alternative food source for the fish. Their dynamics are simple, with a constant weight assumed. Their change in biomass is the difference between temperature dependent production and mortality. Predation mortality is from fish feeding. Natural mortality is temperature dependent to simulate emergence of insects during the warm months.

Zooplankton have equations for both the change in weight and the change in numbers (density). Their weight dynamics depends on the difference between the amount of food consumed (a function of weight, prey density and temperature) times assimilation efficiency and the amount loss due to metabolism (a function of weight and temperature). The adult zooplankton have a constant weight, their excess food intake being converted into eggs. The change in numbers in a zooplankton size class results from predation and natural mortality (assumed to be a constant rate) and recruitment into and out of the size class. Both fish and zooplankton can prey on a zooplankton size class. Recruitment out of a size class is a nonlinear function of the current average

weight relative to the maximum and minimum weight of that size class.

Since fish dynamics were the major emphasis in this model and in the alternative processes considered, fish processes will be described in greater detail. The change in numbers of fish in a size class is the net result of predation and natural mortality and recruitment into and out of the size class. Natural mortality is a constant ratio. Recruitment between size classes is a nonlinear function of the current weight relative to the maximum and minimum weight of that size class.

Fish weight change is the most complicated process in the model. As with zooplankton, the rate of change is the difference between assimilated ration and metabolism. Several alternative subprocesses were considered for each.

Fish ration is computed by adjusting the maximum rate at 10C by temperature, weight and prey density effects:

$$Q_{SRN} = K_{SRNMX} * Q_{SRNT} * Q_{SRNW} * Q_{SRNP}$$

where: K_{SRNMX} = max. ration at 10C
 Q_{SRNT} = temperature effect on ration
 Q_{SRNW} = weight effect on ration
 Q_{SRNP} = prey density effect on ration

The notation used here and throughout the paper has intermediate variables beginning with Q, parameter variables beginning with K and state variables beginning with X (e.g. X*FW is fish weight). The \$ is a delimiter that separates the type of variable from the mnemonic ending which identify the variables.

Temperature effect on ration has two alternative forms. One uses the classical Q_{10} relation.

$$Q_{SRNT1} = K_{SRNQT} ** ((TEMP-10)/10).$$

where: K_{SRNQT} = Q_{10} parameter
TEMP = lake temperature driving variable

This relation can only apply over a limited range of temperatures beyond which it has the unrealistic property of continuing to increase with temperature. The second temperature formulation addresses this problem by using a function similar to the gamma density function which resembles a Q_{10} at low temperatures but reaches a maximum and then decreases with higher temperatures (Kitchell et al., 1977).

$$Q\&RNT2 = (T4 ** (T1 * T3)) * \exp(T1 * T3 * (1 - T4))$$

where: $T1 = (\log(K\&RN\>) * (K\&RNTU - K\&RNT0)) ** 2$
 $T2 = 40 / (\log(K\&RN\>) * (K\&RNTU - K\&RNT0 + 2))$
 $T3 = ((1 + T2) ** 0.5 + 1) ** 2 / 400$
 $T4 = (K\&RNTU - TEMP) / (K\&RNTU - K\&RNT0)$
 $K\&RNT0 = \text{optimal temp. for feeding}$
 $K\&RNTU = \text{temp. above which feeding stops}$

In our model $Q\&RNT2$ is multiplied by a normalizing factor to equal one at 10C standardizing the effect at 10C to the $Q10$ formulation. The two forms are shown in Exhibit 2.

Only one formulation for the effect of weight on ration is used. The power function has received widespread usage in models due to extensive experimental usage supporting its form (Winberg, 1956, Ursin, 1967).

$$Q\&RNW = X\&FW ** K\&RNEX$$

where: $X\&FW = \text{fish weight}$
 $K\&RNEX = \text{weight exponent}$

The prey density effect also has two forms. Both formulations increase with increasing prey density, eventually leveling off at a value of one for high prey densities where food does not limit ration. The first formulation, $Q\&RNP1$, is the Michaelis-Menton formulation modified by including a minimum prey density representing a refugium from predation (Anderson and Ursin, 1977, Steele and Frost, 1977, Scavia et al., 1976).

$$Q\&RNP1 = (Q\&PYTT - K\&RN\&MN) / (Q\&PYTT - K\&RN\&MN + K\&RN\&HS)$$

where: $Q\&PYTT = \text{total prey available}$
 $K\&RN\&MN = \text{minimum prey biomass for feeding}$
 $K\&RN\&HS = \text{half saturation parameter}$

The second formulation, $Q\&RNP2$, is the Ivlev function which has arisen from experiments on fish feeding at different prey densities (Ivlev, 1961).

$$Q\&RNP2 = 1 - \exp(-Q\&PYTT * K\&PDEX)$$

where: $K\&PDEX = \text{prey density exponent}$

Examples of the two equations are displayed in Exhibit 3.

The calculation of total biomass perceived by a predator (Q_{PYTT}) also involves alternative formulations. The proportions of various prey in fish diets are usually not the same as the relative concentrations in the environment. The preference of predators for certain prey types is often modeled as being dependent on the size of the prey relative to the predator (Andersen and Ursin, 1977, Steele and Frost, 1979). Q_{PYTT} is the sum of the biomasses of all prey items each weighted by a preference factor (Q_{RNS}). An additional weighting factor (K_{VUL}), specific to the prey item adjusts for the differences in availability or vulnerability of prey items of the same size.

$$Q_{PYTT} = \sum_k X_{PREYB}(k) * Q_{RNS}(k) * K_{VUL}(k)$$

where: X_{PREYB} = biomass of prey item k

The alternative formulations differ in how Q_{RNS} is computed. The first method uses a table look-up approach in which the table elements are values of Q_{RNS} for different predator-prey combinations. The second approach assumes each predator has a prey size preference based on the logarithm of the ratio of its weight to that of its prey. A normal distribution is assumed for prey size preference with parameters K_{MU} (the mean of the log ratio) and K_{SD} (the standard deviation of the log ratio). Q_{RNS} is the value of the normal density (without the normalizing constant) for the logarithm of the weight ratio. This approach is due to Andersen and Ursin (1977) and Steele and Frost (1977), and is also used for zooplankton feeding in LAKONT. The two formulations are compared in Exhibit 4.

The alternative representations of metabolism differ from the other choices presented in that in addition to a choice of equation forms, there is also a choice of which subprocesses to include. Two alternative metabolism formulations are considered. The first, Q_{MBA} is based on weight and temperature

$$Q_{MBA} = K_{MBMX} * Q_{MBW} * Q_{MBT}$$

where: K_{MBMX} = max. metabolism rate
 Q_{MBW} = weight effect on metabolism
 Q_{MBT} = temperature effect on metabolism

The second approach includes the effects of weight and temperature plus additional sub-processes for foraging and food utilization cost. Foraging costs are affected by temperature via its effect on metabolism whereas food utilization metabolism is affected by temperature through its effect on ration.

$$Q_{M} = K_{M} \cdot (Q_{M} + Q_{M}) + (Q_{R} \cdot Q_{M})$$

where: K_{M} = basal metabolism rate
 Q_{M} = foraging metabolism costs
 $= (K_{M} - K_{M}) \cdot Q_{R} \cdot Q_{M}$
 K_{M} = maximum metabolism rate
 Q_{M} = food utilization costs
 $= K_{SDA} \cdot K_{AS} \cdot Q_{R}$
 K_{SDA} = fraction of assim. energy used for std. metab.
 K_{AS} = fixed assimilation coefficient

The same power function used to represent the effect of weight on ratio is used for the weight effect on metabolism. and the effect of temperature on metabolism is modeled using equation forms analogous to those presented for ration calculation. In fact, when the GIO equation form is used for ration it is also used for metabolism and the same for the gamma function form. This avoids having the unrealistic possibility of having a very high ration and very low metabolism (or vice-versa) at higher temperatures.

