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Model Evaluation Workgroup Technical Memorandum 7b

Review of the Green Bay Food Web Model

Prepared for

Fox River Model Evaluation Workgroup

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Prepared by

Exponent
15375 SE 30th Place, Suite 250
Bellevue, Washington 98007

Edited by

Wisconsin Department of Natural Resources
P.O. Box 7921
Madison Wisconsin 53707-7921

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Acronyms and Abbreviations

BAF	bioaccumulation factor
GBFWM	Green Bay Food Web Model
GBMBS	Green Bay Mass Balance Study
NRDA	natural resource damage assessment
PCB	polychlorinated biphenyl
SDA	specific dynamic action
YOY	young-of-the-year

1. Introduction

This technical memorandum is provided in partial fulfillment of the Memorandum of Agreement between the State of Wisconsin and seven paper companies, dated January 31, 1997. The model review presented in this document has been performed in accordance with the *Workplan to Evaluate the Fate and Transport Models for the Fox River and Green Bay*. Its purpose was to determine the applicability of the Green Bay Food Web Model (GBFWM) to Green Bay, as well as to the upper and lower portions of Lower Fox River.

This review was performed from the perspective that the best value of any model coefficient is presumed to be that specified in the model input, even if it differs from any written documentation. In addition, the written documentation is expected to be the source of information describing any methods of analyses used to generate model coefficients. The one exception to this perspective is the translation of the conceptual food web to numerical model input. In this case, the documented conceptual food web (Connolly et al. 1992, HQI 1995) is presumed to be the actual representation, whereas the coefficients in the model input are its approximation. The primary perspective, and its one exception, were adopted because it is very difficult to evaluate numbers in the input files without justification to support them.

The GBFWM was developed by HydroQual, Inc. (Connolly et al. 1992; HQI 1995) for the U.S. Environmental Protection Agency as part of the Green Bay Mass Balance Study (GBMBS) conducted in 1989. This model focuses on calculating polychlorinated biphenyl (PCB) bioaccumulation in several representative fish species collected in Green Bay and the last seven miles of the Lower Fox River.

The GBFWM model consists of four components: 1) a conceptual food web, which describes the predator-prey relationships between the target fish species, 2) a numerical model framework that is general in nature and performs the PCB bioaccumulation calculations based on the predator-prey relationships defined in the model input, 3) the numerical model input, in which the site-specific conditions of the application are defined, and 4) model calibration. The four components combined constitute the complete GBFWM.

Each of the first three components is equally important in the evaluation of the performance of the GBFWM during model calibration. A conceptual food web that does not reasonably represent the environment will result in implementation of a numerical food web model that does not reasonably represent the environment. A model framework with a flawed numerical representation will calculate less meaningful results. Model input developed using inappropriate assumptions will cause even a sound model framework to calculate less meaningful results.

The bottom line is that model calculations that reasonably approximate measured environmental conditions may not be meaningful if one of the first three components is flawed. In addition, model calculations must be interpreted in the context of the assumptions used to develop any of the first three components. Finally, correction of flaws in any of the first three components may not significantly change the model calculations that result during calibration with respect to data variability, but may have long-term implications when the model is used for either hindcast or forecast simulation.

Model documents (Connolly et al. 1992; HQI 1995, 1996) that describe the development of the GBFWM conceptual model, the theory behind the model framework, the analysis of data for developing model input, and model calibration were reviewed in conjunction with the calibrated model input files (Slawecki 1997, pers. comm.). In many instances, review of the GBFWM source code (Slawecki 1997, pers. comm.) was also required to facilitate understanding how theories were implemented in the model framework. The result of these reviews for each model component is presented below.

2. Conceptual Food Web Description

Conceptual food webs are simplified representations of the predator-prey relationships that exist between key fish species within specified habitats. The conceptual food web supports the implementation of the numerical (e.g., bioaccumulation) model by providing specific ecological information on important habitats, species, and their interactions within the environment. Conceptual food webs that sufficiently represent the environment will result in a numerical model that reasonably predicts the bioaccumulation of PCBs in Green Bay fish. Developing a representative conceptual food web for Green Bay relies on the availability of several key sources of information:

- Nature and extent of habitats that reflect the variation in environmental characteristics of the system
- Presence and abundance of representative biological species that utilize important habitats
- Functional attributes of each species that reflect prey selection (e.g., food type) and preference (e.g., food fraction of total diet)
- Life history characteristics (e.g., foraging, spawning) of biological species that reflect the ecological preference for a specific habitat.

The conceptual food webs presented by Connolly et al. (1992) are good conceptual models for representing habitats associated with the pelagic zone of Green Bay. Appropriately, the authors use valuable site-specific information on predator (e.g., walleye [*Stizostedion vitreum*] and brown trout [*Salmo trutta*]) stomach content data collected by Smith and Magnuson (1987, as cited by Connolly et al. 1992) at the University of Wisconsin's Center for Limnology. This information is used to identify major prey preferences that represent the Green Bay forage base (e.g., alewife, rainbow smelt, and young-of-the-year [YOY] gizzard shad) so that trophic transfer in walleye and brown trout is accounted for in the model. As a final step in the development of key species in the conceptual model, Connolly et al. (1992) account for prey items of the forage species through an evaluation of published literature.

The first food web in Connolly et al. (1992) includes the following species and food sources: walleye, rainbow smelt, gizzard shad, alewife, zooplankton, and phytoplankton (Figure 1). This food web is specific to species and habitat within the inner portion of Green Bay. Inner Green Bay is divided into two zones: inner Green Bay (Zone 2) and the mouth region (the last 7 miles) of the Lower Fox River (Zone 1). The GBFWM documentation (Connolly et al. 1992) indicates that alewife, gizzard shad, and walleye migrate from inner Green Bay to the Lower Fox River during the spring, each for about a month, for spawning. The second food web includes walleye, brown trout, rainbow

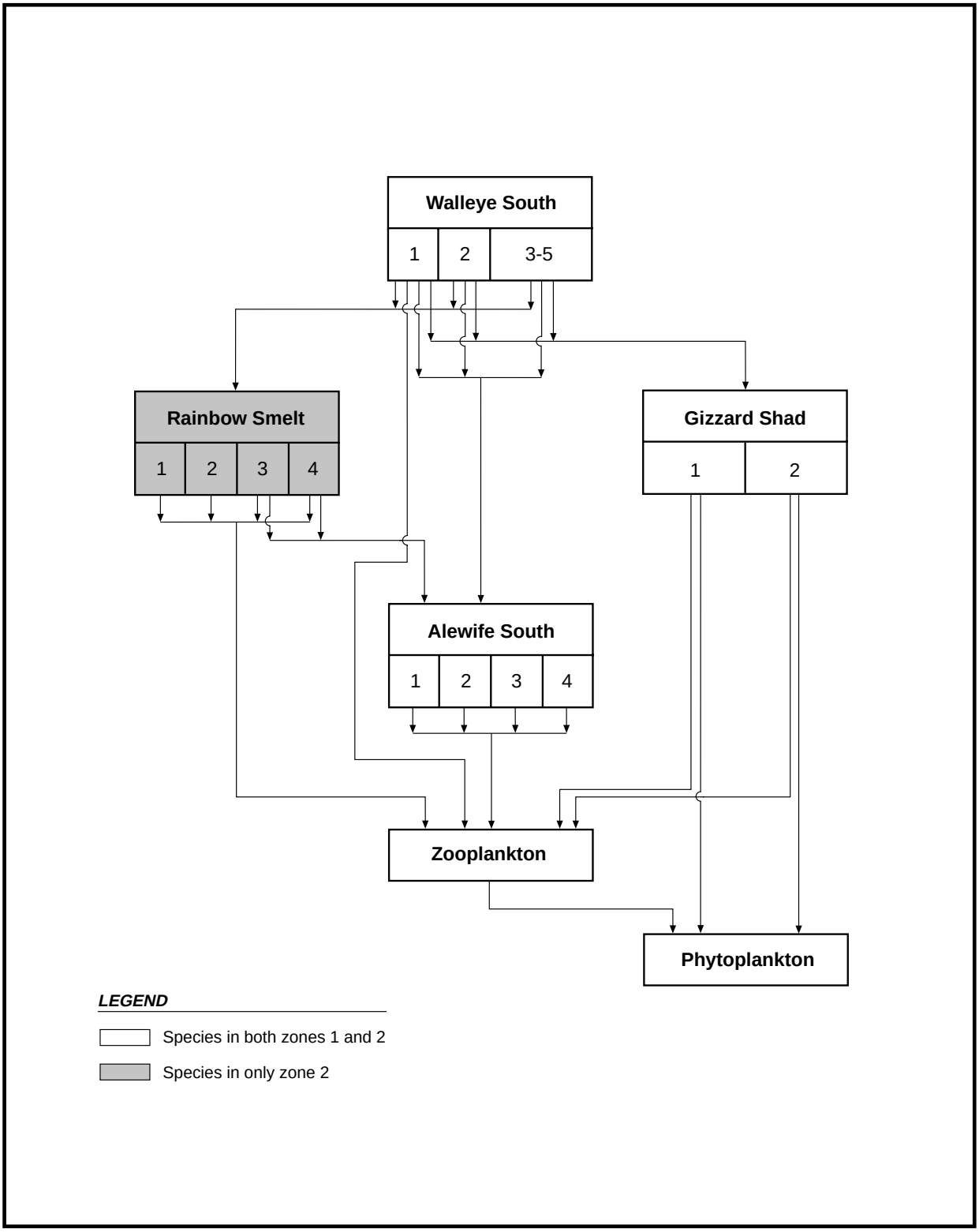

Figure 1. GBFWM—zones 1 and 2 food web.

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smelt, alewife, zooplankton, and phytoplankton (Figure 2). It represents species and habitat associated with the middle and outer portions of the bay. Middle and outer Green Bay are divided into three zones: middle zone west (Zone 3A), middle zone east (Zone 3B), and outer Green Bay (Zone 4).

Zooplankton and phytoplankton represent the primary forage base to the existing Green Bay conceptual food web models. The absence of benthic macroinvertebrates or the sediment organic complex as food sources in the diet of fish species in these models indicates that the conceptual food webs are principally pelagic in nature. The pelagic zone of Green Bay is a combination of the open surface waters of the limnetic zone (e.g., surface waters above the light compensation level but where light does not penetrate to the bottom), and deeper surface waters of the profundal zone (e.g., surface waters below the light compensation level).

The following sections of this memorandum review the conceptual food webs presented in Connolly et al. (1992) in the context of key sources of information that are important in developing these models.

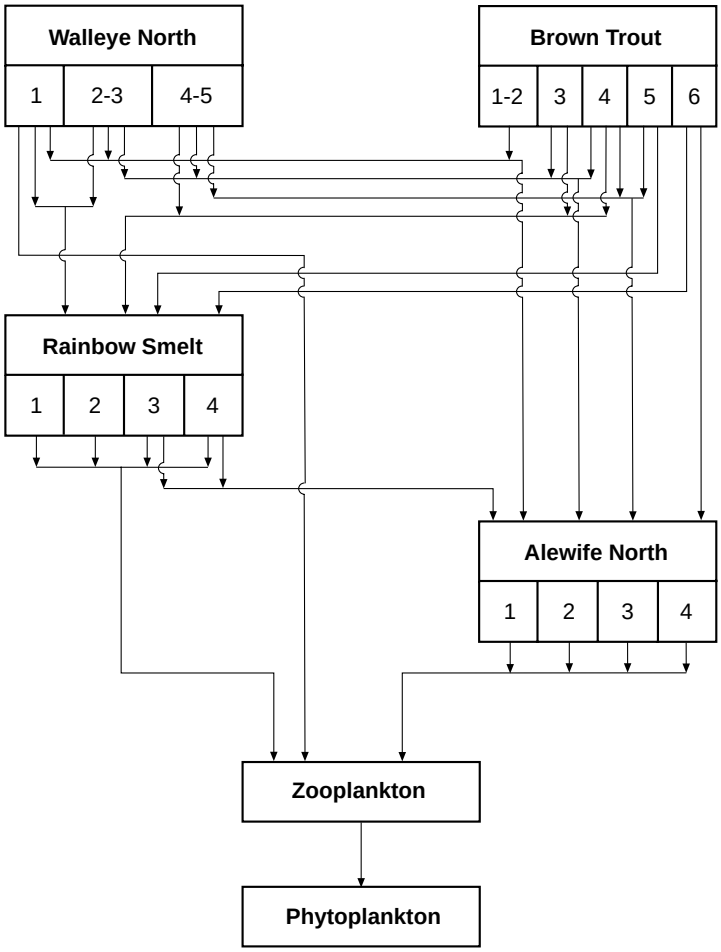

Figure 2. GBFWM—zones 3A, 3B, and 4 food web.

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3. Critique of Conceptual Food Web

As stated above, the conceptual food web models that are input to the GBFWM are reviewed herein according to the adequacy of their representativeness in terms of habitats that reflect environmental variation in Green Bay, the presence and abundance of species utilizing those habitats, the predator-prey dietary relationships of each species, and the life history characteristics that reflect the species' habitat preferences.

3.1 Habitat Representativeness

Green Bay, as a large open body of water with a lengthy shoreline, contains many different types of aquatic habitat. There are two major zones in Green Bay that would support fish habitat: the pelagic and littoral (near-shore) zones. The pelagic zone, defined above, provides habitat for open-water (often coolwater) fish species, planktonic organisms, and a variety of other macroinvertebrate species.

The littoral zone, or surface waters above the light compensation level where light penetrates to the bottom, contains two key types of habitat for fish (primarily warmwater), planktonic organisms, and macroinvertebrates: inshore habitat and coastal wetlands. Inshore habitats consist of shallow, warm surface waters (vegetated or unvegetated) directly exposed to wave action from Green Bay. Coastal wetlands also contain shallow, warm surface waters; however, they are almost always vegetated with submergent or emergent plants. Coastal wetlands are usually protected from wave action of bay surface waters as well.

Although important in describing the ecological function of the Green Bay system, there are fish species and habitats within the bay that cannot be represented by a pelagic–based food web alone. The conceptual food web models described by Connolly et al. (1992) appear to accurately represent the pelagic habitat of Green Bay. The five species chosen to represent the Green Bay conceptual model—walleye, brown trout, gizzard shad, alewife, and rainbow smelt—are common in pelagic environments. The aquatic habitat represented by these species (and collectively, the food web in this habitat) is characteristic of those in the pelagic open waters of Green Bay. However, shallow water habitats of the bay are not considered, addressed, or represented by species in the existing GBFWM.

3.2 Representativeness of Biological Species

An additional step in developing a conceptual food web model is selecting key, representative species. The selection of key fish species is generally be based on a number of factors that consider, but are not restricted to:

1. Position within the food web (e.g., trophic level);
2. Representativeness: integrates localized prey; found throughout the system;
3. Relevance: PCBs known to accumulate based on an adequate time series of data; and
4. Angler harvest.

The five fish species selected by Connolly et al. (1992)—alewife, brown trout, gizzard shad, rainbow smelt, and walleye—are commonly considered major species in Green Bay and are appropriate in meeting the selection criteria described above.

Another way to evaluate the species to use in a conceptual food web model is to examine observed PCB tissue concentrations in species from a variety of key habitats. Lipid-normalized PCB tissue concentrations measured in Green Bay fish in 1998 (Exponent, unpublished data) indicate that predators (walleye, northern pike, and smallmouth bass) have higher concentrations of PCBs than omnivorous (carp) or invertivorous (white sucker, yellow perch) fish. Of the predators analyzed, walleye tissue concentrations (mean = 81 ppm, n = 3) were roughly twice as high as those of northern pike (mean = 43 ppm, n = 3) or smallmouth bass (mean = 33 ppm, n = 6). However, carp concentrations (mean = 32 ppm, n = 8) were just slightly lower than those of the predators sampled in these littoral habitats.

While piscivores, invertivores, and omnivores are included in the GBFWM, other species (e.g., yellow perch and carp) may represent these functional feeding groups in other habitats. For example, although yellow perch (a piscivore) is described in the GBFWM documentation, it is not included the conceptual food webs. Moreover, carp forage and spawn regularly in shallow waters (Epstein et al. 1974; Edwards and Twomey 1982; Harris 1987; Stephenson 1990; Danzmann et al. 1992; Kwak et al. 1992; Weaver et al. 1997). As indicated in tissue samples collected in Green Bay (Exponent, unpublished data), carp have PCB concentrations within approximately a factor of two of the concentrations observed in walleye. It is possible that surface sediment PCBs contribute to the food web of some species. If so, additional components could be added to the conceptual food web to simulate a greater proportion of the food web.

3.3 Diet Composition and Prey Preferences

The development of conceptual food webs requires incorporation of information on species' diets and prey preferences for estimating trophic transfer. Site-specific stomach content data provide a solid foundation for determining predator diets in the Connolly et al. (1992) food web model. This information is valuable to construct a biologically sound conceptual model for the bay and establish an accurate picture of the Green Bay forage fish that support these top predators.

In addition to predator diets, much of the information presented in Connolly et al. (1992) appears to be accurate regarding prey selection and diet composition of forage fish presented in the conceptual model. However there are some cases where the primary citations used in describing forage fish prey were inconsistent with the source of information presented. For example, the statement that "the main diet for yellow perch consists of zooplankton, benthic species, and possibly, as the fish ages, a small percentage of YOY and larval fish" is unsupported by the referenced work of Kitchell et al. (1977) and Henderson and Nepzy (1989). Although this generalized statement does not appear to be inconsistent with the diets of yellow perch, the references mentioned here do not support this statement.

Similar observations are noted for other species of forage fish presented in the Connolly et al. (1992) document. Alewife, bloater chub, rainbow smelt, gizzard shad, and yellow perch are identified in the report as forage fish that generally occupy the same feeding niche. This feeding niche is comprised of both plankton and benthic prey communities that are common residents in Green Bay. Connolly et al. (1992) appropriately acknowledges the connection of the forage base to benthic macroinvertebrate communities. However, most of the remaining sections of the report focus on articles that emphasize the importance of planktonic species to these particular species. It appears that only in yellow perch are benthic macroinvertebrates a more important dietary component than planktonic species. However, yellow perch was not used in the development of the food web models.

Connolly et al. (1992) reports that gizzard shad feed on organic detritus, algae, and plankton, with the diet shifting from algae to organic detritus and zooplankton as the species ages. This is consistent with other references in the primary literature (Jude 1973; Williamson and Nelson 1985; Mundahl and Wissing 1987, 1988; Hartman et al. 1992; Roseman et al. 1996; Shepherd and Mills 1996; Yako et al. 1996) and those that have been reviewed and are cited in Connolly et al. (1992). However, organic detritus can refer to either particles settling through the water column or sediment particles that have been resuspended by the foraging actions of benthic feeders such as carp. Gizzard shad are opportunistic feeders (Mundahl and Wissing 1987, 1988; Yako et al. 1996) that do not distinguish between settling particles and resuspended particles. Therefore, this may indicate a benthic food web connection in addition to the pelagic one considered in Connolly et al. (1992).

Several observations on gizzard shad diet and feeding behavior are made in Connolly et al. (1992) that reference the work of Mummert and Drenner (1986). However, most of these observations were a result of several authors' contributions (e.g., Tiffany 1921, as cited by Mummert and Drenner 1986; Kutkuhn 1958, as cited by Mummert and Drenner 1986; Cramer and Marzolf 1970, as cited by Mummert and Drenner 1986) that were referenced accordingly by Mummert and Drenner (1986). This suggests that the Mummert and Drenner (1986) article is inaccurately referenced as a primary source of this information in the Connolly et al. (1992) document.

Connolly et al. (1992) also reports that rainbow smelt feed primarily on invertebrates, though they also occasionally prey on YOY fish. However, invertebrates can either be located in the sediment, on the surface of the sediment, on aquatic vegetation, or in the water column. The type of invertebrate was not documented; therefore, it cannot be determined if any additional invertebrate food web links are applicable and/or complementary to the pelagic food web. In addition, a compilation of the Foltz and Norden (1977) rainbow smelt diet data by Amin in 1981 is mentioned; however, Amin's work in 1981 is not cited in the reference section of the report. This indicates that Amin's work was either not published or unintentionally left out of the references.

3.4 Species Life History Characteristics and Habitat

Another step in the development of conceptual food webs is the evaluation of fish-habitat associations to estimate habitat function and value as related to life history requirements (e.g., spawning and nursery areas). These attributes are often important to develop habitat rankings for the numerical model. Site-specific measurement of the fish populations modeled by Connolly et al. (1992), their reported abundance in pelagic environments, and their reliance on suspended prey (e.g., zooplankton and phytoplankton) indicate that the existing pelagic food web is appropriate.

As indicated in Connolly et al. (1992), the predators walleye and brown trout are common and appropriate for representing pelagic habitats. Similarly, the forage fish (e.g., rainbow smelt, alewife, and young gizzard shad) are equally important in open (and deep) water habitats and have been shown by Smith and Magnuson (1987, as cited by Connolly et al. 1992) as key species that support the predators selected to represent the GBFWM. The reliance on the fish forage base on key pelagic species of zooplankton (e.g., *Mysis relicta, Pontoporeia hoyi*, etc.) and phytoplankton is also accurately documented and representative of the GBFWM.

3.5 Summary

In summary, the conceptual food webs presented by Connolly et al. (1992) are representative of the pelagic community of Green Bay and are based on field-collected stomach data and a review of the primary literature. This food web provides an accurate assessment of trophic transfer to brown trout and walleye, predators that rely on a forage base that is heavily reliant on planktonic prey. Overall, this is an accurate and important part of the ecosystem function. However, the importance of other forage fish, predators, feeding strategies, or predator-prey associations that represent other components of the food web in Green Bay could be evaluated further.

4. Model Framework Description

The general nature of the GBFWM framework permits bioaccumulation calculations for fish, mammals, and birds. The discussions below focus on the characteristics of the GBFWM as they relate to fish and their prey.