It should be noted that since fish are considered to move among the four regions they would encounter different temperatures and prey densities in each. In the model the effect of temperature and prey density on ration and metabolism are weighted by the time that fish spend in each region.

3 Factorial Designs

A factorial experiment design has a fixed number of levels for each of a number of variables (factors). All possible combinations of factors are run in a full factorial design. The simplest factorial designs are those with k factors each appearing at two levels. These are referred to as 2^k designs since there are 2^k factor combinations.

The main advantage of factorial experiments over varying factors individually is that they allow estimation of interaction effects among factors. If the response to factor A depends on the level of factor B then there is an interaction between factors A and B. Higher order interactions are also possible. One would not discover this interaction if one varied the factors one-at-a-time.

Consider an experiment with 3 factors (A, B and C) each at two levels (high and low). There are 8 (2^3) combinations of factors, which will be denoted in the standard design of experiment notation: (1), a, b, c, ab, ac, bc, abc. The lower case letter denotes the upper level of each factor. The lower level is represented by the digit 1 which is handled in combination with letters using the usual algebraic conventions, that is ab represents ab(1), the treatment combination made up of the upper levels of A and B and the lower level of C. The main effect of A, denoted by A, is the difference in the means of the response when A is at its high level and when it is at its low level:

$$A = (a+ab+ac+abc)/4 - ((1)+b+c+bc)/4$$

Here the lower case letter denotes the mean of the response with that combinations of factors. Of course with deterministic simulation experiments there is no replication so the means are the observations themselves. The interaction between A and B is the difference between the effect of A at the upper and lower level of B. The effect of A when B is at its low level is $(a+ac-(1)-c)/4$. The effect of A when B is at its high level is $(ab+abc-b-bc)/4$. The interaction is the difference between these two effects:

$$\begin{aligned} AB &= (ab+abc-b-bc)/4 - (a+ac-(1)-c)/4 \\ &= ((1)+c+ab+abc)/4 - (a+b+ac+bc)/4 \end{aligned}$$

Other main effects and interactions are defined similarly.

A fractional factorial design has only a fraction of all possible treatment combinations included in the experiment. The main effects and interactions are then confounded with each other e.g. the same combination of means that defines the main effect of A can also define the BC interaction. By carefully choosing the fraction to be run, main effects and lower order interactions will be confounded only with higher order interactions which are usually assumed negligible.

Fractional factorial designs are useful when the number of factors is large and the number of runs must be kept small. In simulation modeling these designs are often used for sensitivity analysis where the factors are the parameters in the model (Rose, 1983). A nominal value and a perturbed value (+/- 10% say) are the levels. Fractional designs are needed here because of the large number of parameters and the large amounts of computer time needed for each model run.

4 Methods for Analysis

Standard statistical techniques (e.g. F-tests, t-tests) should not be applied to experiments on deterministic simulation models because there is no random component included in the model. There are many other ways of judging factor effects, none of them objective. Here we present several methods, most of them graphical.

The first step is to compute the factor effects as described in the previous section. There is no need to then compute the sums-of-squares and form an ANOVA table although some advocate this (Steinhorst, 1979), mainly for sensitivity analysis. Since there is no true error term F statistics cannot be calculated and, since the sums-of-squares are monotone functions of the effects, the effects themselves contain the same information as the F statistics.

The simplest approach is look at the relative magnitudes of the effects. Suppose in a 2^{*4} factorial experiment the four largest

effects, A, C, D, and AD are separated by a wide gap from the remaining 11 effects. One way of expressing the dominance of these four largest effects is by computing the coefficient of determination, R^{*2} . This is the fraction of the total scatter of the original 16 observations about their mean that is accounted for by the 4 effects:

$$R^{*2} = \frac{(A^{*2} + C^{*2} + D^{*2} + AD^{*2}) / 16}{\sum_{i=1}^{16} (y(i) - \bar{y})^{*2}}$$

where $y(i)$ = the i -th observation

$$\bar{y} = \frac{\sum_{i=1}^{16} y(i)}{16}$$

A graphical display using this technique can easily be constructed. Let $R^{*2}(i)$ be the coefficient of determination for the first through i -th largest (in absolute value) effects. Plotting $R^{*2}(i)$ versus i gives a cumulative variance explained plot. After the largest effects are included the plot should look relatively flat, approaching the value one.

A linear rank plot can be formed by plotting the ordered effects versus their ranks. The effects that are near zero will lie along a horizontal line in the middle, the largest effects will be at the ends, the negative ones at the lower left and the positive ones at the upper right. Unlike the above graph, one can tell the sign of the effects on this plot. The actual size of the effects can be measured along the y -axis.

Another graphical analysis technique is a normal quantile-quantile (Q-Q) plot. The i -th smallest effect is plotted against the inverse cumulative normal distribution evaluated at $(i-.5)/n$ where n is the total number of effects. (This is equivalent to plotting the effects on normal probability paper). For a sample from a normal distribution with mean zero this should give an approximately straight line passing through the origin. Values that greatly deviate from the line are assumed to arise from some other distribution. Although we do not assume normality for model output these plots are still useful for looking at simulation experiment results. Like the linear rank plot above this plot allows one to see the sign of the effects. However, because of the scales used the large effects are better identified than with the linear plot. or

5 Discussion of Experiment Results

We have applied the above techniques to a 2*4 factorial experiment with the LAKONT model. We were interested in how different process formulations and equation forms for fish effect model output. The four factors and their levels are:

Factor		Low	High
A	Prey Selectivity	Constant	Size Selective
B	Metabolism	MetabA	MetabB
C	Temp. Effect	G10	Gamma
D	Prey Density Effect	M-M	Ivlev

The designation of low and high levels is arbitrary and is only used to aid interpretation of the signs of the effects. The average response of the low levels are subtracted from the high level average response in computing main effects. Thus a negative C effect indicates that the G10 results in higher values.

In order to compare the process formulations and not the differences due to improper calibration of parameters we attempted to standardize both forms of each factor. For feeding, we adjusted the parameters to give diets that were comparable to the fish diets available in the literature. No goodness-of-fit criterion was available; the adjustment was purely subjective. Standardization of the two metabolism formulations was difficult because of their complexity. However both forms used the same temperature and weight effect subprocesses. Also metabB had a basal metabolism weight of one half the maximum used in metabA. The temperature equations were normalized to 1.0 at 10 C, and KERNGT (or KMBGT) was used in both equations. The two prey density effects were standardized to a value of one half at KERNHS.

Since the experiment involved fish processes we primarily looked at the fish model output. The zooplankton varied little across experiment runs and phytoplankton were virtually the same for all runs. Biomass, which combines both weight and numbers was the main response variable considered. Other model outputs that could be used include growth increment (GSDWDT) at various times of the year or timing of maximums (this latter response is more important for plankton than fish). Rather than look at all 39 fish size class biomasses we grouped them by life stage (larval, juvenile and adult) within a species. Usually two size classes made up one life stage.

We analyzed average fish biomass over the year to get an indication of overall factor effects. Fish biomass at day 180, a time of high larval fish abundance, was also looked at to assess a point effect of the factors.

To conserve space we present the analysis in detail only for average larval alewife biomass. Exhibit 5 shows the ordered (by magnitude) effects. C, A and AC stand far out from the remaining effects. From the cumulative variance explained plot (Exhibit 6) we

see that these three effects account for 89 percent of the total variation. The linear rank plot (Exhibit 7) show the significant effects at the two ends of the plot however the normal G-G plot (Exhibit 8) separates them out better. A, C and AC stand far out from the line made by the remaining effects. From these displays we conclude that for larval alewife feeding (A), temperature effects (C) and the interaction between these factors have the greatest effect on average biomass. None of the other factors have as large an effect as these three.

The results for the other species, life stages and times are summarized in Exhibit 9.

Perhaps the most striking thing about Exhibit 9 is how different the results are, among species and life stages and between average biomass and day 180 biomass. On day 180, the most important effects across species and life stages are prey selection and metabolism. For adults it appears that size selective feeding gives a higher biomass (since the effect is positive), but for juveniles size selective feeding results in a lower biomass and larval fish are split half and half. These results could indicate a problem with the way the feeding formulations were standardized. For adult fish on day 180, the difference between prey density equations also seem important. The estimated effect is always positive implying that the Ivlev formulation results in higher biomass. During this part of the year fish prey is abundant resulting in available prey being above the half saturation level. At these levels of prey abundance the Ivlev function gives larger feeding rates than the Michaelis-Menton.

The temperature effect has the most significant effect on average biomass for all life stages. The estimated effect is always negative indicating that the G10 function gives higher biomasses on the average. This is probably due to the gamma function decreasing for temperatures above the optimal while the G10 continues to increase. Temperature effects are not as important on day 180 because both equations are similar for the range of lake temperature values up to that time of year.

The significant interactions for average biomass involving temperature indicate that temperature is not independent of the other factors. There is a strong interaction between temperature and prey selection for adult perch, juvenile perch, alewife and sculpin and larval alewife, shiner and sculpin. Temperature and metabolism have a significant interaction for adult carp, alewife, and sculpin, juvenile perch, carp, and alewife and larval perch and carp. The nature of these interactions can be examined with interaction diagrams. The four averages of the responses, one for each combination of the two factors involved are plotted versus the first factor's levels (-1 = low, 1 = high, say). Lines are then drawn between the means with the same level of the second factor. For example, for the AC interaction, let $z(1) = ((1)+b+d+bd)/4$, $z(2) = (c+bc+dc+cdb)/4$, $z(3) = (a+ab+ad+abd)/4$, $z(4) = (ac+abc+acd+abcd)/4$. One plots the points $(-1, z(1))$, $(-1, z(2))$, $(1, z(3))$ and $(1, z(4))$ and draws lines from $z(1)$ to $z(3)$ and $z(2)$ to $z(4)$. The lines indicate the change in response as A changes from its low level to its high level. In one case the change is measured at the lower level of B ($z(1)$ to $z(3)$), in the other case the change is measured at the upper level of B ($z(2)$ to $z(4)$). Parallel lines

indicate no interaction, i.e. the response to A is the same for both levels of B. The diagram could be redrawn with the abscissa giving the levels of C without altering the conclusions.

Interaction diagrams for the temperature by prey selection and the temperature by metabolism interactions are shown in Exhibits 10 and 11 respectively. There does not seem to be any pattern among the species and life stages for the feeding by temperature interaction. In some cases the Q_{10} response stays the same as the prey selection function changes while the gamma function response increases. In other cases the gamma function response stays the same while the Q_{10} response increases or decreases. For two of the cases (juvenile and larval sculpin) the lines crossed. This usually results in the main effects of the factors involved being not significant while the interaction as it is here for temperature for juveniles and both temperature and prey selection for the larval stage. From the diagrams we can see that temperature is important, but which function gives the higher biomass depends on what prey selection formulation is used. At this time we have no interpretation of this interaction, especially since its form varies so much among the species and lifestages.

The temperature by metabolism interaction shows a more consistent pattern across species and lifestages. The Q_{10} function response always results in a higher average biomass than the gamma function and the biomass is lower with the Q_{10} -metabB combination than with Q_{10} and metabA together. The gamma function produces slightly higher biomass with the metabB formulation, just the opposite of the Q_{10} result. The lower biomass with the Q_{10} -metabB combination is probably because temperature effects are involved more in the metabB formulation. There is a temperature effect on metabolism (Q_{MBT}) just as in metabA, but there is also a temperature effect on food utilization. Food utilization is a function of ration (Q_{RN}) which has its own temperature effect (Q_{RNT}). The Q_{10} function increases with temperature, thus higher temperature results in higher metabolism which results in less biomass produced. On the other hand, the gamma function decreases at high temperatures leading to lower metabolism and so the gamma-metabB combination gives slightly higher average biomasses than the gamma function with metabA.

6 Summary

We have discussed and displayed here a group of methods for intercomparing alternative process formulations in a large ecosystem simulation model. These methods illustrate many of the difficulties of conducting such experiments and in analyzing and interpreting results. Several important conclusions are discussed below.

(1) The comparability of alternative equation forms for various processes demands standardization of the equations at some average level such as half saturation level for prey density effects, or at 10C for temperature effects. Furthermore the model must be calibrated to field data. It is not always possible to do this with all output criteria in a complex model such as LAKONT and the simulation experiment differences might be due to calibration differences instead of (or in addition to) intrinsic differences between alternatives. In fact

calibration might be looked as a source for parameter variability in model analysis.

(2) The factorial design and subsequent graphical analysis illustrated the ability of the graphical techniques to display the most significant differences between alternative equations. Since the burgeoning ecological modeling literature has given rise to alternative equation forms for many processes (Sullivan et al., 1983) intercomparisons of equations using these methods should prove useful in future modeling efforts.

(3) The example experiments illustrate the great complexity of model behavior and the difficulty of tracing model response to single processes. Witness the large number of interactions that were significant and how the relative importance of the various equation differences and the interactions changes not only from species to species but also from lifestage to lifestage within a species.

(4) Although the methods are excellent for exploring the relative differences between equation forms the comparison is only relative. As mentioned earlier, some measure of acceptability of performance must be defined in order to choose between alternatives. Although we know in this example which equation gives higher biomass, we don't know which is better. The problem of acceptability is exacerbated by having validation data that is highly variable and even missing for some biota in the model and which was not well fit by the model for all biota. The problem of choice is difficult because we prefer to have a single process representation for all species and lifestages while results show the differences between equation forms is not consistent between species or lifestage.

(5) Choosing the best between alternatives requires a data set to compare model output that we are confident represents the real dynamics of the biota. For almost all complex ecosystems this is not presently possible and thus the comparison of equation forms can only focus on relative importance and where the emphasis of future process study should be put. Our suggestion is to use these methods for choosing between optional process representations only when the supporting data are good enough to provide a measure of what the system dynamics really are. Smaller systems or microcosms are promising in this regard.