The GBFWM framework defines the numerical expressions used to make PCB bioaccumulation calculations for two types of dynamic food web components. These components are referred to in the Green Bay Food Chain Model Documentation (HQI 1996) as "steady state" and age-specific species. Fish generally fall into the category of age-specific species. Other lower-trophic-level components, such as zooplankton, can fall into the category of steady state species. Steady state species respond immediately to changes in their exposure levels. Age-specific species are computed dynamically. In addition, the calculations for age-specific species are dependent upon body weight, while those for steady state species are not.

The GBFWM framework also includes a third type of food web component. This third component is not actually modeled. Rather, the PCB concentrations in these components are specified directly in the model input. Food web components such as sediment and phytoplankton fall into this category. The current framework allows for specification of one temporally variable history of water column particulate and dissolved PCB concentrations along with one temporally variable history of sediment particulate PCB concentrations for each model segment. The model can include many segments between which species move.

The calculation of PCB bioaccumulation in the GBFWM is a two-step process for both steady state and age-specific species. For either species, the framework first performs a simplified energy balance. The word *simplified* is used here to describe this balance because the balance accounts for just the major bioenergetic processes (respiration, activity, specific dynamic action [SDA], and growth). After calculating the amount of energy the species uses for respiration, activity, and SDA, the framework balances this energy usage with growth to determine the consumption necessary to supply sufficient energy for these major bioenergetic processes. The numerical expressions that define the bioenergetic process rates, and implementation of the simplified energy balance, are discussed in the section entitled *Bioenergetics and the Energy Balance*.

Continuing, the framework then performs a chemical balance. The chemical balance tracks the intake and release of PCBs associated with the major bioenergetic processes of the fish. Specifically, the framework balances consumption of PCBs with prey, intake of PCBs from water through respiration, and release of PCBs from the body through respiration to calculate any change in PCB body burden. The numerical expressions that track PCB intake and release associated with the bioenergetic process rates are also discussed in *Bioenergetics and the Chemical Balance*.

The GBFWM framework also defines how specified, but temporally variable, model input is manipulated during a simulation. Temporal histories of fish body weight and fraction lipid, water temperature and salinity, exposure concentrations (water column dissolved and particulate PCB concentrations and sediment dissolved and particulate PCB concentrations), prey preferences, and migration patterns are all examples of this type of model input. Three methods are employed in the GBFWM framework for determining the intermediate value of each of these specified, but temporally variable inputs, between time breaks.

The first method is a step function, which means the value applies from the previous time break until the time break it is associated with. If the previous time break is the start of the simulation, then the value applies from the start of the simulation until the time break it is associated with. Intermediate exposure concentrations, prey preferences, and migration patterns are determined by step function.

The second method is linear interpolation, which means the value of a history between time breaks is determined from the line that passes through both time breaks. Intermediate water temperature and salinity, and fraction lipid, are determined by linear interpolation.

The third method is an exponential interpolation, which means the value of the history between time breaks is determined from the exponential relationship that passes through both time breaks. Intermediate body weight is determined between successive time breaks by exponential interpolation using the following expression:

$$W(t) = W_0 e^{G(t-t_0)} \quad (1)$$

where:

$W(t)$	=	body weight at time t [g]
W_0	=	body weight at time t_0 [g]
T	=	current simulation time [d]
t_0	=	time of starting time break [d]
G	=	$\ln(W_e-W_0)/(t_e-t_0)$=growth rate [1/d]
W_e	=	body weight at t_e [g]
t_e	=	time of ending time break [d]

5. Critique of the Model Framework

The general nature of the GBFWM framework permits its application to new sites, such as the Lower Fox River. The approach of calculating PCB bioaccumulation using bioenergetic processes for determining PCB intake and release more closely resembles the physical reality of the environment. This approach models the effect of diet preferences and fish age on PCB bioaccumulation, which can result in changes in tissue PCB concentrations over time, even when sediment PCB concentrations are constant. These and other factors that lead to variations in bioaccumulation can be considered and evaluated using the GBFWM framework.

It is possible for prey species to be exposed to localized conditions while the predator species is exposed to regional conditions. If there is evidence that two prey species in the same area have different sediment exposure levels, then the model can be used to simulate a predator that eats both by specifying prey to be exposed in two segments, and the predator to switch frequently between them.

The use of step function assignment and linear interpolation is reasonable for approximating intermediate values between time breaks for exposure concentrations, prey preferences, migration patterns, water temperature and salinity, and fraction lipid. However, using exponential interpolation to determine the intermediate values of body weight will be inappropriate under certain circumstances, such as when the body weight history is limited to just two time breaks (starting and ending for the year). In this case, the exponential interpolation calculates the majority of the body weight change to occur at the end of the year, contrary to the accepted trend that fish grow most during the warm summer months. This skewed growth pattern can result in overestimated PCB bioaccumulation during the warm summer months and overestimated growth dilution at the end of the year. Unless the overestimated PCB bioaccumulation matches the overestimated growth dilution, this misalignment of within-year growth may have an effect on year-to-year trends. Additionally, when the measured annual average fish tissue PCB concentration is based on samples collected during only a portion of the year, it becomes appropriate to compare within-year model calculations to seasonal measurements. Using linear interpolation to determine intermediate body weights would produce less misalignment of the within-year growth when few time breaks are specified in the model input, as is sometimes the case.

6. Bioenergetics Description

As mentioned previously, the calculation of PCB bioaccumulation in the GBFWM is a two-step process. For each steady state species or age-specific species, the framework first computes the energy balance associated with ingestion, respiration, and growth. Uptake, loss, and growth dilution of PCB is then computed in the chemical balance using the ingestion rate estimated from the energy balance. The bioenergetic rates calculated by the model framework participate in both energy and chemical balances as described below.

6.1 Bioenergetics and the Energy Balance

The energy balance used in the GBFWM is described as:

$$G = E_U - E_L \tag{2}$$

where:

G	=	growth, rate of change in body weight [kJ/g wet-d]
E_U	=	energy uptake rate [kJ/g wet-d]
E_L	=	energy usage/loss rate [kJ/g wet-d]

If the energy uptake is greater than the energy usage, the individual fish gains weight. If the energy usage is greater than the energy uptake, the individual fish loses weight. In the GBFWM, energy uptake is defined as assimilated energy consumed by the individual fish. Energy usage is defined as energy utilized in the performance of the major metabolic processes.

The GBFWM solves the energy balance above for energy uptake in terms of energy usage and growth. Growth is determined from the history of body weight supplied in the model input for each individual species age class. This growth rate is augmented to consider energy required for egg production when spawning for female fish. Energy usage is determined from several mathematical expressions that typically relate the rate of each metabolic process considered to body weight and water temperature. The major bioenergetic processes that are considered by the GBFWM for the energy balance of each individual fish are basal respiration, activity, and SDA.

Basal respiration is expressed as:

$$R_b = \beta W^{-\gamma} e^{\rho T} \tag{3}$$

where:

Rb	=	basal respiration rate [kJ/g wet-d]
β	=	intercept of the allometric weight function for respiration [kJ/g wet$^{(1-\gamma)}$-d]
W	=	body weight [g wet]
γ	=	slope of the allometric weight function for respiration [unitless]
ρ	=	exponential coefficient relating changes in respiration to water temperature [1/°C]
T	=	water temperature [°C]

Activity related to swimming is expressed as:

$$A = (S-1)R_b \tag{4}$$

$$S = e^{X_\eta U} \tag{5}$$

$$U = \Omega W^{\delta} e^{\Phi T} \tag{6}$$

where:

A	=	rate of activity related to swimming [kJ/g wet-d]
S	=	swimming activity increment to basal respiration rate determined from swimming speed [unitless]
X_η	=	exponential coefficient of swimming speed for determining S [s/cm]
U	=	swimming speed [cm/s]
Ω	=	intercept of the allometric weight function for swimming speed [cm/s-g wet$^{\delta}$]
δ	=	slope of the allometric weight function for swimming speed [unitless]
Φ	=	exponential coefficient relating changes in swimming speed to water temperature [1/°C]

SDA, which is defined as the energy required for non-autonomic processes, is expressed as a fraction of total assimilated energy:

$$SDA = f_{sda}(R_b + A + G + SDA) \tag{7}$$

where:

SDA = specific dynamic action rate [kJ/g wet-d]

f_{sda} = the fraction of total assimilated energy lost to SDA [unitless]

Rearranging the above equation for SDA results in the following expression:

$$SDA = \frac{f_{sda}}{1 - f_{sda}}(R_b + A + G) \tag{8}$$

The final step in the energy balance calculation is to use the rearranged energy balance equation and substitute the expressions for the required bioenergetic processes:

$$E_U = G + E_L \tag{9}$$

where:

E_L = basal respiration + activity + SDA rates

E_U = $G + R_b + A + SDA$

E_U, which is the rate of energy assimilation, is then converted into the rate of energy gained by consumption:

$$C = \frac{E_U}{\alpha_p} \tag{10}$$

where:

C = consumption rate [kJ/g wet-d]

α_p = prey assimilation efficiency [unitless]

6.2 Bioenergetics and the Chemical Balance

The GBFWM framework calculates bioaccumulation of PCBs in fish tissue by finding the difference between PCB uptake by the fish and PCB loss from the fish. PCB uptake occurs via consumption of PCB-containing prey and respiration of PCB-containing water. PCB loss occurs via excretion, and the change in PCB concentration resulting from growth (growth dilution). The PCB chemical balance that is used in the GBFWM framework is:

$$\frac{dc_f}{dt} = M_p + M_b - M_e - M_g \tag{11}$$

where:

c_f	=	concentration of PCB in whole body fish [g PCB/g wet]
M_p	=	rate of consuming PCB with prey [g PCB/g wet-d]
M_b	=	rate of uptake of PCB through breathing [g PCB/g wet-d]
M_e	=	rate of excretion of PCB through breathing [g PCB/g wet-d]
M_g	=	rate of change in whole body concentration due to growth dilution [g PCB/g wet-d]

Consumption of PCB with prey is determined from the consumption rate calculated from the energy balance of the fish and the concentration of PCB in the prey:

$$M_p = C c_p \alpha_c \tag{12}$$

where:

C	=	consumption rate [g-wet/g wet-d]
c_p	=	concentration of PCB in prey [g PCB/g wet]
α_c	=	PCB assimilation efficiency [g PCB assimilated/g PCB eaten]

The consumption rate is converted from an energy basis to a prey weight basis using the energy density of the prey. The energy density is calculated using:

$$\lambda = 39.5 f_L + 20 f_P \tag{13}$$

where:

λ	=	energy density [kJ/kg wet]
f_L	=	fraction lipid [g lipid/g wet]
f_P	=	fraction protein [g protein/g wet]

These calculations are carried out for each prey item that makes up the diet of a fish, with the intake from each prey species weighted according to the diet fraction of that prey species.

Uptake of chemical via respiration is determined from the calculated respiration rate, the water column oxygen concentration, and the efficiency of chemical transfer through the gill membrane relative to oxygen:

$$M_b = \frac{r}{c_{O_2}} \frac{E_c}{E_{O_2}} c_d \tag{14}$$

where:

r	=	respiration rate [g O_2/g wet-d]
c_{O_2}	=	water column oxygen concentration [g O_2/L]
E_c/E_{O_2}	=	ratio of efficiency of chemical transfer to oxygen transfer across the gill [unitless]
c_d	=	dissolved water column chemical concentration [g chemical/L]

The respiration rate, r, in terms of oxygen, is related to R in terms of energy:

$$r = R * 0.073 \quad (15)$$

where:

R	=	respiration rate [kJ/g wet-d]
0.073	=	oxygen mass equivalent for energy [g O_2/kJ]

The respiration rate, R, as discussed in Connolly et al. (1992) appears to represent routine respiration. It is not clear in the discussion if routine respiration implies basal respiration or more than basal respiration. Regardless, respiration in the GBFWM source code used to calculate chemical uptake from water is total respiration defined as:

$$R = R_b + A + SDA \quad (16)$$

The ratio of chemical transfer efficiency to oxygen transfer efficiency across the gill is a constant, chemical-specific parameter specified in the model input. Connolly et al. (1992) discusses estimation of this ratio.

The transfer of a chemical through the gill can be affected not only by the properties of the chemical and the gill membrane, but also by the relative rate of supply and removal of the chemical (i.e., by gill morphology and the water and blood flow rates [Hayton 1990]). Thus, the rate of chemical uptake via the gill may differ depending on the physiological condition, age, and activity of the fish. The expression presented by Connolly et al. (1992) does not account for these effects and is therefore a simplified representation of uptake via the gill.

Elimination of chemical via excretion through breathing is presumably the result of a gradient from a higher chemical concentration in the aqueous phase of the organism (blood) to a lower dissolved chemical concentration in the water column. This process, discussed by Connolly et al. (1992), is in terms of gill elimination described mathematically as:

$$M_e = \frac{r}{c_{O_2}} \frac{E_c}{E_{O_2}} \left(\frac{\rho_a}{x_a + \pi_L x_L} \right) c_f \quad (17)$$

where:

ρ_a = density of aqueous blood [g/L]

x_a = fraction aqueous of the organism=1-x_L

x_L = fraction lipid of the organism [g lipid/g wet]

π_L = equilibrium partition coefficient of the chemical between the lipid and aqueous phases of the organism

However, the GBFWM offers four options for calculating elimination of chemical via breathing:

$$M_e = K_u f_a * 1000 * c_f \quad (18)$$

$$M_e = \frac{K_u}{BCF} * c_f \quad (19)$$

$$M_e = BCF * R * f_a * x_L * c_f \quad (20)$$

$$M_e = EXC * c_f \quad (21)$$

where:

K_u = uptake rate = $\frac{r}{c_{O_2}} \frac{E_c}{E_{O_2}} + D$ [L/g wet-d]

D = drinking rate [m^3/g wet-d]

f_a = $\left(\frac{1}{x_a + {}_L x_L} \right)$ [g/L]

BCF = bioconcentration factor, either calculated from % lipid and $K_{ow,}$ or aqueous phases of the organism specified in the model input file [unitless]

EXC = input specified excretion rate [1/d]

The first mathematical expression for M_e (Equation 18) appears to be a simplification of the expression discussed by Connolly et al. (1992). There are two differences between the expression discussed in Connolly et al. (1992) and the expression implemented in the GBFWM framework: the inclusion of drinking rate with uptake due to respiration to form a total uptake rate (K_u), and the exclusion of aqueous phase (blood) density. Connolly et al. (1992) indicates that uptake of chemical via drinking is insignificant relative to uptake via consumption because the concentration of chemical in water is so

much less than the concentration of chemical in prey. The apparent exclusion of aqueous phase density is probably because the density of blood is similar to the density of water, which is generally taken as 1 g/cm^3. The factor of 1,000 included in this equation converts cm^3 to L so the units properly cancel.

Neither Connolly et al. (1992) nor HQI (1995, 1996) documents the theory behind the remaining three options (Equations 19–21) for calculating chemical excretion via gill elimination.

Growth dilution is defined as:

$$M_g = G * c_f \quad (22)$$

Growth dilution is the reduction in PCB tissue concentration resulting from the increase in body weight.

7. Critique of Bioenergetics

As with the bioenergetics description, the critique of the bioenergetics is separated into two topics: energy balance and chemical balance.

7.1 Critique of Bioenergetics and the Energy Balance

The use of allometric weight functions for expressing the relationships between the rates of the major bioenergetic process rates, fish body weight, and water temperature is consistent with other models. Similar expressions are utilized in Fish Bioenergetics Model 2 (Hewett and Johnson 1991).

The energy balance is not entirely complete with respect to the pathways of energy loss. Specifically, there are two additional bioenergetics processes that are not addressed in the calculation of the energy balance: excretion and egestion. Excreted energy is energy that was assimilated but is released typically as urea. Egested energy is energy that was ingested but could not be assimilated (i.e., remains in, and passes through, the gut).

The simple energy balance performed by the GBFWM addresses only assimilated energy. Therefore, egestion is appropriately not considered in this calculation. However, excretion is not clearly addressed in the GBFWM energy balance. Depending upon how the authors of the GBFWM defined SDA, excretion may or may not be included in this term. The result of not including excretion in the energy balance is underestimation of the rate of assimilated energy usage E_U, total prey consumption C, and ultimately the consumption of PCB with prey M_p. Model coefficients from Fish Bioenergetics Model 2 (1991) suggest that excretion can be equivalent to approximately 5–15 percent of assimilated energy. This percentage will not likely alter model performance in the context of the expected uncertainty in model predictions.

The written documentation for this model (Connolly et al. 1992; HQI 1995, 1996) is incomplete in its discussion of bioenergetics and the energy balance used in the GBFWM. These topics are discussed only in relation to their participation in the chemical balance. Much of what was learned about the functioning of this model with respect to bioenergetics and the energy balance was determined by examining the source code and any available documentation statements provided in the source code in detail.

7.2 Critique of Bioenergetics and the Chemical Balance

The chemical balance is also not complete in its consideration of the pathways of PCB release. Calculations of PCB bioaccumulation can be affected by the exclusion of excretion from of the energy balance. Again, given the expected uncertainty in model predictions, the exclusion of the excretion term from the chemical balance will not likely alter model performance.

8. Translation of Conceptual Food Web to Numerical Model

The translation of the conceptual food web model into a numerical representation using the GBFWM framework is a complex process that results in the site-specific application of the numerical model framework. The target fish species, and their predator-prey relationships, identified in the conceptual food web models are the basis for determining the additional data required to create the numerical model input for a site-specific application.

Because the GBFWM framework is designed to model individual age classes for each fish species, versus general age groupings such as juveniles and adults, much of the model input is specified on an age-class basis. However, some of the model input can be duplicated from age class to age class as it applies to the general age groupings such as juveniles and adults.

The species-specific bioenergetic coefficients are an example of model input that might be duplicated from one age class to another. The only age-specific variation might be that of coefficients for juveniles versus adults. Other model input, such as body weight history and prey preferences, must be age-class-specific in nature. For prey preferences, the age-specific requirement is in the age of the prey items eaten, not necessarily in the variation of prey preferences from age class to age class.

The specific discussion of the translation of the conceptual food web models into the numerical model to create the site-specific application to Green Bay is divided into three sections: food web connections, bioenergetics coefficients, and temporal histories.

8.1 Food Web Connections

The discussion of the translation of the conceptual food web model links to numerical model links needs to be divided into food webs with migration (Zones 1 and 2) and food webs without migration (Zones 3A, 3B, and 4). The discussion of links is based on the final GBFWM calibration files (128d.inp, 3a8.inp, 3b8.inp, and 48.inp) provided by HydroQual through LimnoTech, Inc. (Slawecki 1997, pers. comm.). The discussion also focuses on the translation of the conceptual food webs prior to critique to determine if the translation of the target conceptual food web, as it currently exists, was reasonable.

8.1.1 Food Webs With Migration

The conceptual food web model for Zones 1 and 2 (Figure 1) is embodied in a single input file (128d.inp). Within this file, there are two populations each of alewife, gizzard shad, and walleye and one population of rainbow smelt. Both populations of alewife,

gizzard shad, and walleye, as well as the single population of rainbow smelt, spend the majority of their time in Zone 2 (inner Green Bay). Population 1 alewife, gizzard shad, and walleye are specified to migrate to Zone 1 (mouth of the Lower Fox River) for a period of approximately 1 month per year (from day 150–180; approximately the month of May). Population 2 alewife, gizzard shad, and walleye are specified to remain in Zone 2 all the time. As discussed in HQI (1995), calibration to PCB levels measured in the last seven miles of the Lower Fox River was only possible if fish resident in lower Green Bay experience short term exposure to Lower Fox River conditions due to periodic migration. The PCB levels measured in the Lower Fox River fish did not appear to be consistent with the concept of fish populations that reside exclusively in the last seven miles of the Lower Fox River on a year-round basis.

The model input is set up with the following number of age classes for each species of fish: alewife–10, gizzard shad–2, rainbow smelt–10, and walleye–15. These numbers of age classes are greater than the actual number of age classes specified in the conceptual food web model: alewife–4, gizzard shad–2, rainbow smelt–4, and walleye–5.

The diet of alewife and gizzard shad, as depicted in the conceptual food web model (Figure 1), is relatively simple. Alewife eat only zooplankton and gizzard shad eat a combination of phytoplankton and zooplankton. The diet of rainbow smelt is a bit more complicated. Rainbow smelt age classes 1 and 2 eat zooplankton, while age classes 3 and 4 eat a combination of zooplankton and alewife. The diet of walleye is even more complicated and variable by age class. Walleye age class 1 eats zooplankton, rainbow smelt, alewife, and gizzard shad, while age classes 2–5 eat rainbow smelt, alewife, and gizzard shad of varying ages and in varying proportions. The diet fractions and prey preferences for these four species of fish, determined from input file 128.inp, are listed in Table 1.

As described in HQI (1995), the input file specifies that population 1 alewife, gizzard shad, and walleye eat Zone 1 prey when present in Zone 1, and Zone 2 prey when present in Zone 2. The input file also specifies that population 2 alewife, gizzard shad, and walleye, as well as rainbow smelt in Zone 2, eat Zone 2 prey when present in Zone 2. Neither Zone 1 fish nor Zone 2 fish are specified to eat Zone 1 fish present in Zone 2.

8.1.2 Food Webs Without Migration

The conceptual food web model for Zones 3A, 3B, and 4 (Figure 2) is embodied in three input files (3a8.inp, 3b8.inp, and 48.inp). Each file is set up with a single population of each species (alewife, rainbow smelt, walleye, and brown trout).

The model input is set up with the following numbers of age classes for each species of fish: alewife–10, rainbow smelt–10, walleye–15, and brown trout–10. As was found in the input file for Zones 1 and 2, these numbers of age classes are greater than the actual

number of age classes specified in the conceptual food web model: alewife–4, rainbow smelt–4, walleye–5, and brown trout–6.