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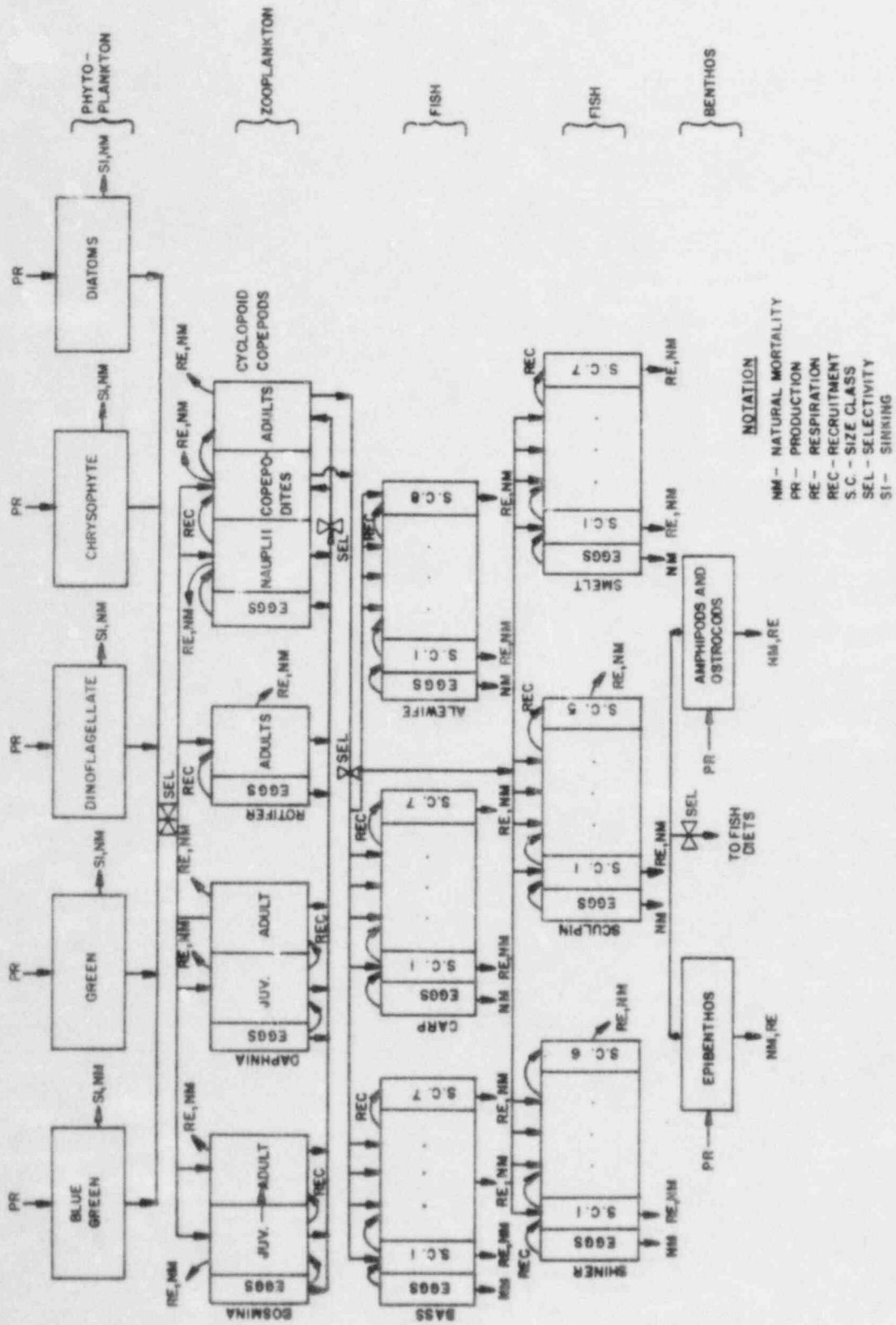


Exhibit 1 Flow diagram for LAKONT model

Exhibit 2 Comparison of temperature effects

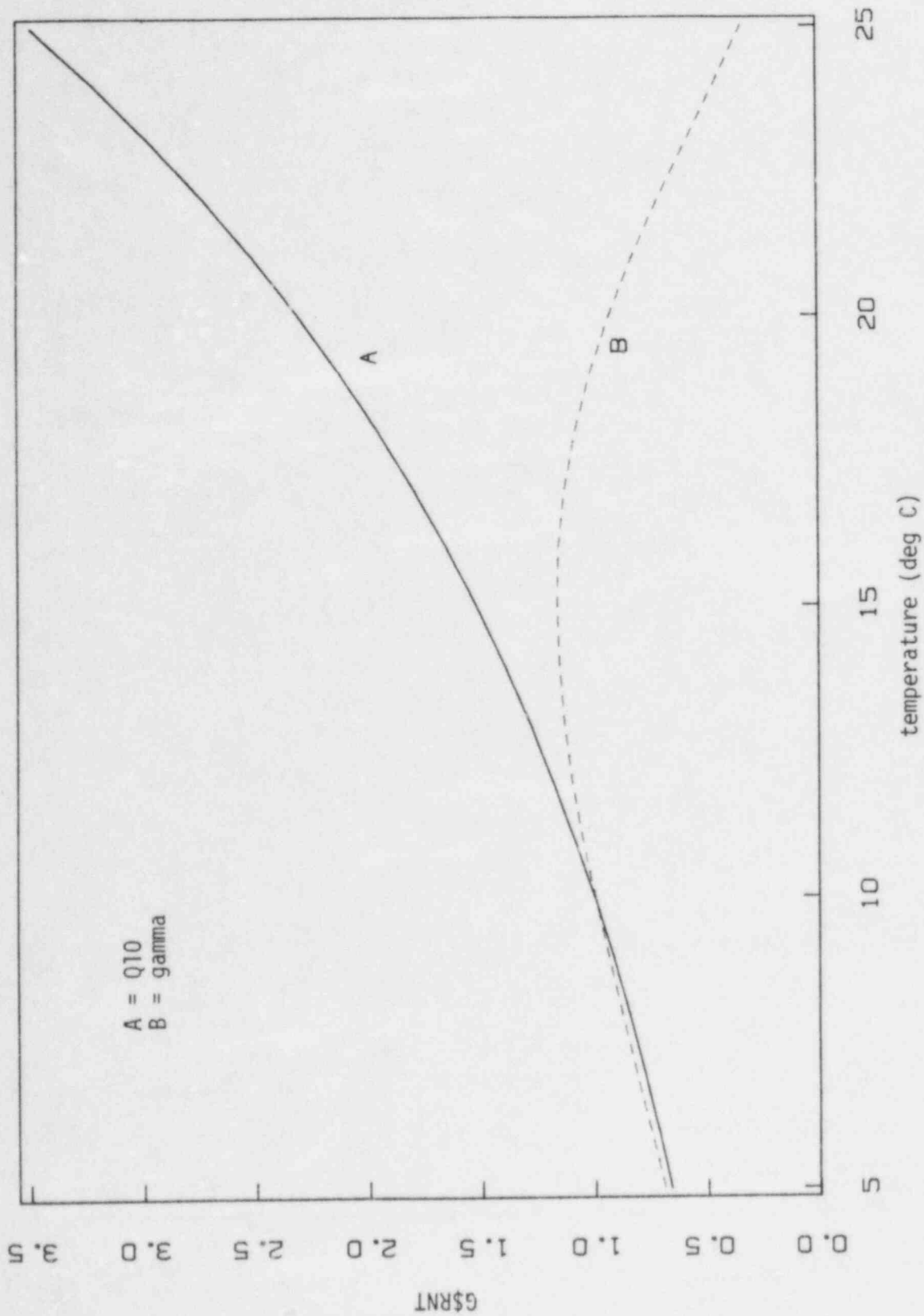


Exhibit 3 Comparison of prey density effects

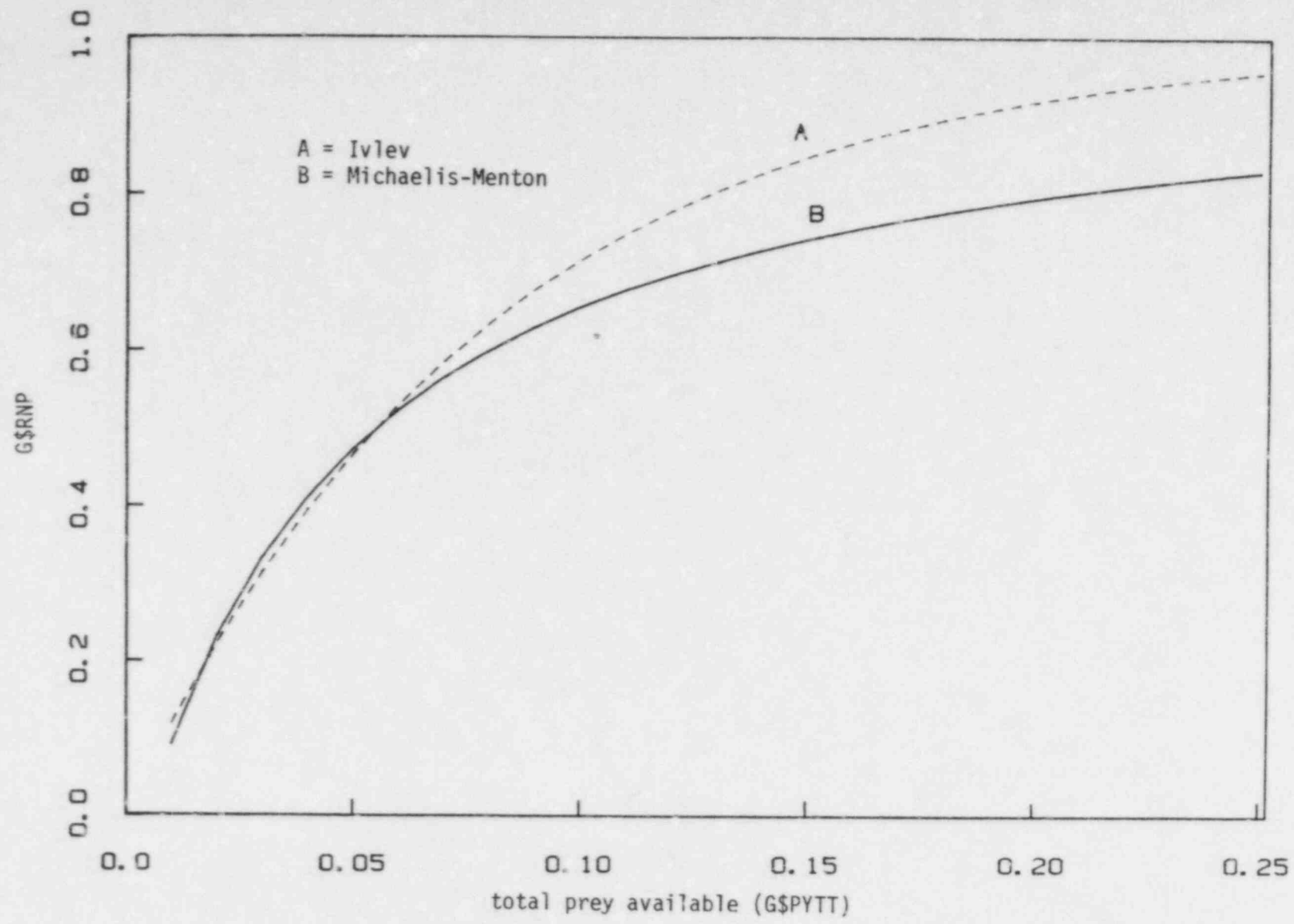


Exhibit 4 Comparison of prey selectivity functions

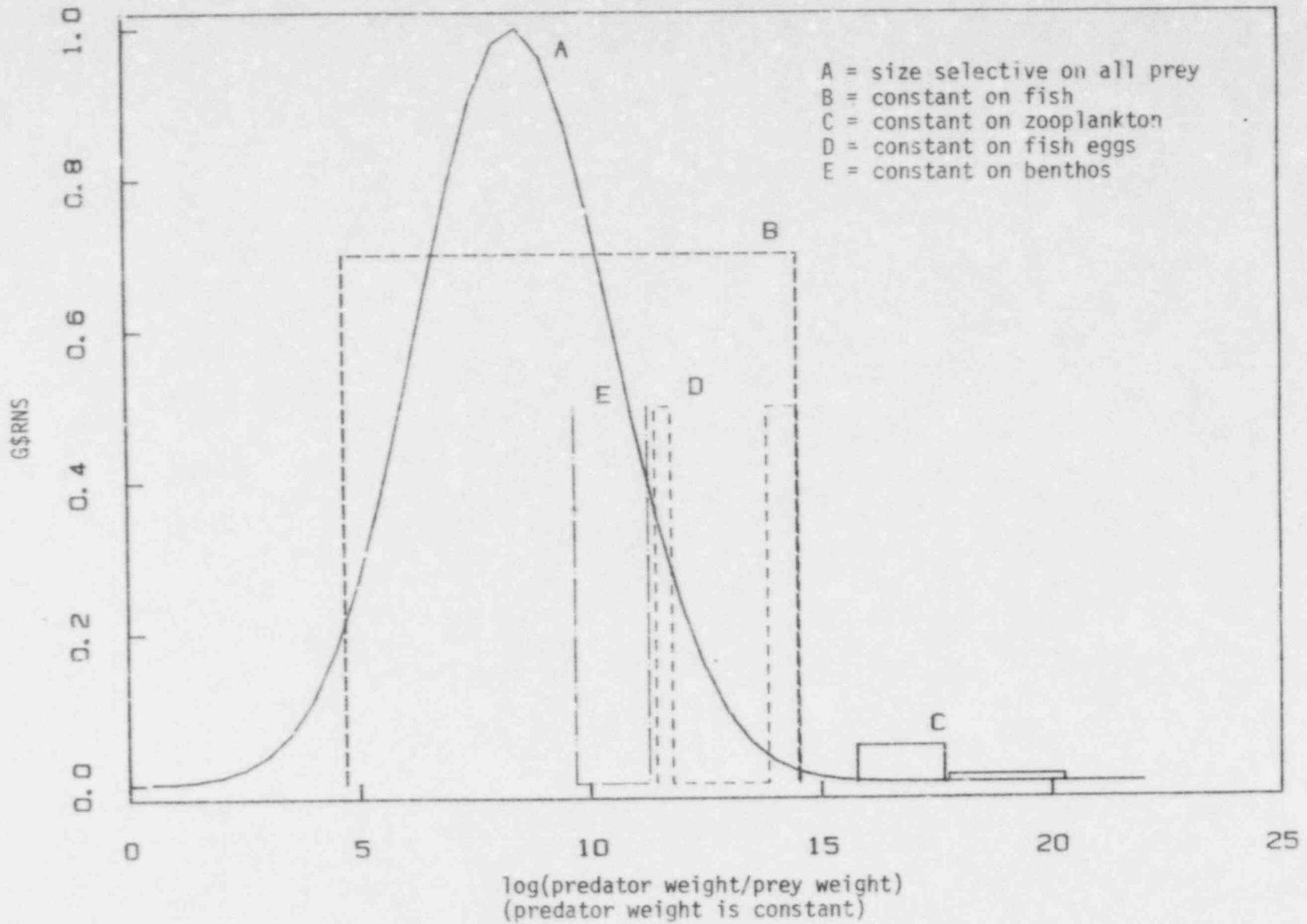


Exhibit 5 Ordered Effects for Average Larval Alewife Biomass

Effect	Value
C	-19.42
A	-15.44
AC	13.56
BC	5.21
B	-5.02
D	3.18
AB	2.97
ABC	-2.96
CD	-2.86
AD	-1.51
ACD	1.33
BD	-0.90
BCD	0.87
ABD	0.25
ABCD	-0.23

A: feeding selectivity
B: metabolism
C: temperature
D: prey density

Exhibit 6 Cumulative percent variance explained plot for larval alewife average biomass