Table 1. Prey preferences and diet fractions for Zones 1 and 2 fishes

Predator and Age Class	Prey: Zoo-plankton	Phyto-plankton	Alewife 1	Alewife 2	Alewife 3	Gizzard Shad 1	Rainbow Smelt 1	Rainbow Smelt 2	Rainbow Smelt 3
Zooplankton	--	1.00	--	--	--	--	--	--	--
Alewife									
1	1.00	--	--	--	--	--	--	--	--
2	1.00	--	--	--	--	--	--	--	--
3	1.00	--	--	--	--	--	--	--	--
4	1.00	--	--	--	--	--	--	--	--
Gizzard Shad									
1	0.50	0.50	--	--	--	--	--	--	--
2	0.50	0.50	--	--	--	--	--	--	--
Rainbow Smelt									
1	1.00	--	--	--	--	--	--	--	--
2	1.00	--	--	--	--	--	--	--	--
3	0.60	--	0.40	--	--	--	--	--	--
4	0.50	--	0.50	--	--	--	--	--	--
Walleye - Zone 1									
1	0.30	--	0.35	--	--	0.35	--	--	--
2	--	--	--	0.50	--	0.50	--	--	--
3	--	--	--	--	0.70	0.30	--	--	--
4	--	--	--	--	0.60	0.40	--	--	--
5	--	--	--	--	0.60	0.40	--	--	--
Walleye - Zone 2[a]									
1	0.30	--	0.15	--	--	0.15	--	0.40	--
2	--	--	--	0.20	--	0.20	--	0.60	--
3	--	--	--	--	0.20	0.45	--	--	0.35
4	--	--	--	--	0.20	0.40	--	--	0.40
5	--	--	--	--	0.20	0.40	--	--	0.40

Note: -- - not a specified prey item

[a] Diet fractions apply to both Zone 1 and Zone 2 walleye when in Zone 2.

The diet of alewife, as depicted in the conceptual food web model (Figure 2), is relatively simple. Alewife eat only zooplankton. The diet of rainbow smelt is a bit more complicated. Rainbow smelt age class 1 and 2 eat zooplankton, while age class 3 and 4 eat a combination of zooplankton and alewife. The diet of walleye and brown trout is even more complicated and variable by age class. Walleye age class 1 eats zooplankton, rainbow smelt, and alewife, while age classes 2–5 eat rainbow smelt and alewife of varying ages and in varying proportions. The diet fractions and prey items for these four species of fish, determined from input files 3a8.inp, 3b8.inp, and 48.inp, are listed in Table 2.

Table 2. Prey preferences and diet fractions for Zones 3A, 3B, and 4 fishes

Predator and Age Class	Prey: Zoo-plankton	Phyto-plankton	Alewife 1	Alewife 2	Alewife 3	Alewife 4	Rainbow Smelt 1	Rainbow Smelt 2	Rainbow Smelt 3	Rainbow Smelt 4
Zooplankton	--	1.00	--	--	--	--	--	--	--	--
Alewife										
1	1.00	--	--	--	--	--	--	--	--	--
2	1.00	--	--	--	--	--	--	--	--	--
3	1.00	--	--	--	--	--	--	--	--	--
4	1.00	--	--	--	--	--	--	--	--	--
Rainbow Smelt										
1	1.00	--	--	--	--	--	--	--	--	--
2	1.00	--	--	--	--	--	--	--	--	--
3	0.60	--	0.40	--	--	--	--	--	--	--
4	0.50	--	0.50	--	--	--	--	--	--	--
Walleye										
1	0.30	--	0.30	--	--	--	0.40	--	--	--
2	--	--	0.20	0.20	--	--	0.60	--	--	--
3	--	--	0.30	0.30	--	--	0.40	--	--	--
4	--	--	-	0.30	0.30	--	--	0.40	--	--
5	--	--	-	0.30	0.30	--	--	0.40	--	--
Brown Trout										
1	--	--	1.00	--	--	--	--	--	--	--
2	--	--	1.00	--	--	--	--	--	--	--
3	--	--	--	0.50	--	--	--	0.50	--	--
4	--	--	--	0.25	0.25	--	--	0.25	0.25	--
5	--	--	--	--	0.50	--	--	--	0.50	--
6	--	--	--	--	--	0.50	--	--	--	0.50

Note: -- - not a specified prey item

8.2 Bioenergetics Coefficients

Connolly et al. (1992) reports that bioenergetics coefficients for the respiration equation were developed from multiple linear regression of the linearized form of the respiration equation. These coefficients were later modified in HQI (1995) during recalibration of the numerical model. At that time, the model framework was modified to its current version. The specific change was implementation of the direct calculation of energy density based on fractions lipid and protein for determining ingestion of prey (see *Bioenergetics and the Energy Balance*).

Table 1 from HQI (1995) lists the values and literature sources of the bioenergetics coefficients specified in the numerical model input. The values for β, γ, ρ, and SDA listed in this table match those specified in the numerical model input files (128d.inp, 3a8.inp, 3b8.inp, and 48.inp). However, the meaning of "activity multiplier" listed in Table 1 from HQI (1995) is not clear because the model input does not require a coefficient specifically called "activity multiplier." Through review of the input files, in conjunction with the user's guide (HQI 1996) and the information for activity coefficient in Table 1 from HQI (1995), the following conclusions were deduced.

For gizzard shad, rainbow smelt, walleye, and brown trout, the term "activity multiplier" seems to be referring to S (see *Bioenergetics and the Energy Balance*): the swimming activity increment to basal respiration. S is a calculated value determined from other model coefficients (X_η and U). For S to be equal to 1, as specified for rainbow smelt, walleye, and brown trout, either X_η or U must be equal to 0. For U to be equal to 0, Ω must be equal to 0. Both X_η and Ω are set equal to 0 in the model input for rainbow smelt, walleye, and brown trout to give S a value of 1. For S to be equal to 2, as specified for gizzard shad, the product of X_η and U must be equal to 0.693. This is accomplished by setting X_η to 1 and allowing U to be calculated as 0.693 by setting Ω to 0.693, δ to 0, and ϕ to 0.

For alewife, the term "activity multiplier" seems to be referring to U (see *Bioenergetics and the Energy Balance*): swimming speed. The mathematical expression for U is the same form as the expression listed for activity multiplier. Furthermore, the values of 0.32, –0.045, and 0.05 in this expression in Table 1 from HQI (1995) match those specified for Ω, δ, and ϕ in the model input.

Both food assimilation efficiency (α_P) and PCB assimilation efficiency (α_C) are input parameters for the GBFWM. Food assimilation efficiency is the amount of food used for energy relative to the amount of food consumed. Food assimilation efficiency is used in the GBFWM framework to determine the necessary prey consumption from the assimilated energy requirements determined from the energy balance. PCB assimilation efficiency is the amount of PCB absorbed into the fish relative to the amount contained in the food consumed. PCB assimilation efficiency is used in the GBFWM framework to determine the amount of PCB absorbed by the fish from the amount eaten with prey.

Discussions in Connolly et al. (1992) about assimilation efficiency focus primarily on chemical assimilation efficiency and the determination of this value through experimentation. There is no discussion of the specific values of either food or chemical assimilation efficiency selected for the model input in either Connolly et al. (1992) or HQI (1995). Ultimately, in the context of the GBFWM framework, the actual values of α_P and α_C are not important. What is important in determining the amount of chemical assimilated by the fish is the ratio of α_C to α_P. This can be seen by substituting Equation 10 into Equation 12 to achieve the following expression for the rate of consuming chemical with prey:

$$M_P = E_U \frac{\alpha_C}{\alpha_P} c_P \qquad (23)$$

HQI (1995) reports that the ratios of α_C to α_P for zooplankton, gizzard shad, and rainbow smelt were modified during GBFWM recalibration. Table 2 from HQI (1995) provides the original and current values of this ratio used in the model. These ratios are achieved during model calculations by specifying the same value for both α_C and α_P.

The ratio of chemical gill transfer efficiency to oxygen gill transfer efficiency is an input parameter for the GBFWM. This ratio also belongs to the subcategory of toxicokinetic coefficients. Connolly et al. (1992) explains that this ratio is a surrogate for the ratio of mass transfer chemical coefficient to oxygen mass transfer coefficient used to determine chemical uptake from respiration (see *Bioenergetics and the Chemical Balance*). In addition, Connolly et al. (1992) provides a lengthy theoretical discussion of the factors that affect both chemical and oxygen transfer efficiency. HQI (1995) also reports this ratio was modified for all components of the food web during model recalibration. Table 2 from HQI (1995) provides the original and current values of this ratio used in the model.

8.3 Temporal Histories

As mentioned in *Model Framework Description*, the GBFWM required temporal histories of fish body weight and fraction lipid, water temperature and salinity, exposure concentration in water and sediment, prey preferences, and migration patterns. Prey preferences and migration patterns are discussed in *Food Web Connections*. The remaining temporal histories specified in the model input are discussed here.

8.3.1 Fish Body Weight

Changes in fish body weight are an important component in both the energy and the chemical balances calculated by the GBFWM framework. At a minimum, annual changes in body weight must be specified in the model input. Ideally, seasonal variation should be considered if sufficient data are available. The site-specific application of the GBFWM to Green Bay utilizes a combination of annual and seasonal body weight changes in the model input. Seasonal body weight histories are typically specified for predator fish (walleye, brown trout) while annual body weight histories are typically specified for prey fish (rainbow smelt, alewife, and gizzard shad).

Connolly et al. (1992) reports that data from the GBMBS conducted in 1989 were used to develop growth patterns for the modeled fish species. Annual growth was assumed to follow the relationship in Equation 1. The value of G was developed directly from the data for predator fish (walleye and brown trout) because age was determined along with weight and length during the GBMBS.

Connolly et al. (1992) also reports that development of the value of G for prey fish (rainbow smelt, alewife, and gizzard shad) was difficult and based on assumptions because age was classified only as YOY or adult along with weight and length during the GBMBS. Length data were presented graphically with respect to time of capture. Age classes were assigned based on the clusters of data that resulted. Specifically, the smallest length cluster was assigned age class 1, the next length cluster was assigned age class 2, and so on. The age of each cluster was set based on age class and time of

capture relative to an assumed May 1 birthday. Length was equated to weight using semi-log weight vs. length relationships developed from historical Green Bay data for rainbow smelt and alewife, and a semi-log weight vs. weight relationship developed from Chesapeake Bay data for gizzard shad.

8.3.2 Fish Fraction Lipid

Lipid content is important because it is used in the GBFWM framework to calculate both predator and prey energy density (Equation 13), which are used to compute the amount of consumed prey (Equation 10) and chemical (Equation 12). In addition, lipid content controls the PCB elimination rate. Unlike the fraction protein, which is specified in the GBFWM framework as a constant for each species, the fraction lipid is specified as time and age class variable.

HQI (1995) reports that values for fraction lipid were modified during model recalibration because the model was modified. The previous version of the GBFWM framework considered fraction dry a constant, such that fraction protein was computed to vary based on fraction lipid. The current version considers fraction protein a constant such that fraction dry varies based on fraction lipid. HQI (1995) reports that the values of fraction lipid specified in the calibrated model input, and listed in Table 3 of HQI (1995), were developed from a review of the GBMBS data. Connolly et al. (1992) also reports that lipid contents specified in the model input in the original version of the model, for all fish species, were defined from field data. Neither Connolly et al. (1992) nor HQI (1995) provides a discussion of the specific analyses that were performed.

The trends in lipid fraction specified in the model input for each species may vary by age class, season, or by zone. Lipid fraction specified for gizzard shad is a constant. Lipid fraction specified for alewife is occasionally temporally variable for older age classes, spatially variable, and age dependent. Lipid fraction specified for rainbow smelt is both age dependent and spatially variable, but not temporally variable. Lipid fraction specified for walleye and brown trout is temporally variable and age dependent, but not spatially variable. The specific trend for each species is discussed below.

Gizzard shad lipid fraction is a constant and does not vary by age, season, or zone.

Alewife lipid fraction in Zones 1 and 2 is specified as a constant for age classes 1 and 2, and seasonally variable for age classes 3 and 4. In addition, the Zone 1 seasonal variation is different from that specified for Zone 2. Alewife lipid fractions specified in Zones 3A and 3B are constant for all age classes, but are different by zone. In addition, the lipid fraction specified for age classes 1 and 2, which is the same for both, is different from that specified for age classes 3 and 4, which is the same for both. Alewife lipid fraction specified for age classes 1–3 in Zone 4 follow the same trends described for Zones 3A and 3B, but with different constant values. The fraction lipid for Zone 4 age class 4 alewife is specified as seasonally variable.

Rainbow smelt lipid fraction in Zones 2, 3A, and 3B is specified as constant. The lipid fraction specified for age classes 1 and 2, which is the same for both, is different from that specified for age classes 3 and 4, which is the same for both. However, these constant values differ by zone. Rainbow smelt lipid fraction specified for age classes 1–3 in Zone 4 follow the same trends described for Zones 2, 3A, and 3B, but with different constant values. The fraction lipid for Zone 4 age class 4 rainbow smelt is specified as seasonally variable.

Walleye lipid fraction is specified as a constant for age class 1 and seasonally variable for age classes 2–5. The same pattern of values is specified in all zones.

Brown trout lipid fraction is specified as seasonally variable for all age classes. The same pattern of values is specified for each age class in all zones.

8.3.3 Water Temperature and Salinity

The analysis of GBMBS data to determine the temporal and spatial variability of water temperature is not documented in either Connolly et al. (1992) or HQI (1995). As expected, the salinity is set to 0.

8.3.4 Exposure Concentrations

Connolly et al. (1992) reports that GBMBS data from 1989–1990 were used to develop the constant water column dissolved PCB concentrations specified in the model input. Analyses indicated that dissolved concentrations varied spatially, with little temporal variation at each station.

Connolly et al. (1992) also reports that GBMBS phytoplankton data were used to develop the particulate water column PCB concentrations specified in the model input. Again, particulate concentrations were generally found to vary spatially with little temporal variation at each station, with two exceptions. Phytoplankton PCB concentrations were higher in spring in Zones 3A and 4 than at other times. These data were reported to be excluded from the analyses because sampling technique was suspected to have contributed to the higher concentrations.

9. Critique of the Translation of the Conceptual Food Web to Numerical Model

The translation of the conceptual food web to the numerical model was as expected with some exceptions. Critique of the translation follows the same organization as the discussion of the translation: food web connections, bioenergetics coefficients, and temporal histories.

9.1 Food Web Connections

The translation of the conceptual food web models into numerical models was generally as expected with the exceptions presented below. As with the translation discussion, critique of the translation is divided into food webs with migration and food webs without migration.

9.1.1 Food Webs With Migration

The migration patterns specified in the numerical model input file for Zones 1 and 2 (128d.inp) are not entirely consistent with discussions in Connolly et al. (1992), which report that both alewife and walleye may migrate to Lower Fox River in the spring to spawn, while gizzard shad are generally resident in both Lower Fox River or the inner bay year round. Connolly et al. (1992) indicate that alewife spawn in late May to early June, while walleye spawn in mid April to mid May. The specification of migration as approximately the month of May for both species is a reasonable representation of the reported migration pattern of these two species in the context of the GBFWM framework. However, the specified migration of gizzard shad to Lower Fox River for the same period of time as for alewife and walleye is not consistent with the reported general presence of gizzard shad in Lower Fox River and inner Green Bay (Connolly et al. 1992). An alternative representation could be made if gizzard shad were specified to eat prey from both Zones 1 and 2 throughout the entire year. The current model framework can accommodate a single population of gizzard shad that roams the full range of both Zones 1 and 2, obtaining its prey from this combined area at all times, by having it switch frequently between zones.

The prey preferences of Zone 1 and Zone 2 walleye and Zone 2 rainbow smelt, when present in Zone 2, do not include predation of Zone 1 prey that is present in Zone 2. If the population of fish that migrates to Lower Fox River constitutes only a small fraction of the population of fish in inner Green Bay, then the fraction of Zone 1 fish in the diet of fish present in Zone 2 would be small. In this case, the current prey preferences specified in the model input would be a reasonable representation. If, however, the migrating population constitutes a greater fraction of the population of fish in inner

Green Bay, then the fraction of Zone 1 fish in the diet of fish present in inner Green Bay would not be insignificant. In this case, the prey preferences specified in the model input of both Zone 1 and Zone 2 fish, when both are present in Zone 2 (which is specified to be most of the time), should contain some fraction of Zone 1 fish that are present in Zone 2. This will reflect indirect exposure to Zone 1 PCBs through predation of fish directly exposed during periods of migration.

Because the development of the diet fractions of prey preferences (Table 1) in the conceptual food web model (Figure 1) is not thoroughly documented in either Connolly et al. (1992) or HQI (1995), comments on the translation of these fractions, other than those provided above, cannot be made without further information, especially for predators with multiple prey preferences.

Finally, each of the model input files for each zone were found to contain a number of placeholder age classes for each species. This is a recognized common practice intended to minimize input file manipulation, and in and of itself, is not an issue of concern. However, the use of placeholders leads to confusion in the absence of documentation. Specifically, Zone 2 alewife age class 4 appears to be a placeholder because the body weight history does not begin with the ending weight of age class 3. In addition, this body weight history is specified to be the same as the remaining age classes that are clearly placeholders. The issue of concern is not whether Zone 2 alewife age class 4 should or should not be a placeholder, but rather that if the Zone 2 alewife age class 4 is indeed a placeholder, model calculations for this age class should not be used in the model calibration. Further, if this age class is not intended to be a placeholder, then an explanation of the unusual continuation of the body weight history would be necessary for further evaluation because it is inconsistent with the measured data.

9.1.2 Food Webs Without Migration

Table 2 lists the diet preferences for each for food webs without migrating species (Figure 2). Neither Connolly et al. (1992) nor HQI (1995) discuss the analyses used to develop these specific numbers. Critique of the translation of the conceptual food web is limited to observing that input-specified diet preferences for brown trout are not variable by zone, and that the relative predation of alewife and rainbow smelt, with and without the presence of gizzard shad, varies by zone. Verification of these observations is recommended.

9.2 Bioenergetics Coefficients

Based on information available in Connolly et al. (1992) and HQI (1995), the values of the bioenergetics coefficients seem to be well supported by literature. However, the values of the toxicokinetic coefficients (ratios of chemical assimilation efficiency to food assimilation efficiency and chemical gill transfer efficiency to oxygen gill transfer efficiency) are not clearly justified in either Connolly et al. (1992) or HQI (1995).

Specifically, Connolly et al. (1992) provides lengthy theoretical discussions about contaminant assimilation efficiency and the ratio of chemical gill transfer efficiency to oxygen gill transfer efficiency. However, the details of how these theories were applied to obtain the values of these parameters specified in the model input are absent from the discussion. HQI (1995) simply reports that these coefficients were modified during model recalibration.

9.3 Temporal Histories

Analysis of GBMBS data for body weight, fraction lipid, water temperatures, and exposure concentrations for this document generally yielded results that were different from those reported in either Connolly et al. (1992) or HQI (1995). In some cases, the results had to be compared directly to model input because little or no discussion of these parameters was provided in either Connolly et al. (1992) or HQI (1995). Specific critique of each parameter, based on analysis of GBMBS data, is provided below.

9.3.1 Fish Body Weight

Connolly et al. (1992) describes the data analyses performed to determine fish growth rates. These growth rates were used to establish the model-specified body weight histories using the assumption that growth conforms to the first-order exponential model of Equation 1. The approach differs slightly for forage fish, compared to predator fish, because forage fish were generally aged as either YOY or adults.

Connolly et al. (1992) describes the method used for assigning age class to the forage fish. Because this procedure makes use of an idealized weight vs. length relationship for each species, the data were also analyzed using the actual measured weight data for comparison. Both sets of results are compared to the forage fish raw data (Figures 3 through 5), the model input body histories, and the results presented in Connolly et al. (1992) that are reported to be the basis of the model input.

For alewife (Figure 3), the body weight history specified in the model input appears to overestimate body weight for age classes identified as YOY. In addition, while the body weight history appears to have the same growth rate determined from the analyses presented in Connolly et al. (1992), it does not appear to have the same W_0 (Equation 1).

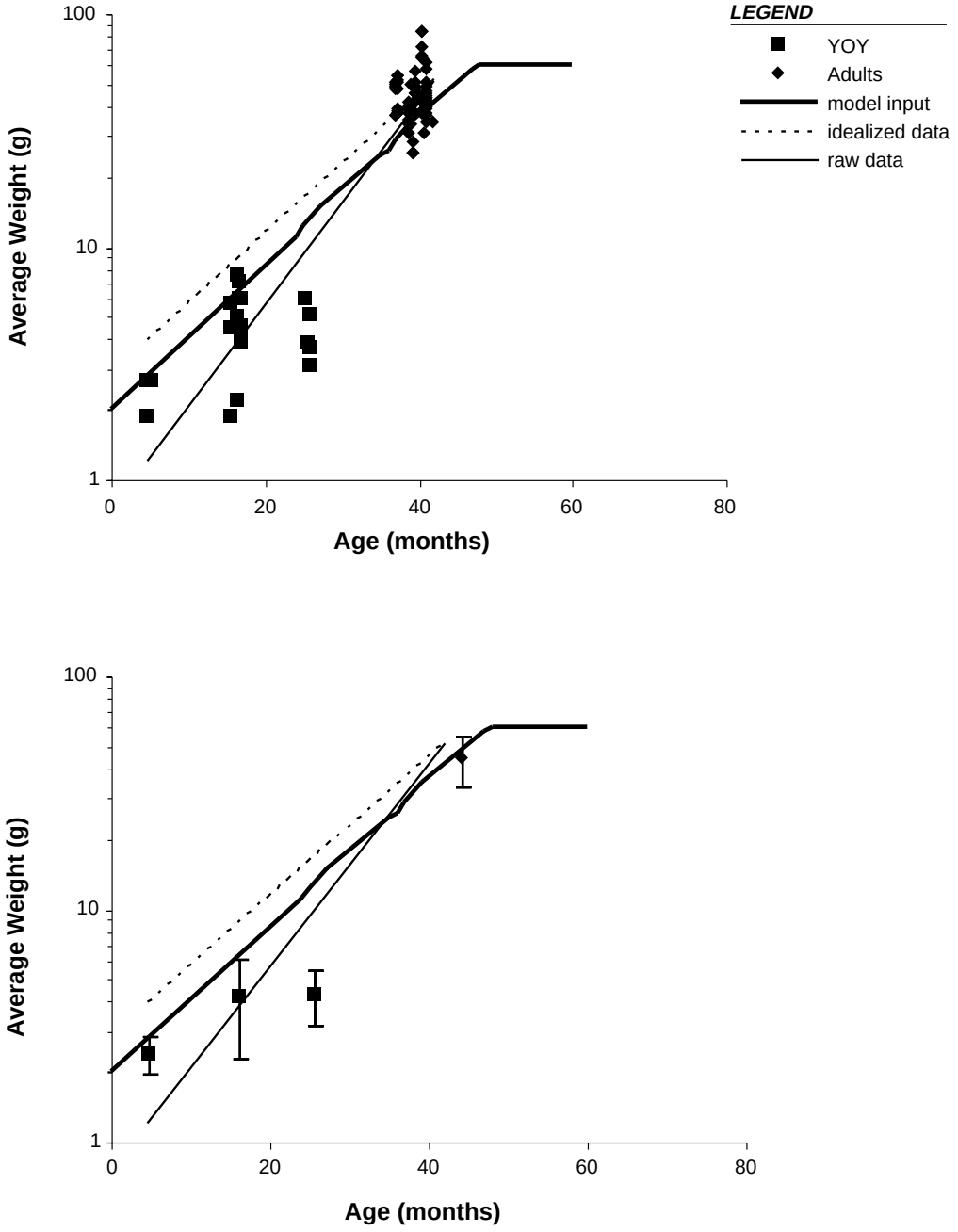

Figure 3. Analysis of alewife weight data.

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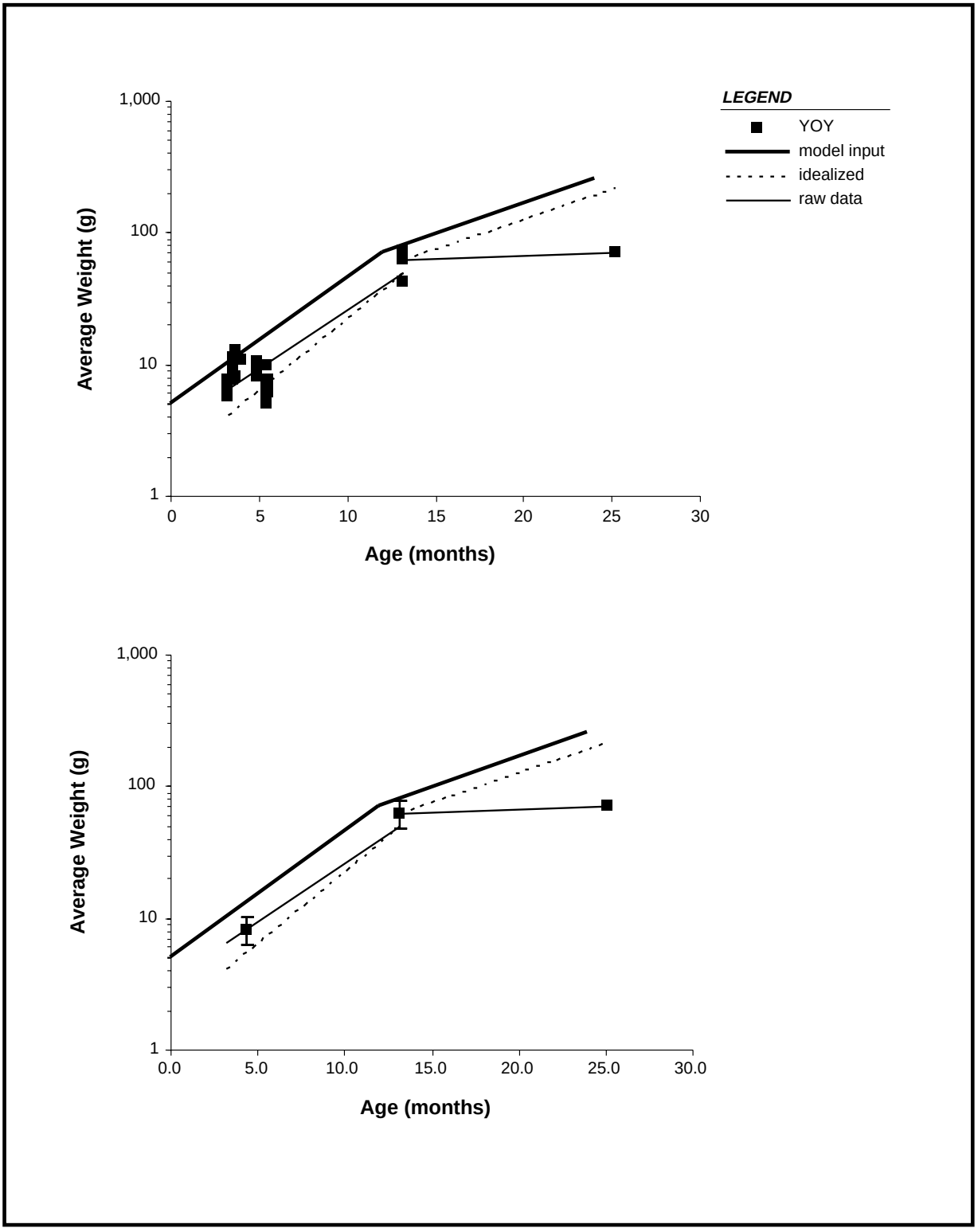

Figure 4. Analysis of gizzard shad weight data.

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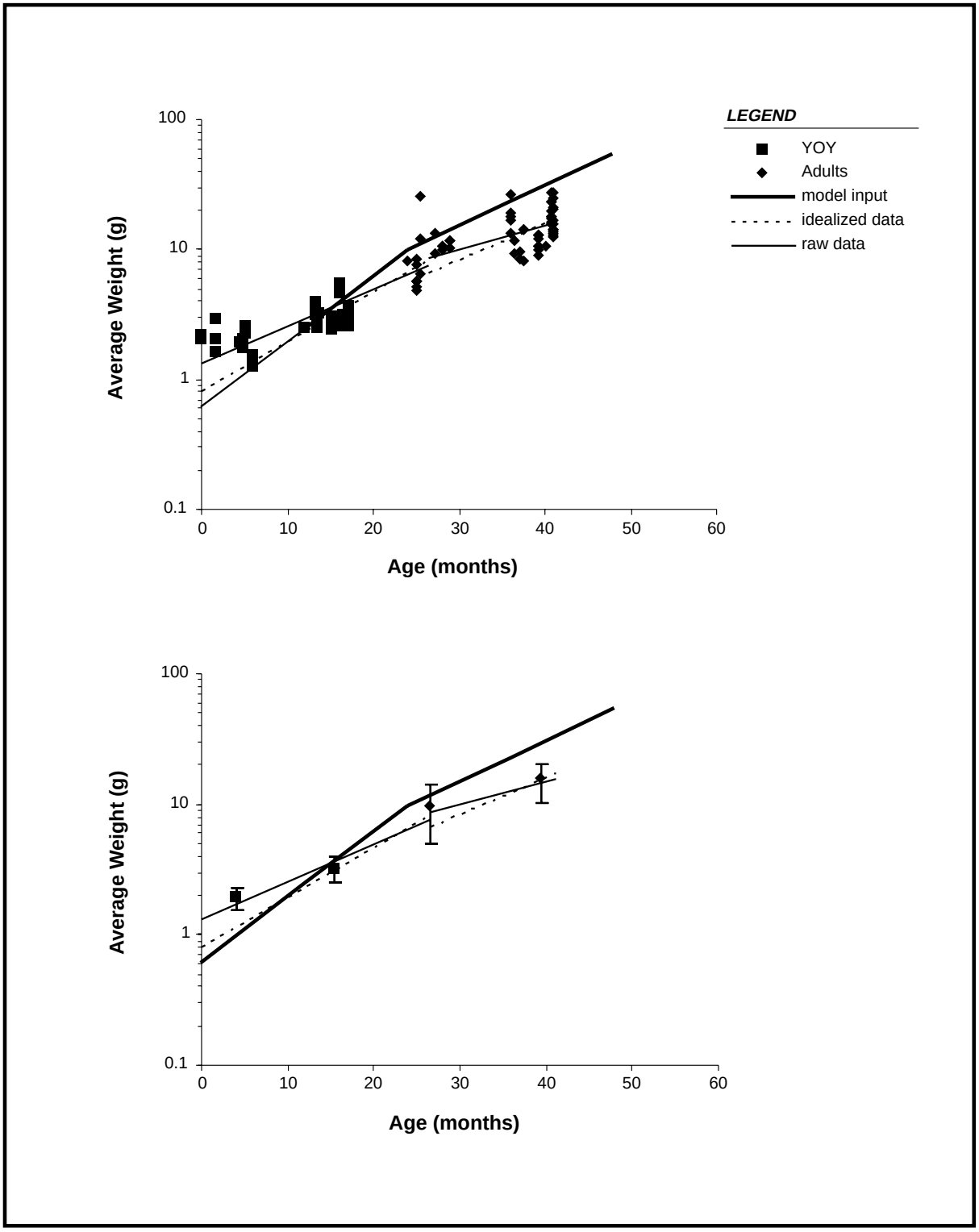

Figure 5. Analysis of rainbow smelt weight data.

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Further, determination of the growth rate using the raw weight data vs. the idealized weight data produces a growth rate (0.00329 1/d) that is nearly 40 percent greater than that apparently used to develop the weight history in the model input and reported in Connolly et al. (1992). The concern about using the idealized weight vs. length relationship for alewife is that it is based on only 12 values vs. 101 paired measurements in the GBMBS alewife data set. In addition, the body weight history established using the raw data represents both the YOY and the adult data, whereas the body weight history specified in the model input appears to overestimate the body weight for YOY data.

For gizzard shad (Figure 4), the body weight history specified in the model input appears to overestimate the body weight for all ages. In addition, while the body weight history appears to have the same growth rates for each leg of the history determined from the analyses presented in Connolly et al. (1992), each leg does not appear to have the same W_0 (Equation 1). Further, growth rate determined from the raw weight data is different from that determined from the idealized weight data. The growth rate for the lower leg (0.0068 1/d) is nearly 30 percent lower than that apparently used to develop the weight history legs in the model input and reported in Connolly et al. (1992), and a growth rate for the upper leg (0.00036 1/d) is 90 percent lower. The concern about using the idealized weight vs. length relationship for gizzard shad is that it is based on data from Chesapeake Bay (n=21) rather than data from Green Bay (n=35 from GBMBS). In addition, the separation of the data to produce two separate growth rates puts significant, and perhaps unnecessary, emphasis on a single data point (greater than 10 in. in length) in the determination of the growth rate of the upper leg of the body weight history.

For rainbow smelt (Figure 5), the body weight history specified in the model input appears to underestimate the body weight for the first age class and overestimate the body weight for the fourth age class. The analyses described in Connolly et al. (1992) indicate that both the adult and YOY data sets were subdivided into two groups. However, the specific length used to make the subdivision was not reported. For the purposes of trying to duplicate the analyses, a length of 5 in. was selected.

As was the case with the analyses of alewife and gizzard shad data, the rainbow smelt body weight history specified in the model input did not match the results of the attempt to duplicate analyses described in Connolly et al. (1992). Comment is refrained on the similarities or dissimilarities of growth rates determined from trying to duplicate these analyses for two reasons: these rates are obviously influenced by the length selected to subdivide the adult data, and the selection of 5 in. did not succeed in reproducing documented growth rates or the growth rates apparent in the specified weight history. Regardless, a concern about using the idealized weight vs. length relationship for rainbow smelt still exists. The relationship documented in Connolly et al. (1992) is based on a very limited data set of 4 observations, compared to the GBMBS data set of 115 observations. Finally, the growth relationship established using the raw data represents both the YOY and the adult data, whereas the body weight history specified in the model input appears to underestimate the body weight for age class 1 data and overestimate body weight for age class 4 data.

There is no discussion of seasonal growth evaluation for predator fish in Connolly et al. (1992), though seasonal variation is included in the model input. The patterns of seasonal variation in the model input are compared to seasonal body weight determined from GBMBS data acquired from http://www.epa.gov/grtlakes/gbdata/gbay2.html in Figures 6 and 7. As can be seen, the seasonal variation in body weight in the model input for both walleye and brown trout shows body weight increasing from spring to summer and decreasing through fall to winter. Although the seasonal data for brown trout (Figure 7) do exhibit a similar pattern, only the summer and fall data for age 3 brown trout are statistically different. This suggests that the pattern of body weight decrease following summer may not be measurable in the context of the data variability. In contrast, the seasonal data for walleye do not exhibit this pattern.

All body weight histories for forage fish species should be determined using measured weight data rather than estimated weight developed from idealized weight vs. length regressions that are based either on limited data sets or data not related to the site. In addition, the body weight histories specified in the model input should be adjusted to better match the data analyses presented in Figures 6 and 7.

9.3.2 Fraction Lipid

GBMBS lipid data reported as the basis of the values specified in the model input were obtained from http://www.epa.gov/grtlakes/gbdata/gbay2.html and were evaluated for spatial and temporal trends for comparison to the values specified in the model input. The analyses described below may not be entirely consistent with the analyses performed to develop the values specified in the model input and listed in Table 3 of HQI (1995) because neither Connolly et al. (1992) nor HQI (1995) provided a discussion of how these values were developed. The data analyses presented below assume that the age assignments of forage fish lipid content was determined from the age assignments made during the analysis of forage fish body weight, as described by Connolly et al. (1992).

The lipid fraction specified for alewife in the model is sometimes temporally variable for older age classes, spatially variable, and age dependent. Zone 1 alewife lipid data are limited to adults. Zone 2A and 2B alewife lipid data are primarily for adults with a few measurements for age classes 1 and 2. The specified lipid fractions for age classes 1 and 2 in both Zones 1 and 2 are assigned the same value of 0.068. The lack of measured data in Zone 1 suggests that the values specified for Zone 1 age class 1 and 2 alewife were based on measurements collected in Zones 2A and 2B. Analyses of the Zone 2A and 2B lipid data suggest that the fraction lipid should be 0.033 for age class 1, and should be 0.077 for age class 2. If, in fact, the data from

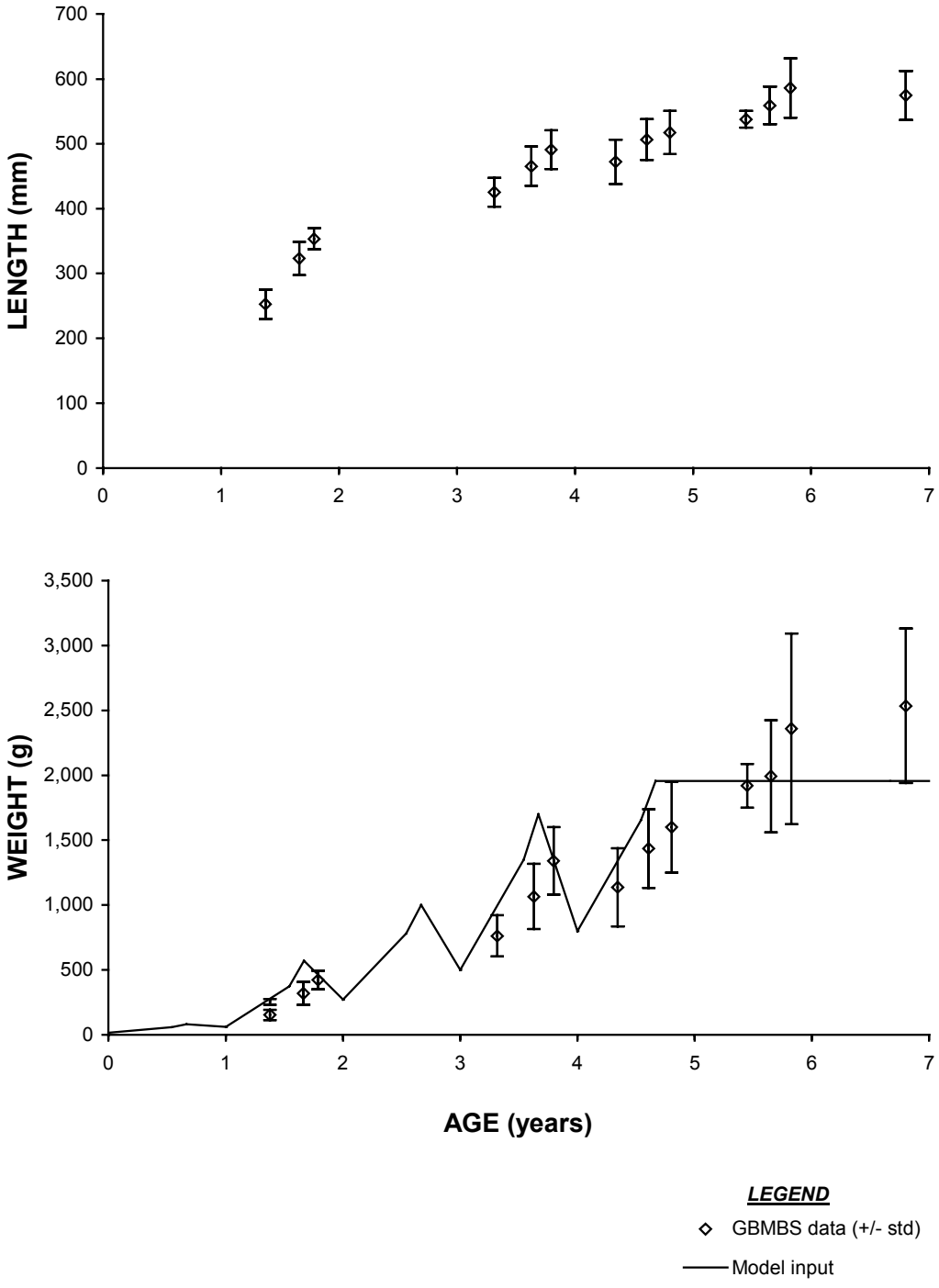

Figure 6. Seasonal body weight history for walleye.

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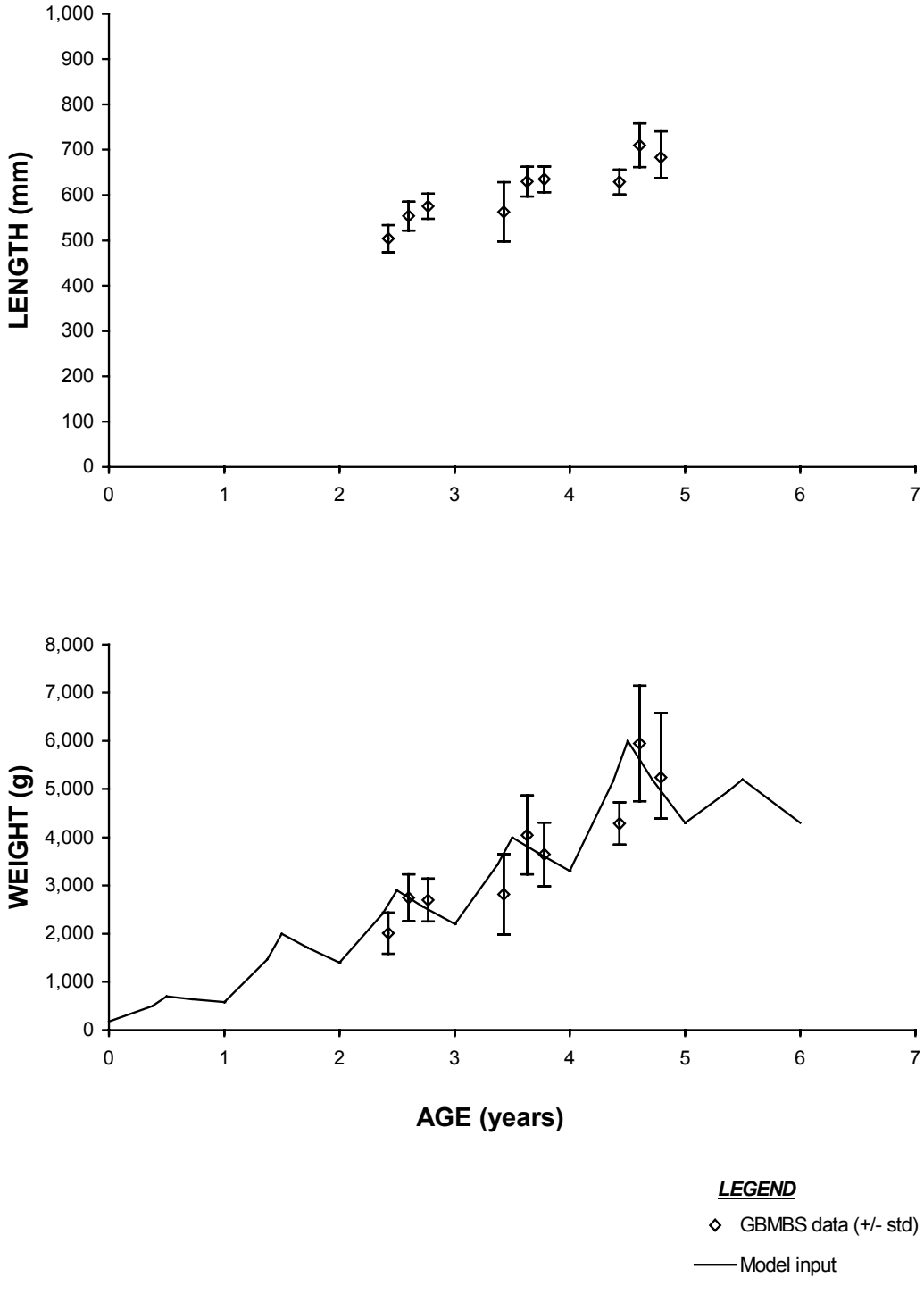

Figure 7. Seasonal body weight history for brown trout.

these two age classes were combined, the average lipid fraction should be 0.066. Because there were no age class 3 measurements collected in either zone, and because age class 3 fish were not identified as adults, the specified lipid fraction could reasonably be assigned the same value as for age class 2. The lipid fraction specified in the model input for age class 4 alewife is both time-variable and different in each zone. Analysis of Zone 1 adult data suggests that a time variable trend may exist in Zones 2A and 2B, but not in Zone 1. Therefore, the specified lipid fraction for Zone 1 age class 4 alewife should be replaced with a constant value of 0.054, determined from the measured data. As discussed previously (*Critique of the Translation of the Conceptual Food Web to Numerical Model, Food Web Connections, Food Webs with Migration*), Zone 2 age class 4 alewife may be a place holder in the model input. If this is intentional, then no change to the model input is necessary. If this is unintentional, then a time variable pattern of lipid fraction may be specified based on measured data collected from June through October in Zones 2A and 2B.