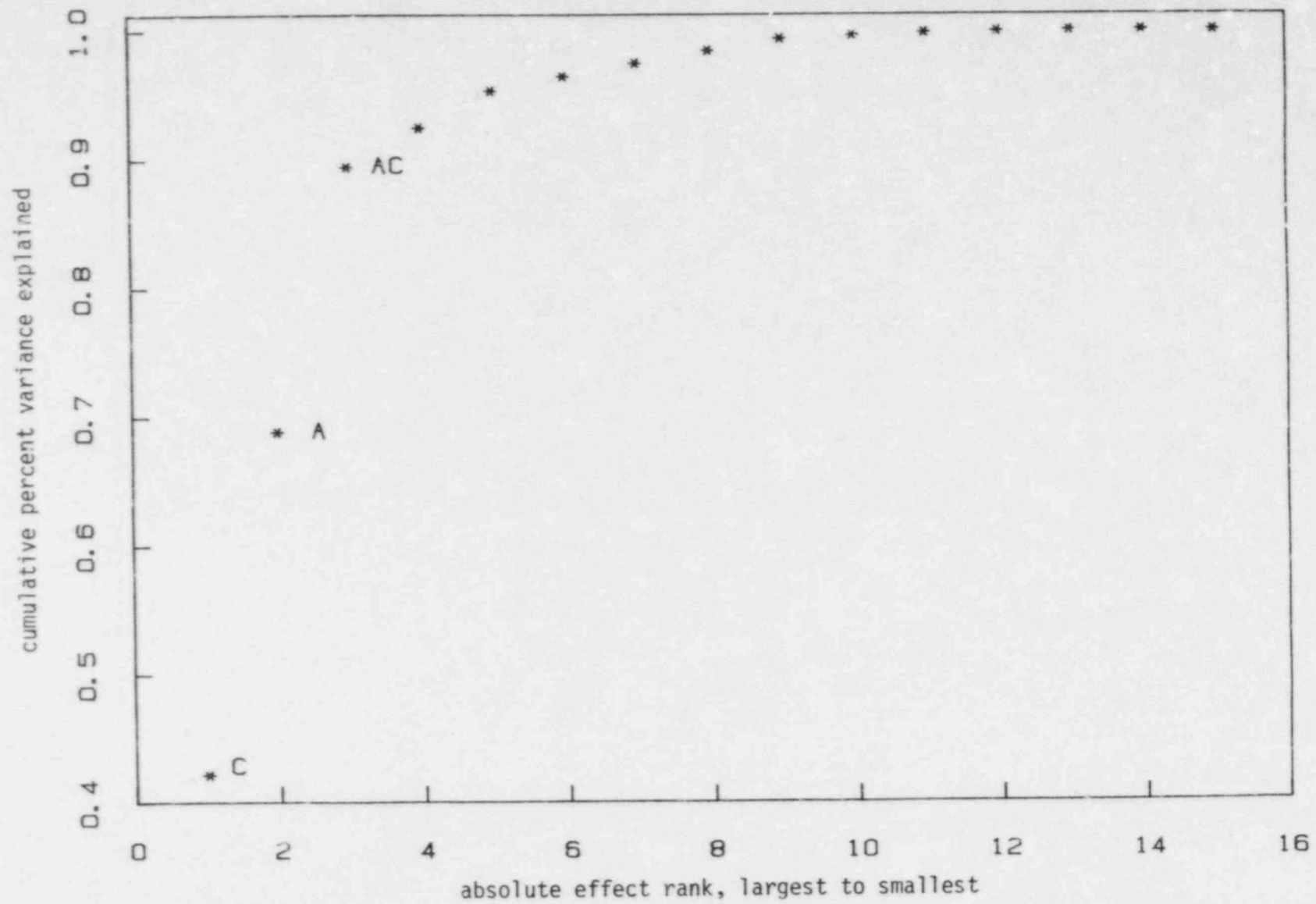


Exhibit 7 Linear rank plot for larval alewife average biomass

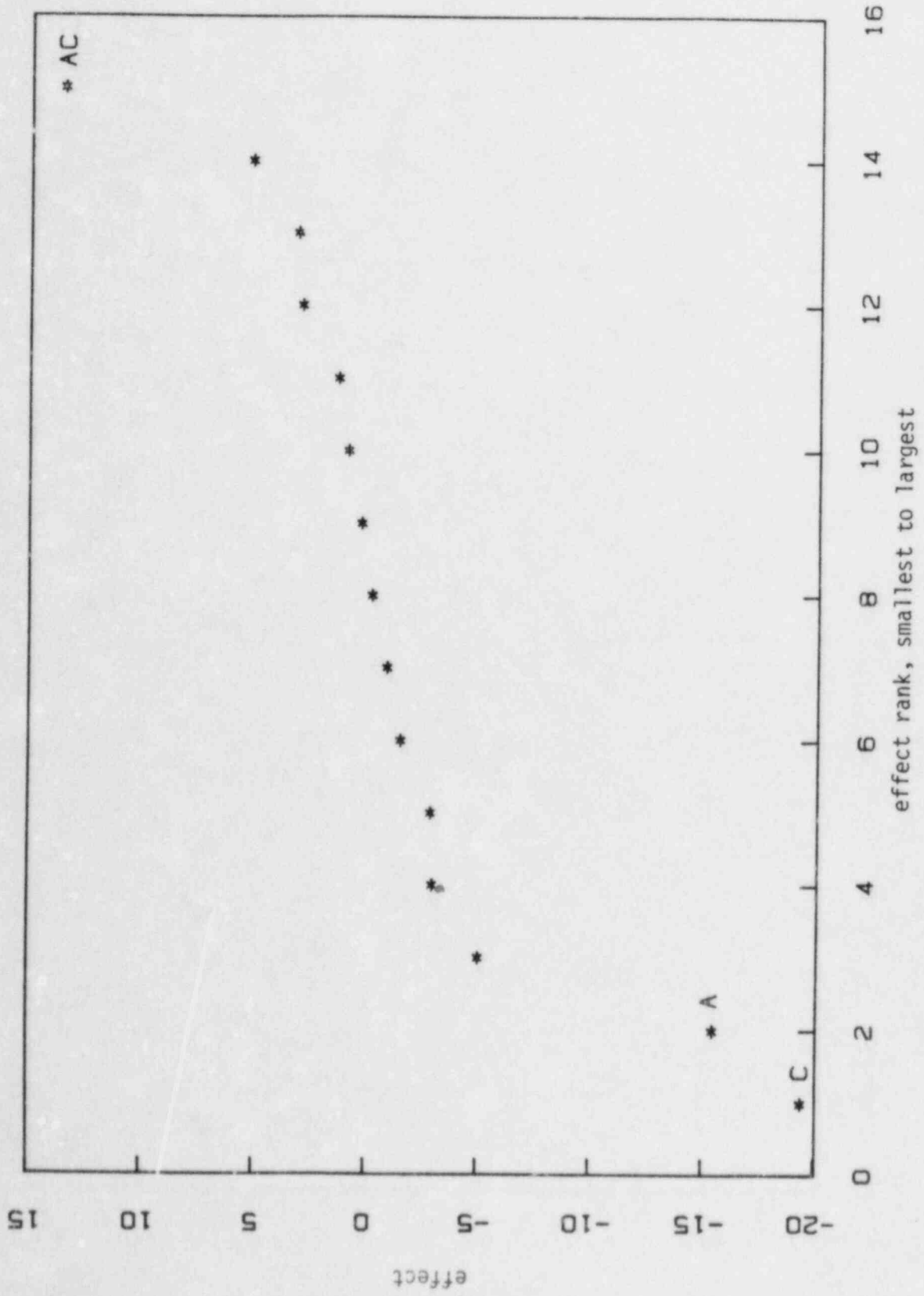


Exhibit 8 Normal Q-Q plot for larval alewife average biomass

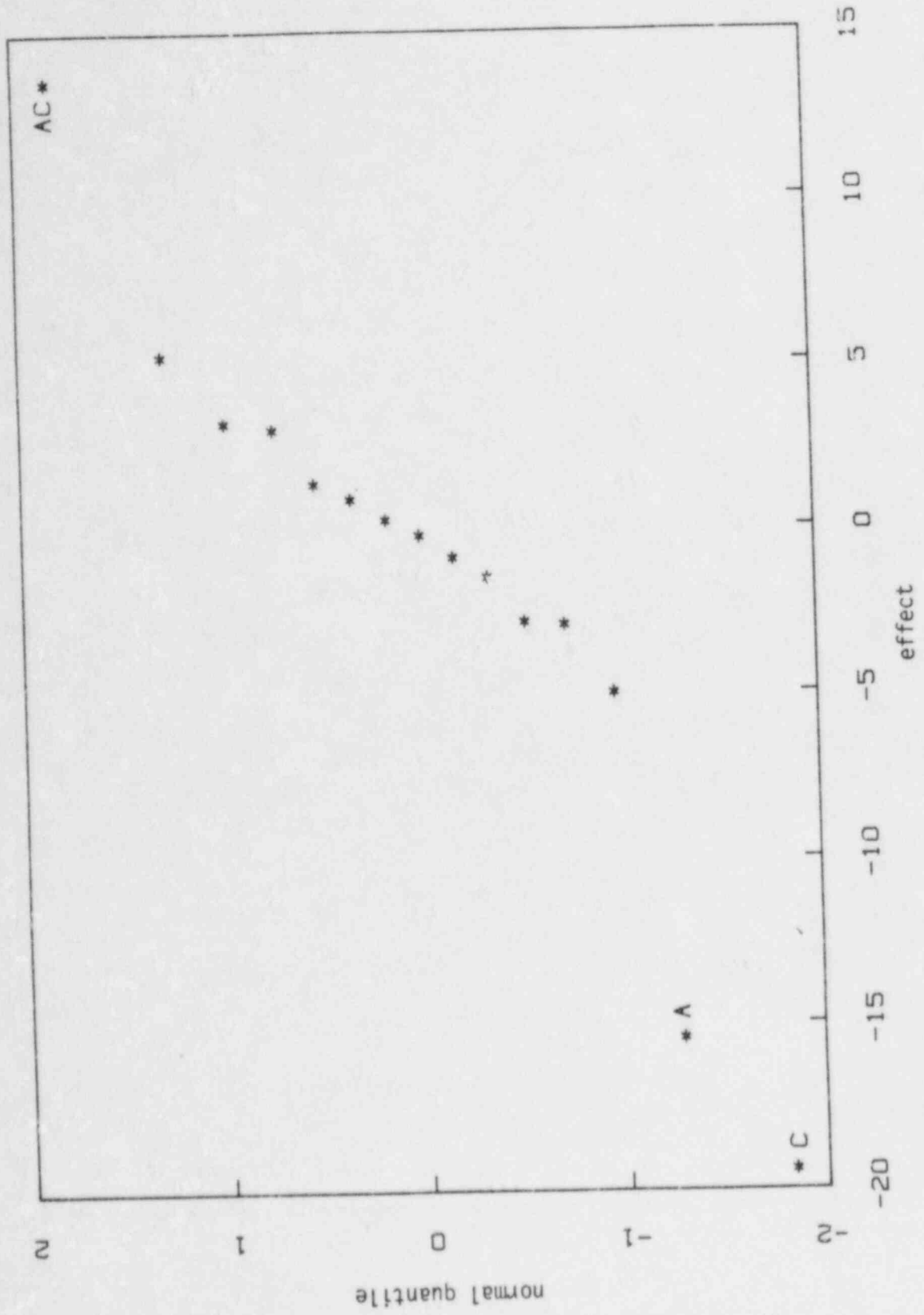


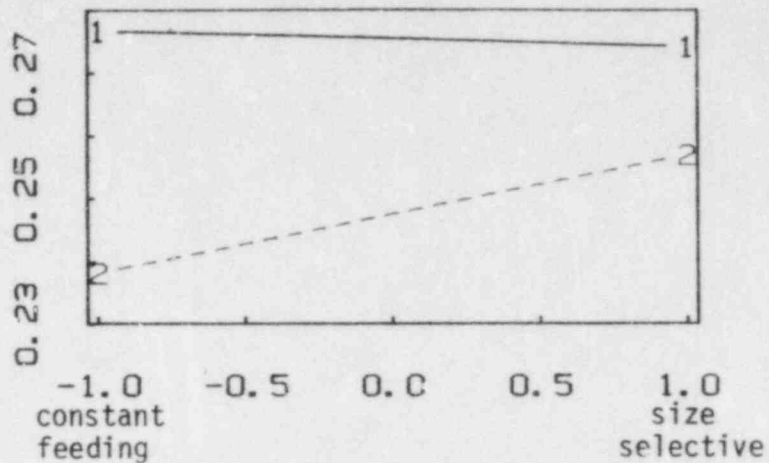
Exhibit 9 Significant Effects by Species, Lifestage and Time
 (listed in decending order of magnitude, a minus
 sign denotes a negative effect)

Species	Adult		Juvenile		Larval	
	Ave.	Day 180	Ave.	Day 180	Ave.	Day 180
Perch	-C	B	B	-A	B	B
	B	A	-A	B	D	A
	A	D	-C	-C	-C	D
	D		D	D	BD	-AB
	-AC		-BC		-BC	-C
	-CD		-AC			-BC BD
Carp	-C	-A	-C	-A	-C	-A
	BC	D	-B		-A	-C
	-B	-C	BC		-B	-B
		-AD B			BC	AC AB
Alewife	-C	A	-C	-A	-C	-A
	D	B	BC	-AB	-A	B
	A	D	AC	B	AC	D
	BC	C				AC
Shiner	A	A	A	A	A	A
	-C	B	-AB	B	-C	B
		D	B		-AC	AD AB D
Sculpin	-C	B	A	-A	B	A
	D	A	-AC	-C	AC	B
	BC	D				AB
	-CD	C				D
	A					
Smelt	-C	B	-C	A	B	-C
	A	A	D	-AB	-A	B
	B	D	A	B	-C	D
			-AB	-C	-AD	-BC
			-AD			

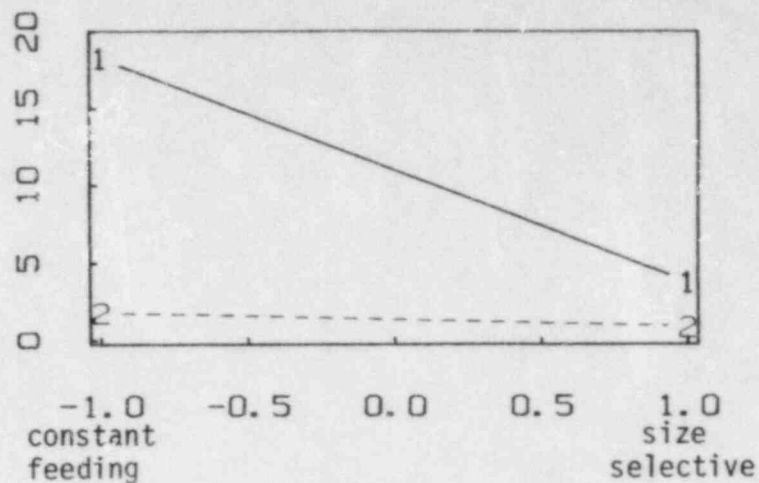
A: feeding selectivity
 B: metabolism
 C: temperature
 D: prey density

Exhibit 10 Temperature - prey selection interaction diagram
 (1 = Q10, 2 = gamma)