Zone 3A alewife lipid data are primarily for adults with one age class 1 measurement, and a few age class 3 measurements, where as Zone 3B data are limited to adult measurements. The specified lipid fractions for age classes 1 and 2 in both Zones 3A and 3B are assigned the same value of 0.063. The specified lipid fractions for age classes 3 and 4 are assigned a constant value of 0.078 for Zone 3A, and a constant value of 0.123 in Zone 3B. Because of the lack of measured data in Zone 3B for non-adult age classes, it is likely that the lipid fraction values specified for Zone 3B were based on Zone 3A data. Analyses of the Zone 3A lipid data suggest that the fraction lipid should be 0.055 for age class 1 and 0.43 for age class 3. If, in fact, the data from these two age classes were combined to develop an average for age classes 1 to 3 inclusive, the average lipid fraction should be 0.045. Analyses of the adult alewife data from both zones suggest that the age class 4 lipid fraction should be 0.072 for Zone 3A, and 0.115 for Zone 3B.

Zone 4 lipid data are limited to two adult measurements and one measurement each for age classes 2 and 3. The specified lipid fraction for age classes 1 and 2 in Zones 4 is 0.031. The specified lipid fraction for age class 3 is 0.102, and the specified lipid fraction for age class 4 varies from 0.123 to 0.102. Analysis of the Zone 4 lipid data suggests the lipid fraction for age classes 2 and 3 should be 0.031. This value may also be assigned to age class 1 because of the lack of data. Analysis of the adult alewife data hints at a temporal trend similar to that observed in Zone 2A and 2B data. However, two data points are insufficient to justify specifying such a trend in the model input. Therefore, a constant average value of 0.123 should be specified in the model input for Zone 4 age class 4 alewife.

Very few lipid fraction data were collected for gizzard shad. All data were aged as YOY. All data were collected in only Zones 1, 2A, and 2B. Because the number of data points is insufficient for trend analysis, a single average was developed from all data. The specification of a single fraction lipid in the model input and Table 3 in HQI (1995) for all gizzard shad is consistent with this analysis. However, the actual value specified in the table is different from the value obtained in this analysis. Unless additional

information is provided to justify the constant value of 0.069 specified for gizzard shad in the model input, this value should be replaced with the average value of 0.091 calculated from the GBMBS data.

The majority of rainbow smelt data were collected in all zones in the spring. The results of analyzing these data in a manner thought to be consistent with the analyses performed by Connolly et al. (1992) support specifying lipid fraction as a constant, but different by age. However, the analyses do not support specifying the lipid fraction for Zone 4 age class 4 rainbow smelt as temporally variable because insufficient data exist to establish a temporal pattern. The lipid fraction values specified in the model input are as follows: 0.034 (Zone 2, age classes 1 and 2), 0.056 (Zone 2 age classes 3 and 4), 0.035 (Zone 3A, age classes 1 and 2), 0.050 (Zone 3A age classes 3 and 4), 0.029 (Zone 3B, age classes 1 and 2), 0.052 (Zone 3B age classes 3 and 4), 0.033 (Zone 4, age classes 1 and 2), 0.058 (Zone 4 age class 3), and 0.58–0.52 (Zone 4 age class 4). Based on the values specified in the model input, it appears the data were grouped, based on age class, for analysis. Specifically, data for age classes 1 and 2 were averaged together, and data for age classes 3 and 4 were averaged together. The results of the data analyses, performed with this grouping, suggest that the values specified in the model input should be changed to the following: 0.038 (Zone 2, age classes 1 and 2), 0.055 (Zone 2 age classes 3 and 4), 0.041 (Zone 3A, age classes 1 and 2), 0.044(Zone 3A age classes 3 and 4), 0.038 (Zone 3B, age classes 1 and 2), 0.037 (Zone 3B age classes 3 and 4), 0.029 (Zone 4, age classes 1 and 2), and 0.053 (Zone 4 age classes 3 and 4).

Table 3 in HQI (1995) reports that, based on an analysis of GBMBS walleye data, lipid fraction varied seasonally, and the variation changed with age, but did not vary spatially. The GBMBS data do show an obvious change in lipid content from age 1 to age 3 and 4 fish. However, the reported seasonal variation does not appear to be statistically significant based on the small numbers of samples that were averaged to obtain seasonal averages by age. Therefore, it is not necessary to specify the walleye fraction lipid as anything but temporally and spatially constant, but variable by age: 0.056 (age class 1), 0.128 (age class 3), 0.120 (age class 4), and 0.086 (age class 5). No age class 2 data were collected, so the average of age class 1 and 3 data could be used as an estimate. In addition, the value for age class 5 is based only on one measurement, so this value should be used with caution.

Table 3 in HQI (1995) reports that, based on an analysis of GBMBS data, brown trout lipid fraction varied seasonally but was neither spatially nor age variant. Very little brown trout data were collected during the GBMBS—a total of nine samples (four collected in the spring and five collected in the fall) collected from Zones 3A, 3B, and 4, split evenly between ages 2 and 3. It is difficult to detect any trend from so little data. However, these data suggest that the lipid content of brown trout may be higher in the spring than in the fall. Nevertheless, a more reasonable representation may be a single age non-specific, zone non-specific, constant value of 0.137 developed from the GBMBS data.

9.3.3 Water Temperature and Salinity

The GBMBS water temperature data for all stations in both Green Bay and the last seven miles of the Lower Fox River, for all months sampled, were acquired from http://www.epa.gov/grtlakes/gbdata/ gbay2.html. Water temperatures typically collected in June, July, September, and October 1989, and April 1990, were occasionally supplemented with temperatures collected in February and April 1989, and February 1990.

Figure 8 in U.S. EPA (1989) shows where Green Bay stations GB0001–GB0027 are located. In general, station numbers increase from inner bay to outer bay. Figure 2 in U.S. EPA (1989) shows where Lower Fox River stations GB0050–GB0055 are located. In general, station numbers increase in the downstream direction.

Temporal trends in the Green Bay data were reviewed by station. However, these trends could not be evaluated statistically because the depth of the temperature measurement was usually different from station to station, as well as month to month at a given station. Therefore the data from multiple depths were averaged by month for each station.

Average monthly water column temperatures were developed for the following station groupings, which are based on the evaluation of water column dissolved PCB concentrations described in the next section (*Exposure Concentrations*): 1–3 (Group 1); 4–12 without 9 (Group 2); 16 and 19 (Group 3); 17, 18, and 20 (Group 4); and 21–24 (Group 5). All Lower Fox River stations were grouped as Group 6. Exclusion of specific stations from any grouping is discussed in the next section.

Table 3 summarizes the monthly average temperatures by group. Table 3 also presents the temperatures (by time break) specified in the model input for each of the zones used in the GBFWM. The values specified in the model input are the only information available for comparison to the analysis of the GBMBS. The comparison is qualitative in nature because neither Connolly et al. (1992) nor HQI (1995) discusses the analyses used to develop the model input.

As discussed in the next section (*Exposure Concentrations*), Groups 3, 4, and 5 are likely comparable to Zones 3B, 3A, and 4. There are some obvious differences in measured temperature between Groups 3 and 4, but this is not reflected in the values specified in the model input for Zones 3A and 3B. Another difference is that the

Table 3. Grouped GBMBS station water column temperatures by month

	Group 1			Group 2			Group 3			Group 4			Group 5			Group 6		
Month	Avg. (°C)	SD	No. of Observations	Avg. (°C)	SD	No. of Observations	Avg. (°C)	SD	No. of Observations	Avg. (°C)	SD	No. of Observations	Avg. (°C)	SD	No. of Observations	Avg. (°C)	SD	No. of Observations
Jan	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Feb	0.8	0.3	3	0.4	0.2	11	0.5	0.1	2	0.5	0.1	3	0.2	--	1	ND	ND	ND
Mar	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Apr	12.4	3.7	2	8.7	2.0	11	7.4	0.3	2	8.0	0.7	3	4.1	1.0	4	ND	ND	ND
May	13.5	0.9	3	7.6	1.9	10	3.6	0.9	2	3.8	1.6	3	2.6	0.2	2	13.6	0.3	6
Jun	23.5	2.1	2	16.9	0.7	11	12.3	0.4	2	12.9	2.2	3	9.4	2.2	4	21.3	0.9	6
Jul	25.0	0.0	3	21.9	1.6	9	18.6	1.5	2	16.0	3.0	3	13.8	0.7	4	26.8	0.6	6
Aug	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Sep	18.7	0.3	3	18.3	0.7	11	14.1	1.3	2	15.9	1.5	3	13.8	1.5	4	20.2	0.4	6
Oct	ND	ND	ND	8.3	1.0	10	10.1	0.2	2	9.7	0.5	3	9.5	0.8	4	8.8	0.6	6
Nov	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Dec	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND

Date	Zone 2			Zone 3A			Zone 3B			Zone 4			Zone 1		
Jan 1	2	NA	NA	2	NA	NA	2	NA	NA	2	NA	NA	0	NA	NA
Feb 1	--	NA	NA	--	NA	NA	--	NA	NA	--	NA	NA	--	NA	NA
Mar 1	--	NA	NA	--	NA	NA	--	NA	NA	--	NA	NA	1	NA	NA
Apr 1	1	NA	NA	1	NA	NA	1	NA	NA	1	NA	NA	3	NA	NA
May 1	4	NA	NA	4	NA	NA	4	NA	NA	4	NA	NA	9	NA	NA
Jun 1	7	NA	NA	7	NA	NA	7	NA	NA	6	NA	NA	16	NA	NA
Jul 1	12	NA	NA	12	NA	NA	12	NA	NA	11	NA	NA	--	NA	NA
Aug 1	16	NA	NA	16	NA	NA	16	NA	NA	13	NA	NA	24	NA	NA
Sep 1	--	NA	NA	--	NA	NA	--	NA	NA	--	NA	NA	22	NA	NA
Oct 1	18	NA	NA	18	NA	NA	18	NA	NA	16	NA	NA	16	NA	NA
Nov 1	12	NA	NA	12	NA	NA	12	NA	NA	10	NA	NA	11	NA	NA
Dec 1	5	NA	NA	5	NA	NA	5	NA	NA	6	NA	NA	5	NA	NA
Dec 31	2	NA	NA	2	NA	NA	2	NA	NA	2	NA	NA	1	NA	NA

Note: -- - no time break specified
GBMBS - Green Bay Mass Balance Study
NA - not applicable
ND - no data collected
SD - standard deviation

warmest temperatures specified in the model input for Zones 3A, 3B, and 4 occur in October, while the warmest temperatures were measured for Groups 3 and 4 in July.

Temperatures for Groups 1 and 2, which represent the inner bay, can be compared to the values specified in the model input for Zone 2. The difference in measured temperatures between Groups 1 and 2 is further support for the separation of the associated stations as described in the next section (*Exposure Concentrations*). When temperatures from Groups 1 and 2 are compared to those from Group 6 (Lower Fox River), the influence of the warmer water can be seen to diminish with distance from the mouth of Lower Fox River. The temperatures specified in the model input for Zone 2, which are the same as those specified for both Zones 3A and 3B, do not reflect the influence of Lower Fox River on temperatures in the inner bay.

Group 6 temperatures can be compared to the values specified in the model input for Zone 1. While some differences between the measured and specified values exist, the values specified for Zone 1 do reflect the warmer temperatures measured in the Lower Fox River.

9.3.4 Exposure Concentrations

Two exposure pathways are specified in the current application of the GBFWM to Green Bay: dissolved water column PCB and particulate water column PCB. These pathways are consistent with the pelagic nature of the current application, and the evaluation of the exposure concentrations for each pathway is discussed below. An exposure pathway that could be added to the existing model is surface sediment PCB. The evaluation of exposure concentrations for this pathway is also discussed below.

9.3.4.1 Dissolved Water Column PCB

The GBMBS water column PCB data for all stations in Green Bay and the last seven miles of the Lower Fox River for the June, July, September, and October 1989 and April 1990 surveys were acquired from http://www.epa.gov/grtlakes/gbdata/gbay2.html. Total PCB was reported as a minimum and maximum. The reported minimum PCB values were used for the purpose of this analysis. Although results are presented for the PCB minimum, the data analysis approach described below is also applicable to assessment of the PCB maximum.

Figure 8 in U.S. EPA (1989) shows where Green Bay stations GB0001–GB0027 are located. In general, station numbers increase from inner bay to outer bay. Figure 2 in U.S. EPA (1989) shows where Lower Fox River stations GB0050–GB0055 are located. In general, station numbers increase in the downstream direction.

Temporal trends in the Green Bay data were reviewed by station. However, these trends could not be evaluated statistically because infrequent collection of multiple monthly

samples prevents the calculation of the variance of each monthly average needed for such a comparison (Table 4). Therefore, the data were averaged by station using monthly averages (when multiple samples were collected) before calculating a station

Table 4. GBMBS water column dissolved total PCB concentrations by station

	June 1989			July 1989			September 1989			October 1989			April 1990			Station Average[a]		
Station	Avg. (ng/L)	SD (ng/L)	No. of Observations	Avg. (ng/L)	SD (ng/L)	No. of Observations	Avg. (ng/L)	SD (ng/L)	No. of Observations	Avg. (ng/L)	SD (ng/L)	No. of Observations	Avg. (ng/L)	SD (ng/L)	No. of Observations	Avg. (ng/L)	SD (ng/L)	No. of Observations
GB0001	10.53	--	1	10.15	0.56	2	22.44	12.87	3	9.01	--	1	13.66	--	1	13.16	5.47	5
GB0002	7.34	--	1	10.23	--	1	6.87	--	1	5.51	--	1	9.81	--	1	7.95	2.01	5
GB0003	7.94	--	1	6.18	--	1	6.51	--	1	18.96	16.72	2	10.39	11.62	2	10.00	5.28	5
GB0004	4.20	--	1	3.00	--	1	2.95	--	1	1.81	--	1	1.21	--	1	2.64	1.16	5
GB0005	1.64	--	1	2.28	--	1	2.82	--	1	1.29	--	1	0.97	--	1	1.80	0.75	5
GB0006	2.38	--	1	4.91	--	1	3.71	--	1	2.11	--	1	1.24	--	1	2.87	1.44	5
GB0007	4.00	--	1	7.06	--	1	3.10	0.22	2	3.77	0.14	2	3.46	--	1	4.28	1.59	5
GB0008	1.59	--	1	11.92	13.79	3	2.64	--	1	3.71	--	1	1.39	--	1	4.25	4.38	5
GB0009	--	--	--	1.72	--	1	31.44	41.20	2	14.85	19.36	2	0.74	--	1	12.19	14.36	4
GB0010	9.57	13.26	3	4.17	0.01	2	1.83	--	1	3.06	--	1	0.66	0.10	2	3.86	3.45	5
GB0011	2.54	--	1	3.88	--	1	2.13	--	1	2.99	--	1	0.85	--	1	2.48	1.12	5
GB0012	3.44	0.15	2	5.54	--	1	2.64	--	1	2.33	--	1	1.12	--	1	3.01	1.64	5
GB0013	1.14	0.04	2	16.23	21.05	2	1.26	0.08	2	1.35	0.11	2	0.77	--	1	4.15	6.76	5
GB0014	1.01	--	1	1.45	--	1	1.10	--	1	2.72	--	1	0.67	0.00	2	1.39	0.79	5
GB0015	2.11	--	1	1.15	--	1	0.90	0.13	2	2.13	--	1	6.92	8.00	2	2.64	2.46	5
GB0016	0.61	--	1	0.78	--	1	0.77	0.14	2	1.05	--	1	0.60	--	1	0.76	0.18	5
GB0017	10.09	11.83	2	1.42	--	1	6.95	10.92	3	1.17	--	1	1.02	--	1	4.13	4.16	5
GB0018	1.28	0.79	2	0.75	0.25	2	0.81	0.28	4	13.00	16.60	2	0.46	--	1	3.26	5.45	5
GB0019	0.51	--	1	0.71	--	1	0.54	0.14	2	1.11	--	1	0.45	--	1	0.67	0.27	5
GB0020	19.37	26.65	2	0.73	0.02	2	0.53	--	1	0.69	--	1	0.54	--	1	4.37	8.39	5
GB0021	9.14	14.99	3	0.47	--	1	0.47	0.04	2	0.80	--	1	0.30	--	1	2.23	3.86	5
GB0022	0.50	0.00	2	0.37	--	1	0.58	0.01	2	0.86	--	1	12.84	17.45	2	3.03	5.49	5
GB0023	0.41	--	1	0.34	0.03	2	0.39	0.07	2	24.48	33.73	2	0.37	--	1	5.20	10.78	5
GB0024	0.51	0.12	3	5.44	9.98	4	0.48	0.06	3	0.63	0.01	2	0.45	--	1	1.50	2.20	5
GB0025	0.45	--	1	0.40	0.12	2	0.68	0.27	3	0.86	--	1	0.32	0.00	2	0.54	0.22	5
GB0026	0.79	0.34	3	0.38	0.05	2	11.89	19.65	3	0.70	--	1	0.42	--	1	2.84	5.06	5
GB0027	0.76	--	1	0.43	0.09	2	0.45	--	1	0.57	0.14	2	0.33	--	1	0.51	0.17	5
GB0050	11.06	--	1	20.60	--	1	18.50	--	1	15.74	--	1	17.42	--	1	16.67	3.59	5
GB0051	14.37	--	1	25.90	--	1	23.37	--	1	16.34	--	1	--	--	--	20.00	5.51	4
GB0052	18.44	--	1	31.18	--	1	26.95	--	1	20.41	--	1	21.97	--	1	23.79	5.19	5
GB0053	12.56	--	1	24.27	--	1	17.40	0.46	2	25.57	0.77	2	20.56	--	1	20.07	5.28	5
GB0054	16.90	0.17	2	24.94	6.48	2	27.82	3.16	2	23.78	--	1	25.04	--	1	23.69	4.08	5
GB0055	16.05	--	1	25.23	--	1	21.18	--	1	24.98	--	1	18.86	--	1	21.26	3.95	5

Note: -- - not applicable or no sample collected
GBMBS - Green Bay Mass Balance Study
SD - standard deviation

[a] Average of monthly averages

average. Connolly et al. (1992) reports that the data were averaged in the same manner because monthly variation was interpreted to be small.

Because neither Connolly et al. (1992) nor HQI (1995) clearly define either the boundaries of the modeling zones (i.e., on a map) or list the water quality stations used for developing water column exposure concentrations, the following was assumed based on the GBTOX model segmentation (Bierman et al. 1992): Zone 1 is the Lower Fox River from the DePere Dam to the river mouth, Zone 2 is GBTOX water quality model segments 1–6, Zone 3A is GBTOX model segment 7 and 10, Zone 3B is GBTOX model segment 8 and 11, and Zone 4 is GBTOX model segments 9 and 12. As a result of these assumptions, the Green Bay sampling stations would be associated with each of the zones as follows: stations 50–55 in Zone 1, stations 1–12 in Zone 2, stations 13, 14, 16, and 19 in Zone 3A, stations 15, 17, 18, and 20 in Zone 3B, and stations 21–27 in Zone 4.

The station average dissolved total PCB concentrations from Table 4 were grouped, as described above, to generate zone average dissolved total PCB concentrations for comparison to the model-specified concentrations. The model-specified concentrations, and those determined from the analyses of the GBMBS data, are presented in Table 5.

Table 5. Grouped GBMBS station water column dissolved and particulate total PCB averages

	Dissolved (ng/L)			Particulate (μg/g C)		
			Number of	Total Homolog		Number of
Zone	Average	SD	Stations	Lower	Upper	Stations
GBMBS						
Zone 1	20.91	2.67	6	29.70	38.47	6
Zone 2	5.65	3.93	12	4.14	5.25	12
Zone 3A	1.74	1.64	4	1.48	1.92	4
Zone 3B	3.60	0.80	4	1.73	2.21	4
Zone 4	2.39	1.67	7	0.98	1.65	7
Model Input						
Zone 1	21.729	--	--	39.032	--	--
Zone 2	5.6058	--	--	5.1224	--	--
Zone 3A	1.7859	--	--	2.9067	--	--
Zone 3B	2.2965	--	--	2.7222	--	--
Zone 4	1.2607	--	--	1.6245	--	--

Note: -- - not provided in the model input files
GBMBS - Green Bay Mass Balance Study
PCB - polychlorinated biphenyl
SD - standard deviation

A comparison of the two shows that the model-specified concentrations for Zones 1, 2, and 3A are similar to those determined from the GBMBS, whereas the model-specified concentrations for Zones 3B and 4 are at least 50 percent lower than those determined from the GBMBS data. In Zone 3B, stations 18 and 20 each have an apparent outlier of very high concentration. Exclusions of these samples from the analyses decreases the

Zone 3B average dissolved PCB to 2.07 (SD=1.64). Five of the seven stations in Zone 4 also each have an apparent outlier of very high concentration. Exclusions of these samples from the analyses decreases the Zone 4 average dissolved PCB to 0.52 ng/L (SD=0.05).

9.3.4.2 Particulate Water Column PCB

Discussions of phytoplankton in Connolly et al. (1992) focus on variation in phytoplankton carbon and lipid contents, and PCB partitioning to phytoplankton. There is no discussion of the development of the water column particulate PCB concentrations, which represent phytoplankton, specified in the model input. There is, however, a brief discussion of the elimination of the April 1989 data from the analyses because high concentrations were suspected of being caused by the sampling technique. The data set from the April 1989 cruise is smaller than for any of the other cruises. In addition, the majority of the samples were depth-integrated during this cruise, whereas they were collected as grab samples during the remaining cruises.

The phytoplankton PCB concentrations (carbon basis) by station were calculated from wet weight PCB and organic carbon content using both lower and upper homolog sums reported in the data. Little seasonal variation in phytoplankton PCB concentrations was observed in data collected in Green Bay, whereas some seasonal variation was noted in the Lower Fox River data. Therefore, it is reasonable to develop a single average phyto-plankton PCB exposure concentration for each of the Green Bay zones. The seasonal variation in the river data may be the result of seasonal variation of flow rate. However, these data are too infrequent to evaluate the influence of flow rate on any other factors on phytoplankton PCB. Therefore, a single average was calculated for the river data as well. Using the same station-to-zone associations assumed for the analysis of water column dissolved PCB, the phytoplankton PCB concentrations were analyzed to develop constant concentration values for each zone. The model-specified concentrations, and those determined from the analyses of the GBMBS data, are presented in Table 5. A comparison of the two shows that the model-specified concentrations for Zones 1, 2, and 4 appear to be based on the reported upper homolog concentrations. In contrast, the model-specified concentrations for Zones 3A and 3B are even greater than the averages estimated from the reported upper homolog concentrations. The difference between the lower and upper homolog concentrations in Table 5 is approximately 30 percent, with the exception of Zone 4, which is approximately 70 percent. To reduce the uncertainty translated to the model calculations by using either the lower or upper homolog estimate, and in the absence of additional information supporting the values currently supplied in the model input, the average of the lower and upper homolog estimates should be used as phytoplankton PCB exposure concentrations in the model input.

9.3.4.3 Surface Sediment PCB

A sediment exposure pathway is not currently included in the existing GBFWM application to the Green Bay system. If such a pathway were to be included, it would be necessary to define surface sediment PCB exposure conditions for the Lower Fox River and Green Bay. Sediment PCB concentrations for the Lower Fox River are presented in Technical Memorandum 2e (WDNR, 1999). Sediment PCB concentrations for Green Bay are presented in Technical Memorandum 2f (draft report) (LTI, 1999). For reference, average sediment PCB concentrations in Green Bay for the 0-10 cm depth interval as computed from 1989-1990 Green Bay Mass Balance Study data are presented in Figure 8.

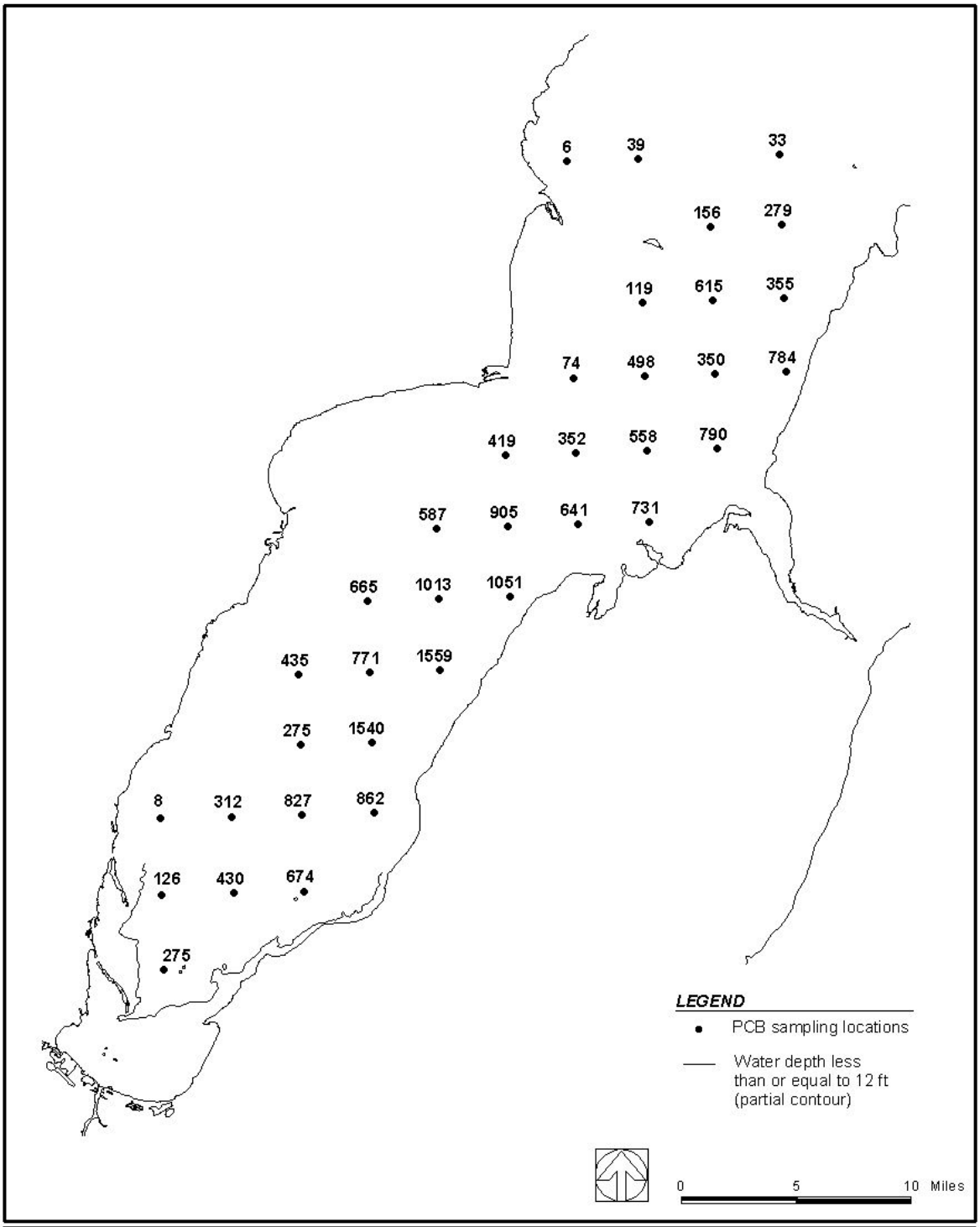

Figure 8. Average 0-10 cm PCB concentrations (μg/kg) in Green Bay based on 1989-90 data.

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10. Model Calibration

The original site-specific application of the GBFWM to Green Bay was set up to model several congeners and total PCBs (Connolly et al. 1992). HQI (1995) reports that the modeling approach was modified to model a range of log K_{ow}s from 5.0–8.0 with a log K_{ow} of 6.1 for total PCB. The goal was to evaluate model calculations with respect to the range of all available congener data without limiting model calculations to a specific congener.

The model was run for a simulated period of 30 years with constant exposure concentrations because the biota was assumed to be at steady state with exposure concentrations (HQI 1995). Running the model long-term under the assumption of steady state precludes the need to specify meaningful initial conditions for all age classes except age class 1 because body burden is tracked from one age class to another in a multiple-year simulation. The initial PCB concentrations in age class 1 fish were specified in the model input as zero. The option to have age class 1 initial body burden determined from spawning adult fish was not selected.

HQI (1995) compares several aspects of the model calculations to data: predator-prey ratios, bioaccumulation factors (BAFs), and body burdens. In all cases, both age-specific data and age-specific model calculations are aggregated by species in each zone for comparison. In addition, both the aggregate data and the aggregate model calculations were averaged on an annual basis prior to comparison. HQI (1995) reports that only data for those congeners with less than 20 percent nondetect values in the water column were used in developing the annual aggregate average concentrations, specifically to reduce variance in the data.

Figures 1–7 from HQI (1995) show the comparisons of species-specific annual average aggregate model calculations to the annual average aggregate data. Predator-prey ratios and BAFs are presented for Zones 3A, 3B, and 4 as a function of K_{ow} in Figures 1–6 from HQI (1995). The spatial trend in total PCB by species is presented in Figure 7 from HQI (1995).

11. Critique of Model Calibration

The approach of modeling a range of log K_{ow}s for comparison to all available congener data is creative because it takes advantage of all available field data without necessitating model runs for each specific congener. Total PCB log Kow is specified in the model input for Zones 1 and 2 as 6.1, and for Zones 3A, 3B, and 4 as 6.3. This log K_{ow} is within the range of congener specific K_{ow}s reported by Hawker and Connell (1988) and is most similar to K_{ow}s measured for pentachloro biphenyls. Typical homolog distributions of fish tissue PCBs show that homologs 4,5, and 6 are the prevalent homologs that make up total PCBs. Using the average log K_{ow} by homolog, determined from the congener specific log K_{ow}s reported by Hawker and Connell (1988), and the typical homolog distributions from the GBMBS fish tissue data, one can calculate an mass weighted average log K_{ow} for each species by zone. With the exception of gizzard shad (log K_{ow} = 5.93) represented in the model in only Zones 1 and 2, the log mass weighted log K_{ow}s for all species by zone, were consistent with the specified values in the model input.

The purpose of the review of the model calibration was to review the manner in which the model calculations were compared to measured data, and to assess if the current calculations represent the measured data. To accomplish this, all values of model coefficients were initially presumed to be correct.

The first step in the review was to run the model with the calibrated input files provided by HydroQual through LimnoTech, Inc. (Slawecki 1997, pers. comm.) and compare the results for total PCBs to data in the same manner as described in HQI (1995). Glaser (1998b, pers. comm.) briefly describes the aggregation of both model calculations and measured data that are presented in HQI (1995). The aggregated data shown in HQI (1995) were also provided by Glaser (1998a, pers. comm.). Aggregate model calculations, along with the data provided by Glaser, are shown on Figure 9.

As can be seen in Figure 9, the current model calculations appear to satisfy the model quality criteria for calculation of total PCB fish tissue concentrations proposed in Technical Memorandum 1 (LTI and WDNR 1998). Specifically, predicted concentrations for fish should be within ± a factor of 3 of observed values for short-term simulations. It is appropriate to apply the short-term criteria to the calibration of the GBFWM because of the steady-state assumption defined in HQI (1995) as well as the period of data to which the model was calibrated (1989 GBMBS).

However, several problems and concerns arose while using the aggregation scheme described by Glaser (1998b, pers. comm.). First, analysis of the raw GBMBS data using the aggregation scheme was unsuccessful in duplicating the aggregate data provided by Glaser. Second, could the inclusion of model calculations from age classes suspected of being placeholders greatly affect the aggregated model calculations? Third, some of the

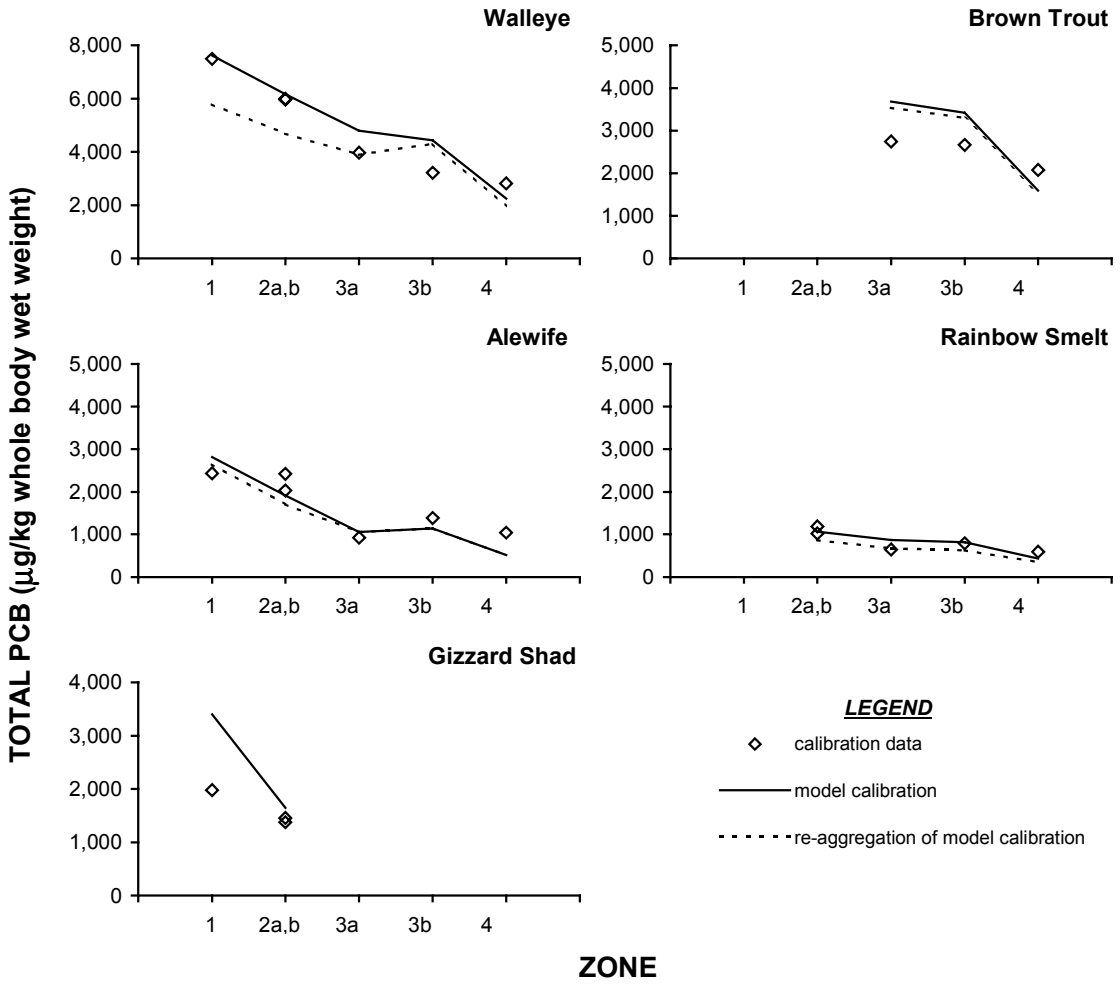

Figure 9. Adult whole body PCB tissue concentration by zone.

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age classes apparently included in the aggregated model output were not actually sampled, and therefore, did not participate in developing the aggregate data. Fourth, could aggregation of age specific data and model calculations obscure any important age specific trends? Fifth, what is the variance associated with the aggregated data provided by Glaser?

To respond to the second concern, the model calculations for all age classes suspected of being placeholders in the input files were removed from the calculation of aggregate model results. This line is shown on Figure 9 as the re-aggregation of model calibration. With the exception of walleye, very little difference is observed between the two lines. And, the re-aggregated calculations also appear to satisfy the model quality criteria for calculation of total PCB fish tissue concentrations proposed in Technical Memorandum 1.

To respond to the first, third, forth, and fifth concerns, the measured data were grouped by age, evaluated for variance, and compared to age specific average model calculations (Figures 10 through 14). Model calculations for walleye and brown trout are generally within the variability of the data and certainly within a factor of 3 of the data. With the exception of YOY rainbow smelt, model calculations for gizzard shad, alewife, and rainbow smelt are again within the variability of the data and certainly within a factor of 3 of the data. This analysis indicates that, in this instance, the aggregation of both measured data and model output did not obscure any unusual age specific trends. Therefore, the model aggregation scheme appears valid.

One-to-one comparisons of model calculations to data are shown in Figures 15–19. In addition, lines that represent the model quality criteria of ± a factor of 3 proposed in Technical Memorandum 1 (LTI and WDNR 1998) are also shown on these figures. Most, though not all, of the calculated values fall within these lines.

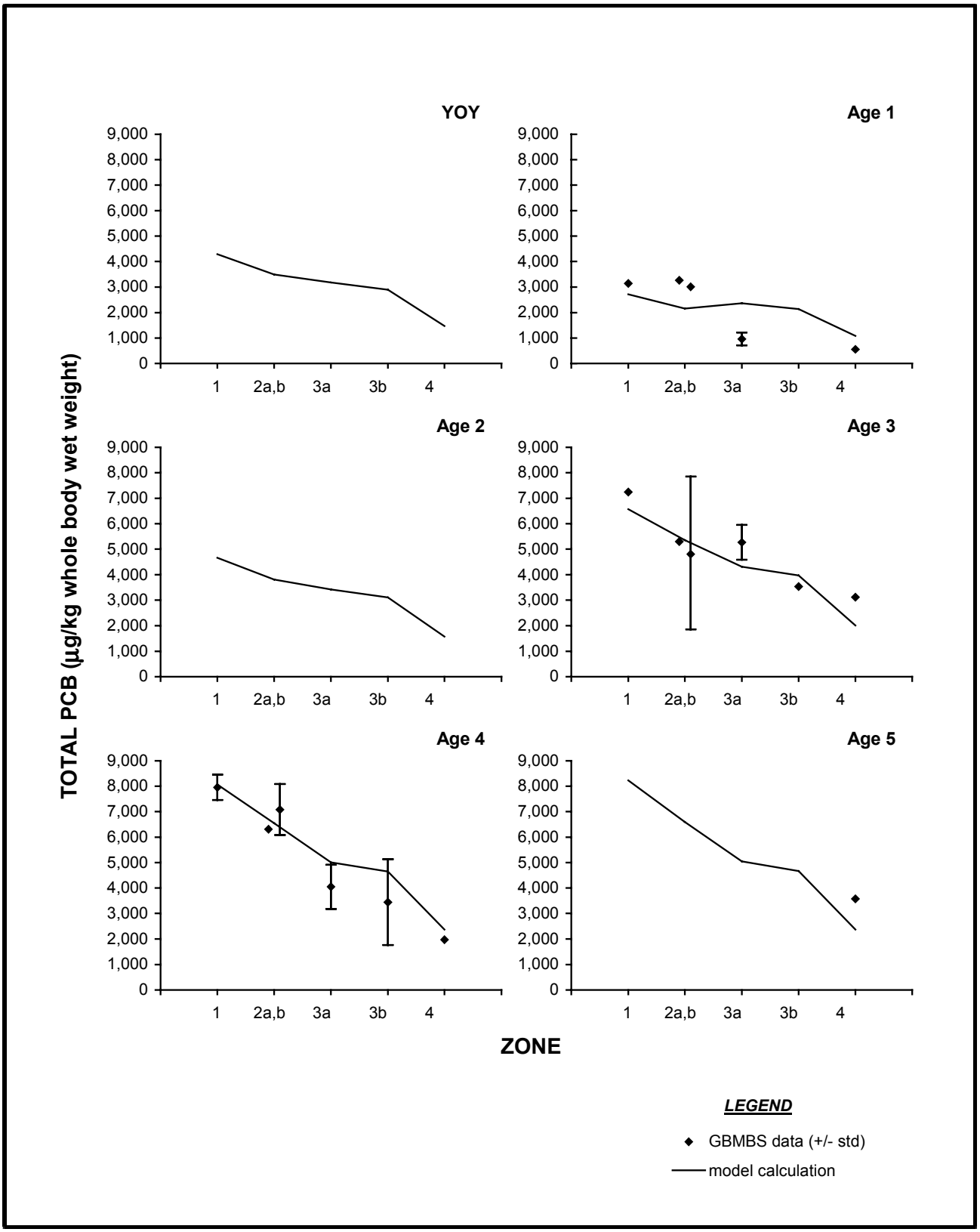

Figure 10. Walleye whole body PCB tissue concentration by zone.

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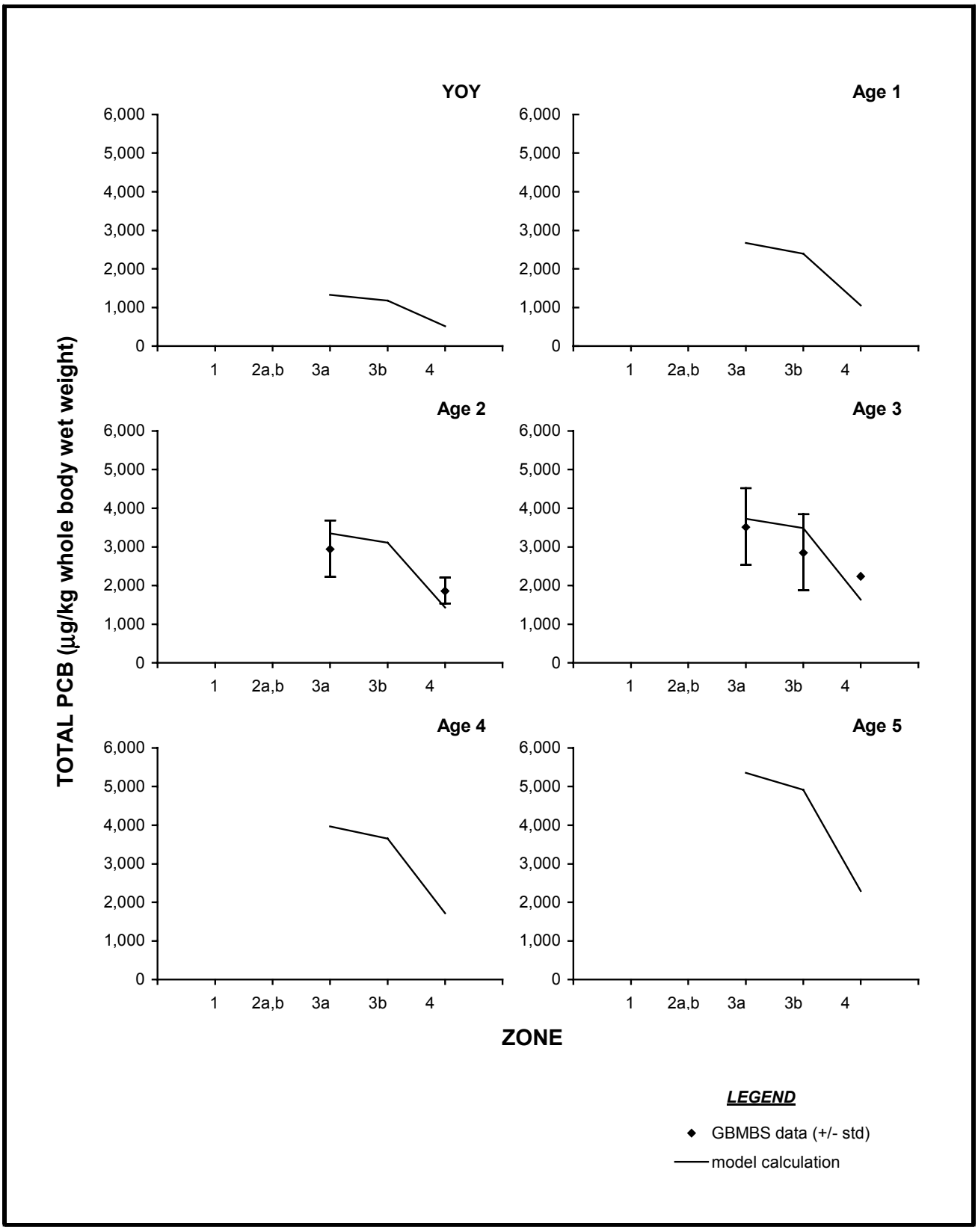

Figure 11. Brown trout whole body PCB tissue concentration by zone.