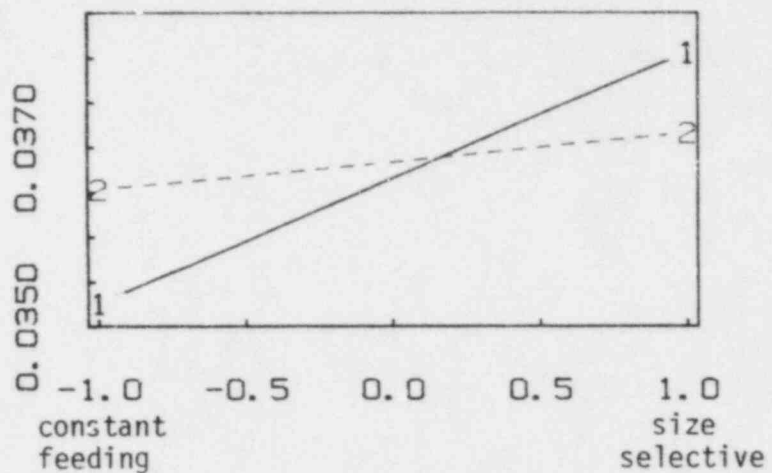
Juv. alewife ave. biomass



Lar. alewife ave. biomass



Juv. sculpin ave. biomass



Lar. sculpin ave. biomass

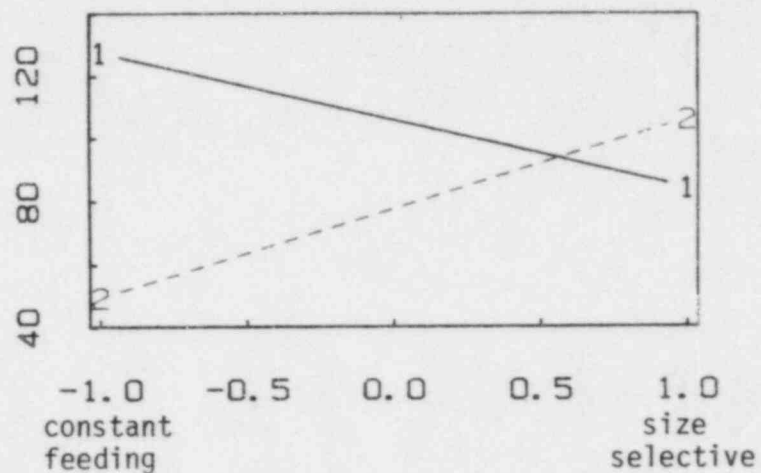
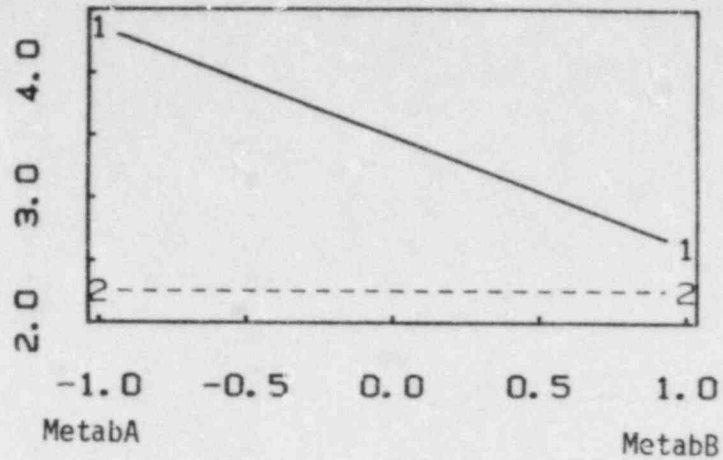
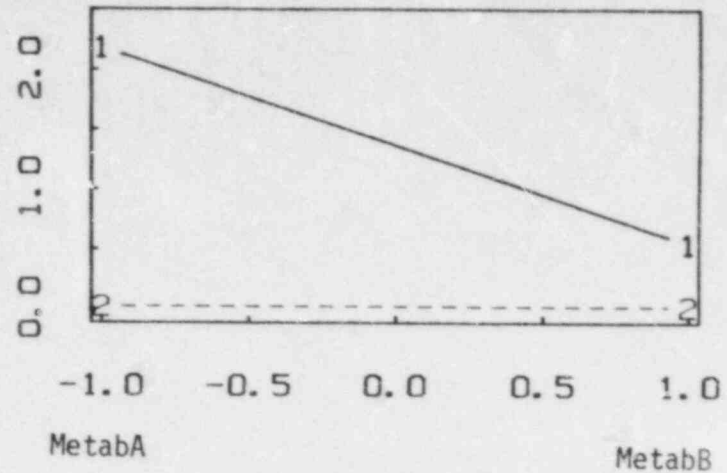


Exhibit 11 Temperature - metabolism interaction diagrams
 (1 = Q10, 2 = gamma)

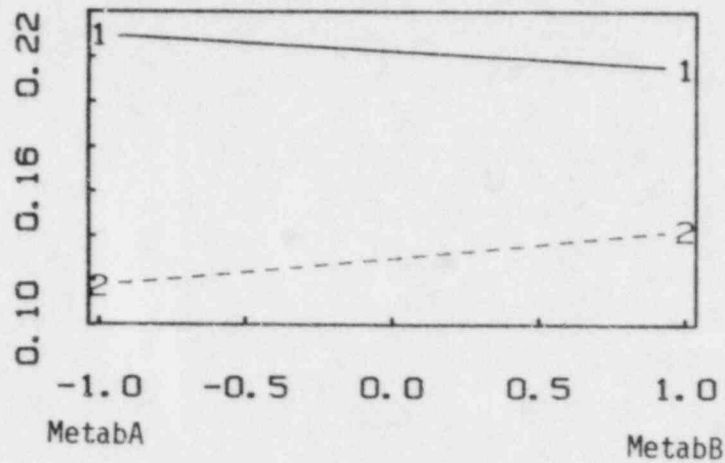
Adult carp ave. biomass



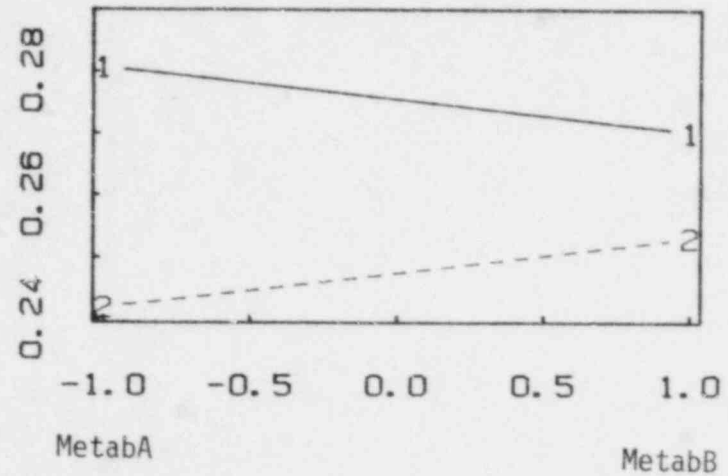
Juv. carp ave. biomass



Adult sculpin ave. biomass



Juv. alewife ave. biomass



NRC FORM 335 (7-77)		U.S. NUCLEAR REGULATORY COMMISSION BIBLIOGRAPHIC DATA SHEET		1. REPORT NUMBER (Assigned by DDC) NUREG/CR-3896	
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16. ABSTRACT (200 words or less) This paper reviews methods for exploring the differences between alternative equations in complex ecosystem models. A factorial design is proposed as a method for exposing possible interactions between equation forms in their effect on model output as well as to clarify differences between the main candidate equations. A number of display methods arising from statistical analysis are used including normal Q-Q plots, linear rank plots, and interaction diagrams. The methods were illustrated using a complex ecosystem model of Lake Ontario. We found the methods effective at illustrating major differences between equations although several difficulties arose due to the complexity of the models and the diffuse nature of the data supporting model validation. Questions of the method for standardization of equation forms so that the compared equations are in some way analogous are important. These methods are probably most useful in cases where the data are of sufficient quality to indicate not only how different equations effect model output but also which forms are to be preferred.				11. CONTRACT NO. FIN B7018	
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SIMULATION EXPERIMENTS COMPARING ALTERNATIVE PROCESS FORMULATIONS
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