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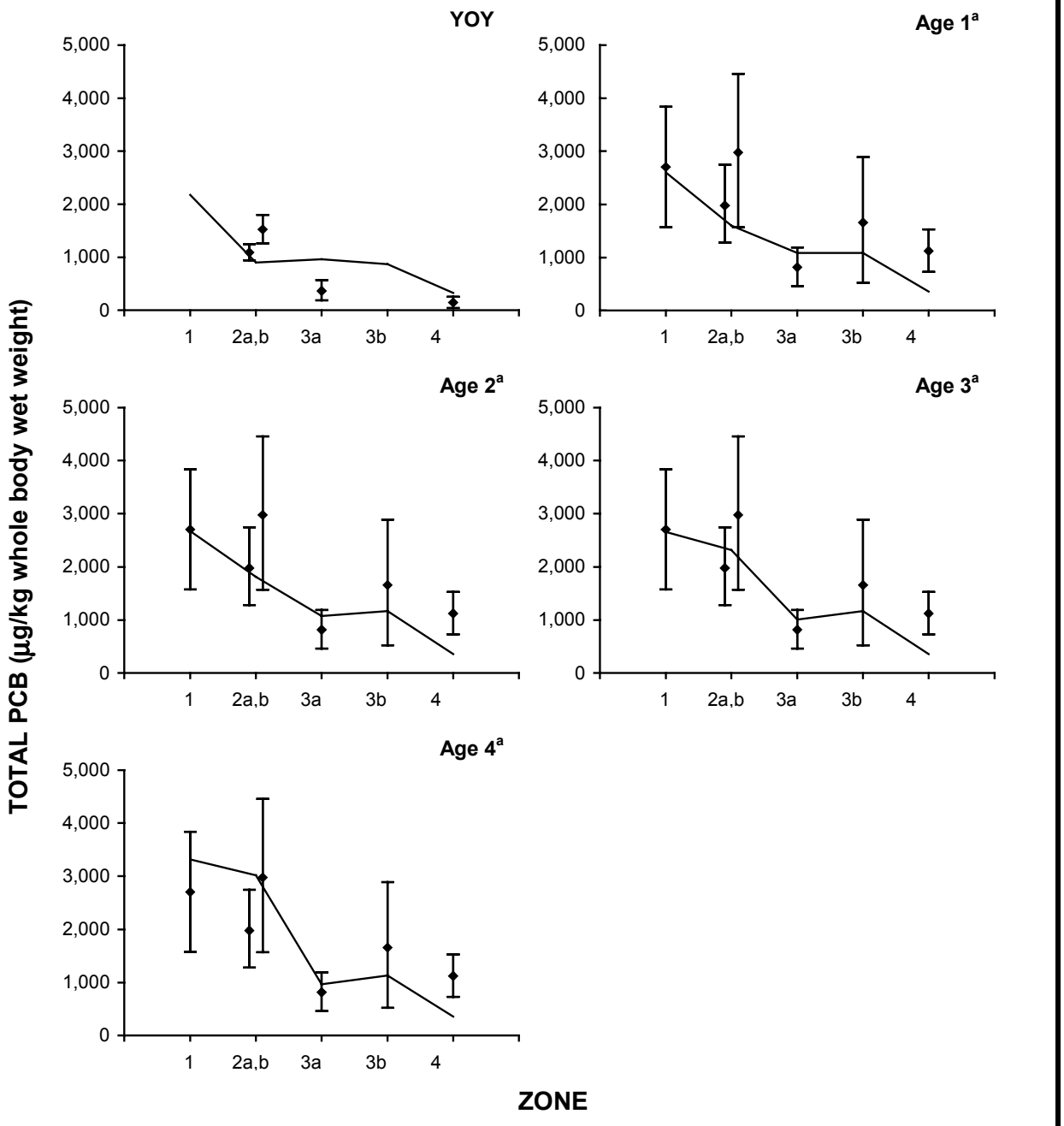

Figure 12. Alewife whole body PCB tissue concentration by zone.

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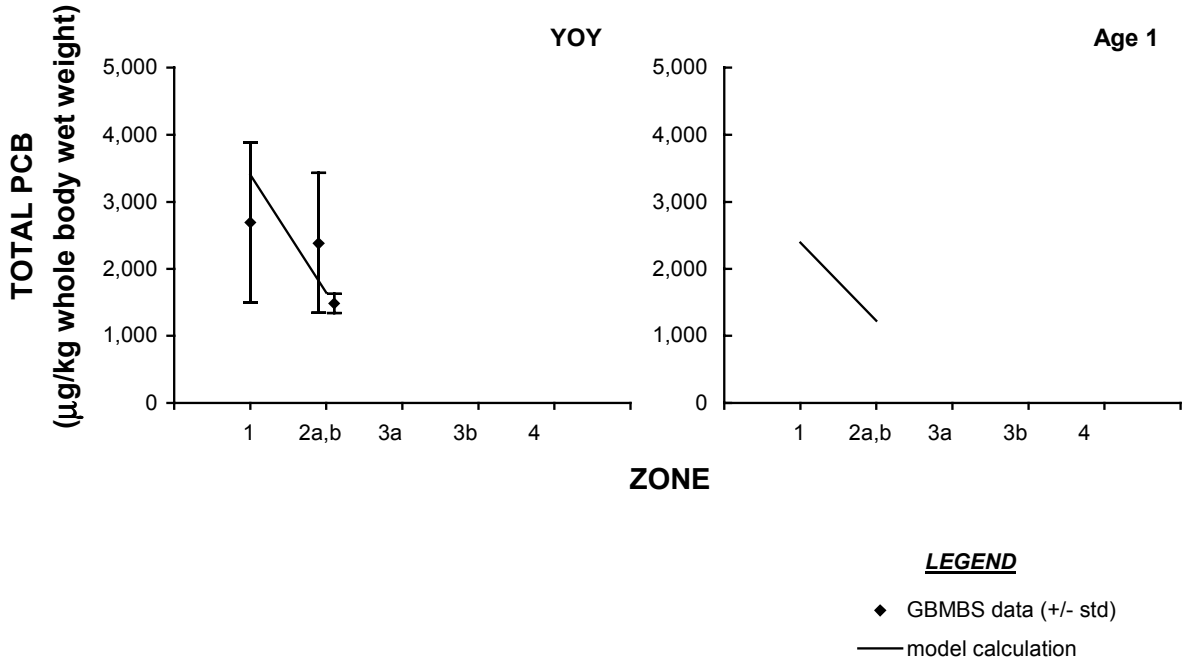

Figure 13. Gizzard shad whole body PCB tissue concentration by zone.

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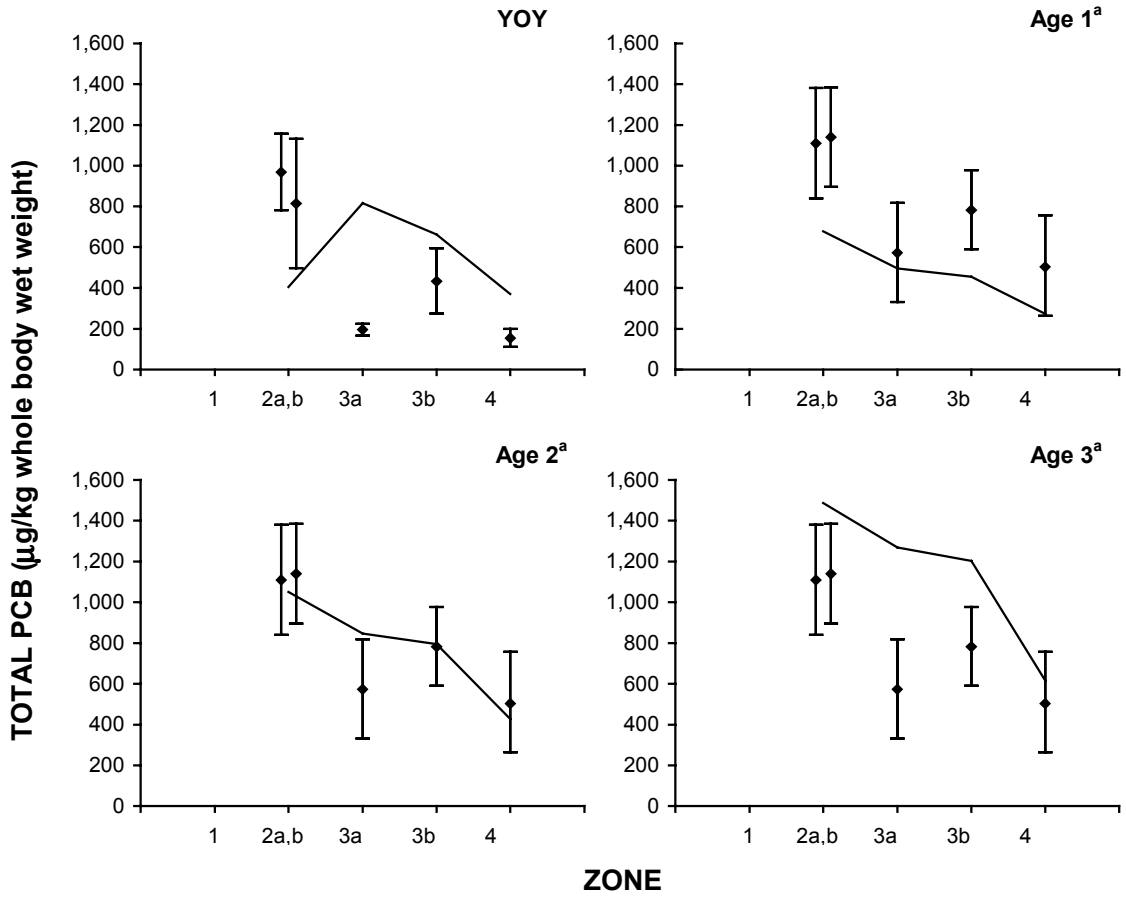

Figure 14. Rainbow smelt whole body PCB tissue concentration by zone.

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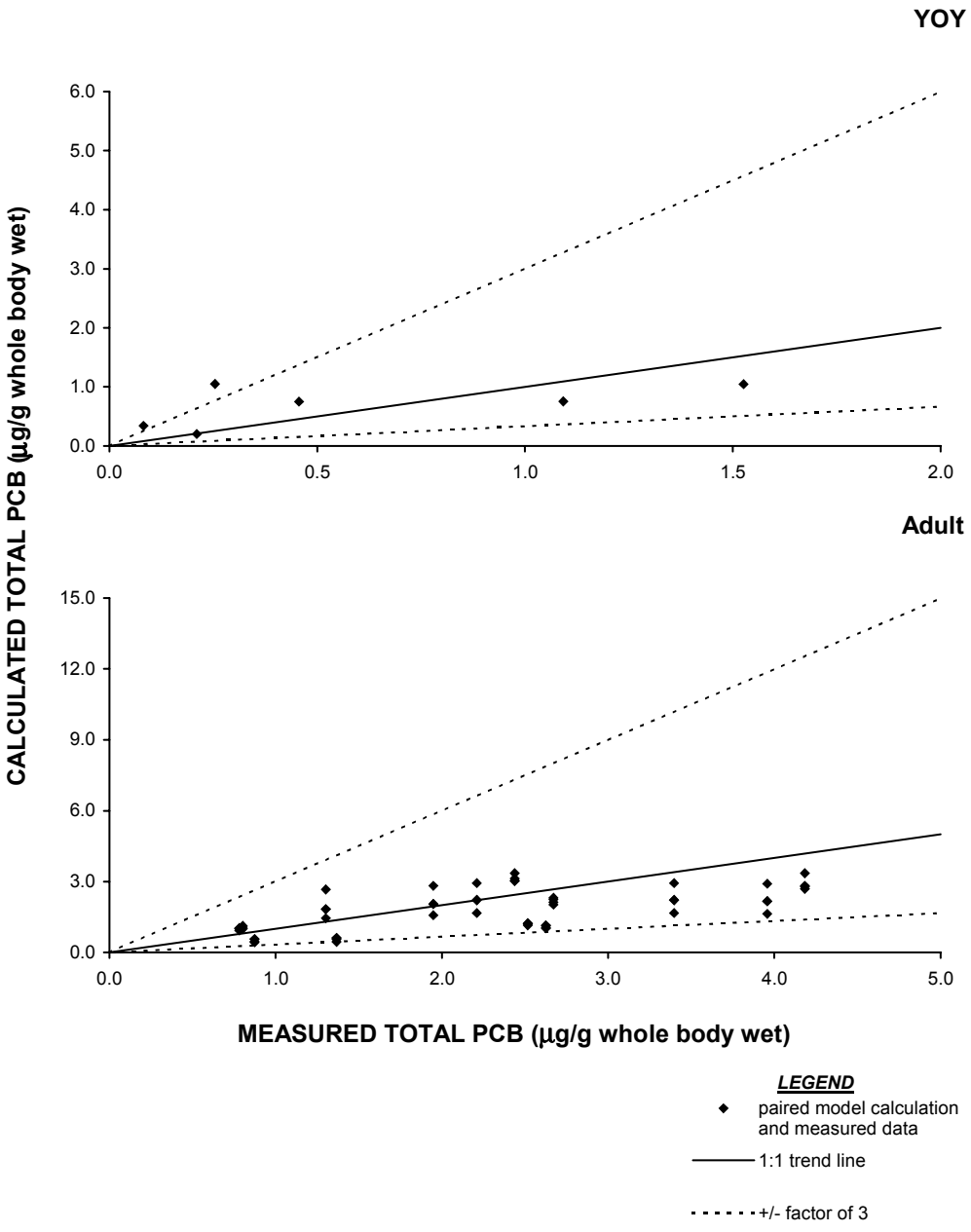

Figure 15. Alewife calculated vs. measured whole body PCB tissue concentrations.

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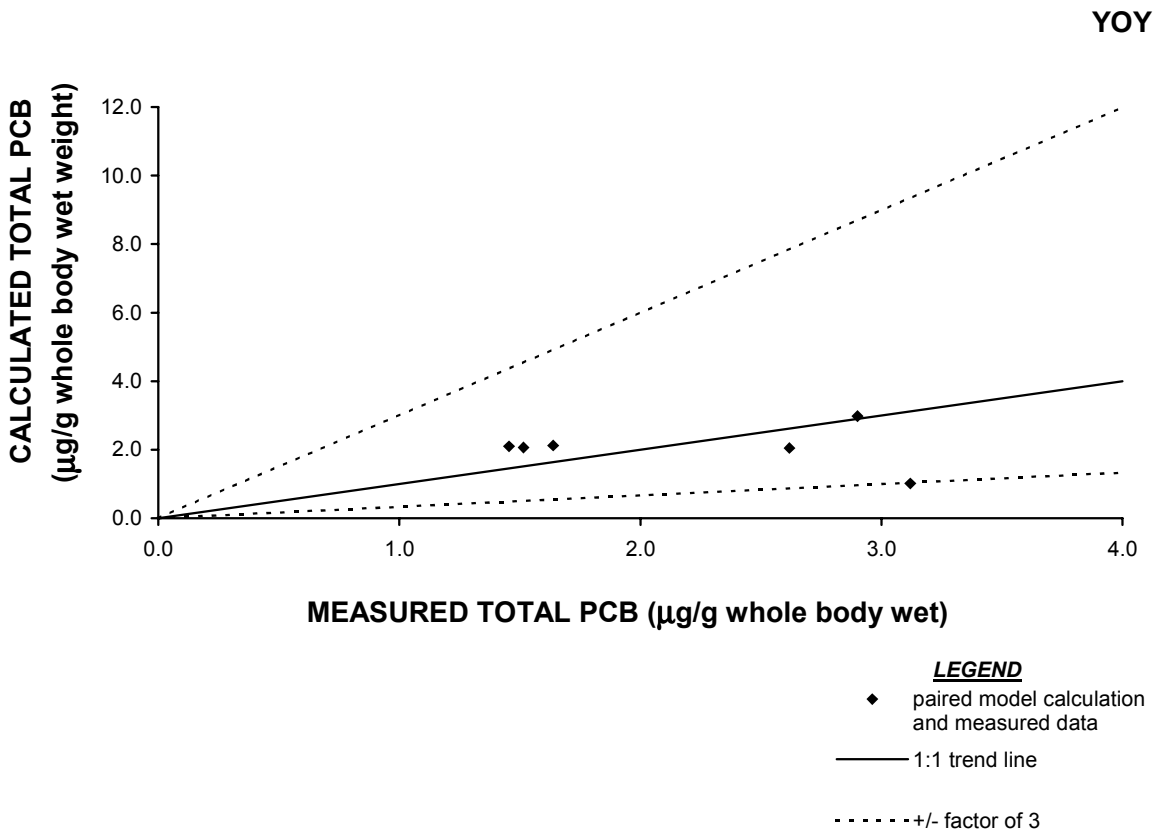

Figure 16. Gizzard shad calculated vs. measured whole body PCB tissue concentrations.

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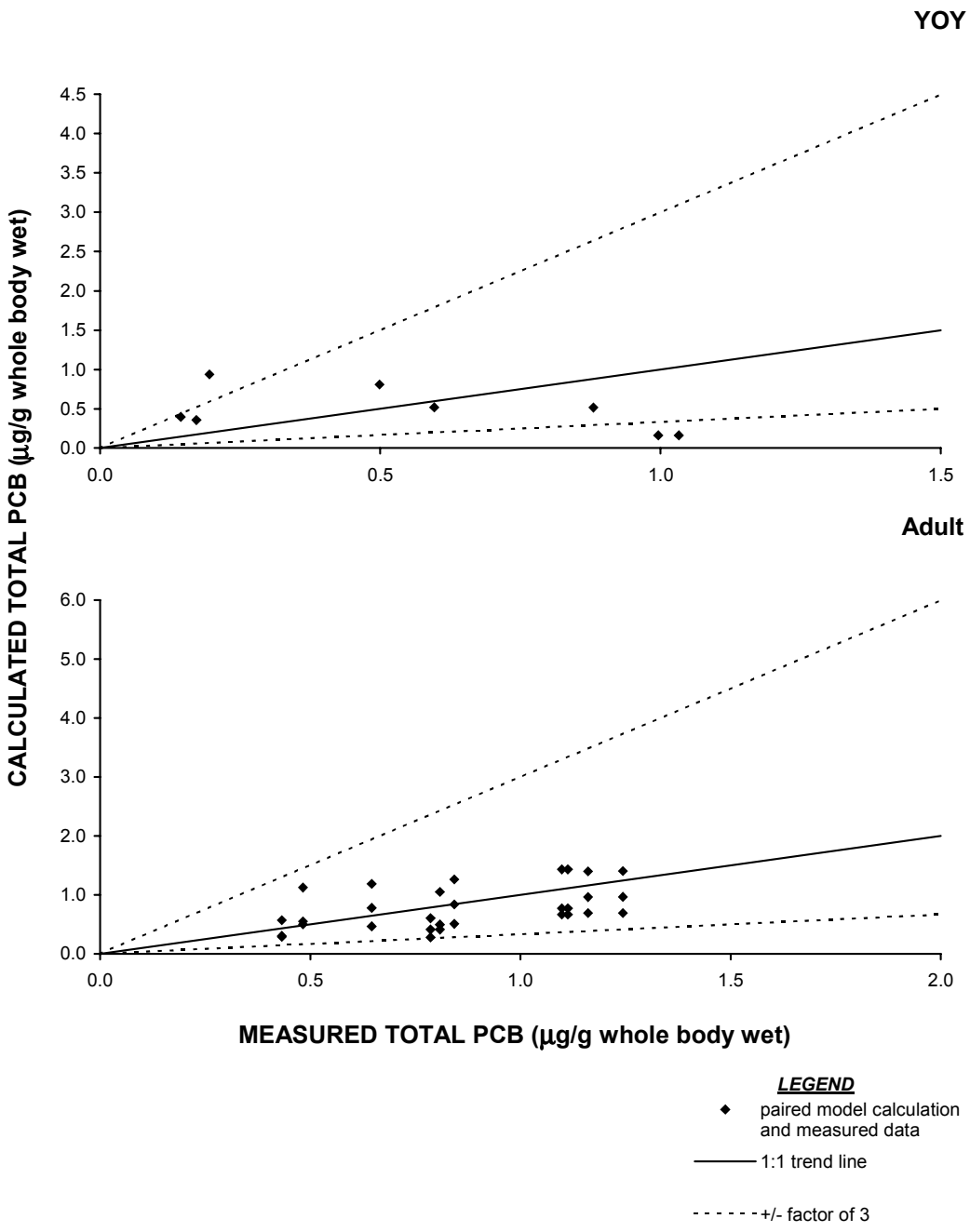

Figure 17. Rainbow smelt calculated vs. measured whole body PCB tissue concentrations.

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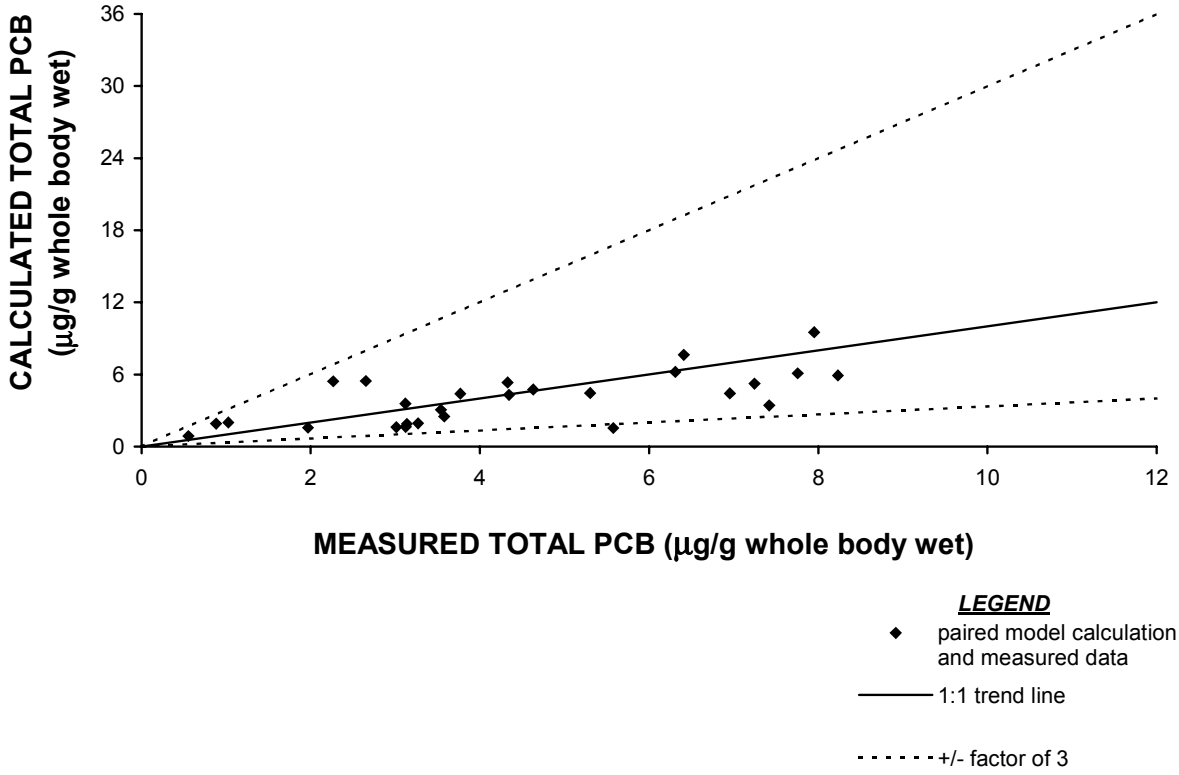

Figure 18. Walleye calculated vs. measured whole body PCB tissue concentrations.

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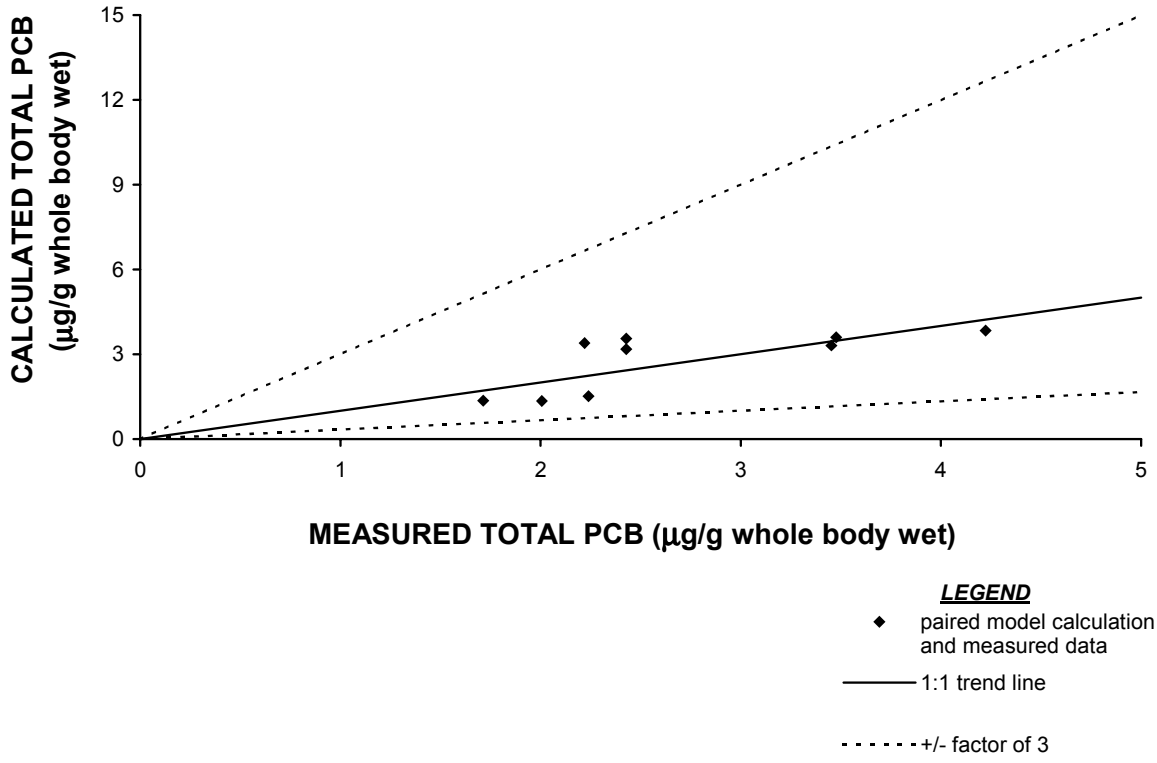

Figure 19. Brown trout calculated vs. measured whole body PCB tissue concentrations.

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12. Appropriate Uses of the GBFWM

The evaluation of the GBFWM presented above was undertaken to determine the applicability of the model to both Green Bay and the upper and lower portions of Fox River. In addition, the evaluation was to determine whether the GBFWM could be used in a hindcast or forecast mode. Each use is discussed below. Consideration of the application of the GBFWM to either Green Bay or Fox River for natural resource damage assessment (NRDA) and remedial alternative evaluation is also considered.

12.1 Applicability to Green Bay and the Lower Fox River

The applicability of the existing GBFWM to Green Bay and Lower Fox River (from the DePere Dam to the river mouth) is determined by the results of the evaluation of the fundamental building blocks of the model: the conceptual food web and the model framework. If the conceptual food web is not representative of Green Bay, or if the calculations made by the model are biased, then the model application would require revision.

In general, the conceptual food web presented from information collected in the GBMBS was determined to be reasonably representative of the pelagic habitat in Green Bay. However, the current pelagic food web does not include biological communities with strong ties to benthic food chains. Littoral habitats have been shown to be highly productive areas. Littoral habitats provide both sediment- and water-based forage attributes that may be important to consider in evaluating PCB bioaccumulation and trophic transfer. In addition, there are other species of forage fish that are abundant in littoral habitats and that may contribute as prey to pelagic predatory fish. Therefore, if littoral food webs accumulate PCBs directly from sediments, then the applicability of the existing conceptual food web to littoral environments would be improved with the addition of a benthic food chain component.

The Zone 1 conceptual food web describes the predator-prey relationships for fish species that migrate from their primary residence of lower Green Bay into the Lower Fox River for a short period of time in the spring for spawning. It does not specifically represent predator-prey relationships for species whose primary residence is Lower Fox River. Therefore, a conceptual food web for fish species resident in the last seven miles of the Lower Fox River would permit further evaluation of the hypothesis that a resident population exists.

In its current form, the GBFWM framework was determined to be a reasonable representation of the environmental processes targeted for modeling. The single recommendation for modifying the model framework does not alter the fundamental concepts incorporated into the model framework. Therefore, the existing framework is

considered applicable to modeling PCB bioaccumulation in fish in both Green Bay and the Lower Fox River.

12.2 Hindcast Simulation

One intended use of a model to predict contaminant concentration is fish tissues is a long-term hindcast simulation. As with any food web model simulation, development of a long-term food web model hindcast simulation requires that exposures be input and a representative food web specified. In this application, it is assumed that exposures will be computed by a coupled suite of water and sediment quality models for the Lower Fox River and Green Bay. Given that Great Lakes fisheries may have been significantly altered over time due to invasions of exotic species that affected predator-prey relationships and the presence of some fish species, it is possible that a food web based on contemporary conditions may not accurately represent the long-term historical food web.

Where possible, food webs representative of historical conditions could be constructed if data exist to define conditions. In the absence of such historical data, the predator-prey relationships specified in the contemporary conceptual food web model would remain unchanged for the hindcast period. However, if the contemporary food web is used, the uncertainty associated with model predictions may increase. In this instance, the uncertainties implicit in a long-term simulation should be considered during the interpretation of food web model hindcast results. Specifically, it should be recognized that model accuracy may decrease if the historical food web differs from the food web represented in the model.

12.3 Forecast Simulation

Another intended used of a model to predict contaminant concentration is fish tissues is a long-term forecast simulation. Again, as with any food web model simulation, development of a long-term food web model forecast simulation requires that exposures be input and a representative food web specified. In this application it is again assumed that exposures will be computed by a coupled suite of water and sediment quality models for the Lower Fox River and Green Bay. It is also further assumed that the predator-prey relationships specified in the contemporary food web would remain unchanged for the forecast period.

Again, given that Great Lakes fisheries structures may change over time, the uncertainties implicit in a long-term simulation should be considered during the interpretation of food web model forecast results. Specifically, it should be recognized the accuracy of predicted future fish tissue contaminant concentration trends may decrease if the underlying structure of the food web in the future differs from contemporary conditions.

12.4 Natural Resource Damage Assessment and Remediation Alternate Evaluation

NRDA or remedial alternative evaluation endpoints may benefit from predictions of PCB bioaccumulation in benthic, as well as pelagic, food webs. In its present form, the GBFWM does not explicitly include a representative food web for benthic-feeding fish which may include, for example, carp. This potential limitation could be addressed by adding a representative benthic food web to the existing GBFWM.

13. Recommendations

The following modifications to the GBFWM in the areas of conceptual food webs, model framework, translation of the conceptual food web to numerical model, and model calibration are suggested to improve use of the model for NRDA and remedial planning in both Green Bay and Fox River. The basis for these modifications is provided in the critique of each model component.

13.1 Modification of the Conceptual Food Webs

The conceptual food web of the existing GBFWM was developed from data collected during the GBMBS and other historical or literature data sources. Since then, a number of studies designed to characterize the habitat and ecology of the Lower Fox River and Green Bay have been completed. The results of these studies should be considered to: 1) determine if the existing conceptual pelagic food web is representative of conditions in the last 7 miles of the Lower Fox River and Green Bay; 2) construct a representative conceptual benthic food web for the river and the bay; and 3) construct pelagic and benthic food webs for the river areas between Lake Winnebago and the DePere Dam. Specifically, the number and nature of species representing the forage base of target top predators (e.g., walleye and brown trout) should be evaluated. Especially for areas upstream of the DePere Dam, data from habitat characterization and fisheries structure studies should also be considered to determine if other predator fish species such as northern pike, smallmouth bass, or yellow perch represent an ecologically important resource for NRDA or remedial alternative evaluations.

13.2 Modification of the Model Framework

The number of sediment temporal histories allowed in the current GBFWM framework should be increased. This proposed modification to the framework will allow more convenient application of the model to areas where multiple habitats exist without altering the underlying conceptual basis of the framework. It will also permit representation of a conceptual food web in which predator species eat several prey species, each of which eat from unique sediment sources (as may be the case in Fox River). This specific scenario cannot be represented in the context of the existing model framework, and cannot be simulated by multiple additive simulations.

The use of Equation 1 to interpolate body weight in between time breaks can skew the body weight profile, particularly when only two time breaks define the body weight history. The effects of a skewed body weight history will influence the selection of input coefficients during model calibration when within-year model calculations are compared to within-year measured data (i.e., comparing summer average model

calculations to summer average measured data). Therefore, the use of linear interpolation is recommended over the use of exponential interpolation.

13.3 Modification to the Translation from Conceptual Food Web to Numerical Model

The body weight histories for alewife, gizzard shad, and rainbow smelt specified in the model input should be based on the analysis of measured body weights rather than idealized body weights. The analyses performed with idealized body weights generally result in an inaccurate representation of the measured body weight data for these species.

Unless documentation supporting the lipid fractions specified in the model input is provided, the lipid fractions should be modified as suggested in Section 9

Unless additional documentation supporting the exposure concentrations specified in the model input is provided, the exposure should be modified as suggested in Section 9.

13.4 Modification of the Model Calibration

Both model calculations and measured data on an age-segregated basis should be compared.

Consider running the model with temporally variable (vs. steady-state) exposure concentrations as a means of model verification, provided, of course, that recent data indicate a temporal trend. The current method of model calibration does not test the ability of the model to calculate changes in PCB body burden in response to temporally variable exposure concentrations. Without such model verification, the usefulness of the model will be limited to similar steady-state simulations with new exposure concentrations that reflect the long-term projection scenarios. The most reasonable approach to verifying the model is to run it for the period 1989–1995. Data collected in 1989 would be used as the basis of initial conditions. Data collected in 1995 would be used for model calibration. However, determination of the usefulness of the 1995 data for calibration purposes is outside the scope of this evaluation and should be addressed during development of the dynamic modeling approach.

14. Conclusions

The GBFWM constitutes a solid foundation for evaluating the bioaccumulation of PCBs in fish tissue in Green Bay. Therefore, the existing model need not be abandoned. However, the existing GBFWM requires some modification before it can be used for the purposes of NRDA and remedial alternative evaluation in either Green Bay or Fox River. The GBFWM, in its existing form, is only relevant for pelagic food webs that occur in selected portions of Green Bay. It does not account for some key species and sediment-based food webs predominant in Green Bay and the Fox River. Adaptation of the model to sediment-based food webs that occur in the Fox River is required before the model will be useful for evaluating potential restoration options under the NRDA.

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Appendix A

Email Communications

From: Tad Slawecki [tad@limno.com]
Sent: Wednesday, November 12, 1997 11:25 AM
To: dodgel@exponent.com
Cc: vbierman@limno.com; Gary Bigham
Subject: Food chain model

Laura,

The attached file FDCHAIN.ZIP contains source code, example inputs, and documentation as received from Hydroqual by LTI. Please let me know if you have any questions.

Tad

==========

Tad Slawecki tslawecki@limno.com
Computer Manager (313) 332-1200

Limno-Tech, Inc. o 501 Avis Drive o Ann Arbor, MI 48108

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Information about this message...


fdchain.zip

From: dg@indimax.hydroqual.com
Sent: Tuesday, January 06, 1998 3:40 PM
To: dodgel@pti-enviro.com
Cc: dbeltman@habaco.com
Subject: Green Bay data analysis fish ages

Laura -

Here is information on age classes in the data:

In the Green Bay Mass Balance Study (GBMBS), age of the fish caught was handled as described below.

DATABASE
The database contained the following information on fish age.
brown trout and walleye: actual age of the fish was determined. The age given is age as of last "birthday", meaning a 3 year old fish is actually between 3 and 4 years old.
alewife and rainbow smelt: determined to be "young-of-the-year" (less than one year old) or mature (greater than one year old).
gizzard shad: only young-of-the-year were caught

BIOACCUMULATION FACTORS
Bioaccumulation factors were calculated using fish of the following ages:
brown trout: ages 2,3,4
walleye: ages 3,4,5,6
alewife: mature
rainbow smelt: mature
gizzard shad: young-of-the-year

TROPHIC TRANSFER FACTORS
The trophic transfer factor = the ratio of concentrations of predator/prey. The predator concentrations were determined using the same age classes as for the bioaccumulation factors (see above). The prey age classes were determined as follows:

For the trophic transfer factors of walleye and brown trout, only adult rainbow smelt and alewife were used.
For the trophic transfer factor of rainbow smelt, young-of-the-year and adult alewife were used.

David

From: dg@indimax.hydroqual.com
Sent: Monday, January 05, 1998 4:00 PM
To: dodgel@pti-enviro.com
Cc: dbeltman@habaco.com
Subject: Green Bay data

Dear Laura,

Enclosed please find a set of files containing the data used in the model recalibration. The file Read.me (ASCII, included below) contains a full description of the data, which I think you will understand. If you have questions, please call anytime.

David
Here are the following files:
Read.me
Data.zip
PKUNZIP.EXE
PKZIP.EXE

FILE Read.me

****
********** GENERAL INFO **********
****

Contents of disk:

1) Read.me (this file you are currently reading)
2) Data.zip - all data files are contained within "Data.zip"
3) pkunzip.exe - will extract data files:
(move to working directory and type "pkunzip Data")

Notes:

1) Any field which has "-999" means data not available
2) In some cases, congeners could not be isolated in the lab. In these cases, the congeners within the peak were reported as a sum of all co-eluting congeners within that peak. The field "cong1" is the lowest IUPAC number in the co-elution and "lgkow" is the average log(Kow) for the congeners within that peak. The file "cong.dat" is a table which reports all congeners within one peak.
3) All files have a field called "cg80". This field was used as a mask for quality control. Many congeners were at or below the detection limit in the water samples. Because of the uncertainty in the actual concentrations for these congeners, those data that had 80% or more of the water samples at or below the detection limit were removed from many of our analyses. These congeners are marked with "888" in the cg80 field.

4) Note that plankton (phyto- and zoo-) BAF's and TTF's were calculated for each matched sample, then an average for each congener within a zone was taken. Therefore, dividing the plankton concentration by the water (or prey) concentration in these files will NOT match exactly the BAF (or TTF) in these files.
5) Format and read statements are written in GDP, but can be easily translated to standard FORTRAN.
NOTE: in order to keep formats consistent, five digits past the decimal were printed for all values. However, all values have only FOUR significant digits.
6) If a concentration in the plankton was reported as zero (rather than flagged as less than detection limit), this zero value was included in all analyses. Through our own QA/QC and discussion with others involved in the Green Bay Mass Balance Study, this was determined to be the appropriate way to handle these data.

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********** BIOACCUMULATION FACTORS **********
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All files to be read have the same format:
ifor:(2f6.0,f9.3,2f15.5);
read:cong1,cg80,lkow,vbiota,baf,/'FILENAME'/;
cong1 - congener numbers, total PCB = 500
cg80 - congener numbers where those at <80% detect in water are flagged with "888"
lkow - Hawker and Connell Log(Kow) values, Log(Kow) for total PCB = "-999"
vbiota - lipid-based concentration in the biota [ug/kg]
baf - bioaccumulation factor = (vbiota/cd)

FILENAME: all filenames are coded as follows
FILENAME = 'bafSPECZONE.crz'

SPEC: bt = brown trout
we = walleye
rs = rainbow smelt
al = alewife
zp = zooplankton
ph = phytoplankton

ZONE: 3a = zone 3A
3b = zone 3B
4 = zone 4

** zooplankton and phytoplankton files have a "4" at the end to indicate
matched samples, with zoo on lipid basis and phyto on oc basis
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****
********** TROPHIC TRANSFER RATIOS **********
********** (TROPHIC TRANSFER FACTORS) **********
****

****
Predator-prey preferences:
****
1. Walleye, adult
Preferences used : rainbow smelt = 0.4
alewife = 0.6

2. Brown trout, adult
Preferences used : rainbow smelt = 0.5
alewife = 0.5

3. Rainbow smelt, adult
Preferences used : zooplankton = 0.8
alewife = 0.2

4. Alewife, adult
alewife diet is constant, all zooplankton
Preferences used : zooplankton = 1.0
****
****

All files to be read have the same format:
ifor:(2f6.0,f9.3,3f15.5);
read:cong1,cg80,lkow,vpred,vprey,ttf,/'FILENAME'/;
cong1 - congener numbers, total PCB = 500
cg80 - congener numbers where those at <80% detect in water are flagged
with "888"
lkow - Hawker and Connell Log(Kow) values, Log(Kow) for total PCB = "-999"
vpred - lipid-based concentration in the predator [ug/kg]
vprey - lipid-based concentration in the prey [ug/kg], where prey is defined
by the predator-to-prey preferences given above
ttf - trophic transfer factor = (vpred/vprey)

FILENAME: all filenames are coded as follows
FILENAME = 'ttfSPECZONE.dat'

SPEC: bt = brown trout
we = walleye
rs = rainbow smelt
al = alewife
zp = zooplankton

ZONE: 3a = zone 3A
3b = zone 3B
4 = zone 4

** zooplankton files have a "4" at the end to indicate matched samples,
with zoo on lipid basis and phyto on oc basis

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****
********** WATER CONCENTRATIONS **********
****

All files to be read have the same format:
ifor:(2f6.0,f9.3,f15.5);
read:cong1,cg80,lkow,cd,/'FILENAME'/;
cong1 - congener numbers, total PCB = 500
cg80 - congener numbers where those at <80% detect in water are flagged
with "888"
lkow - Hawker and Connell Log(Kow) values, Log(Kow) for total PCB = "-999"
cd - dissolved water column concentration [ng/L]

FILENAME: all filenames are coded as follows
FILENAME = 'watZONE.crz'

ZONE: 1 = zone 1
2a = zone 2A
2b = zone 2B
3a = zone 3A
3b = zone 3B
4 = zone 4

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********** FISH CONCENTRATIONS **********
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All files to be read have the same format:
ifor:(2f6.0,f9.3,3f15.5);
read:cong1,cg80,lkow,vlip,vwet,plip,/'FILENAME'/;
cong1 - congener numbers, total PCB = 500
cg80 - congener numbers where those at <80% detect in water are flagged with "888"
lkow - Hawker and Connell Log(Kow) values, Log(Kow) for total PCB = "-999"
vlip - lipid-based concentration in the biota [ug/kg]
vwet - wet weight-based concentration in the biota [ug/kg]
plip - average percent lipid

FILENAME: all filenames are coded as follows
FILENAME = 'concSPECZONE.dat'

SPEC: bt = brown trout
we = walleye
rs = rainbow smelt
al = alewife

ZONE: 1 = zone 1
2a = zone 2A
2b = zone 2B
3a = zone 3A
3b = zone 3B
4 = zone 4

****
****
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Data.zip


PKUNZIP.EXE


PKZIP.EXE