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Forecasting Fish Biomasses, Densities, Productions, and Bioaccumulation Potentials of Mid-Atlantic Wadeable Streams

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ABSTRACT

Regional fishery conditions of Mid-Atlantic wadeable streams in the eastern United States are estimated using the Bioaccumulation and Aquatic System Simulator (BASS) bioaccumulation and fish community model and data collected by the US Environmental Protection Agency's Environmental Monitoring and Assessment Program (EMAP). Average annual biomasses and population densities and annual productions are estimated for 352 randomly selected streams. Realized bioaccumulation factors (BAF) and biomagnification factors (BMF), which are dependent on these forecasted biomasses, population densities, and productions, are also estimated by assuming constant water exposures to methylmercury and tetra-, penta-, hexa-, and hepta-chlorinated biphenyls. Using observed biomasses, observed densities, and estimated annual productions of total fish from 3 regions assumed to support healthy fisheries as benchmarks (eastern Tennessee and Catskill Mountain trout streams and Ozark Mountains smallmouth bass streams), 58% of the region's wadeable streams are estimated to be in marginal or poor condition (i.e., not healthy). Using simulated BAFs and EMAP Hg fish concentrations, we also estimate that approximately 24% of the game fish and subsistence fishing species that are found in streams having detectable Hg concentrations would exceed an acceptable human consumption criterion of 0.185 μg/g wet wt. Importantly, such streams have been estimated to represent 78.2% to 84.4% of the Mid-Atlantic's wadeable stream lengths. Our results demonstrate how a dynamic simulation model can support regional assessment and trends analysis for fisheries. *Integr Environ Assess Manag* 2016;12:146–159. Published 2015 SETAC. This article is a US Government work and, as such, is in the public domain in the United States.

Keywords: Bioaccumulation Biomass Fish Production Simulation modeling

INTRODUCTION

The United Nations' Millennium Ecosystem Assessment (2005) identified commercial, recreational, and subsistence fisheries and other nonexploited fish communities as major providers of ecosystem services that contribute to the health and well-being of humans on local, regional, and national scales. Fisheries (used here to encompass exploited and nonexploited fish communities) provide not only food and recreation to humans but also the resource base for many culturally valued species of piscivorous wildlife. The condition of fisheries is also used as a primary indicator of the condition of other culturally valued habitats and ecosystems (e.g., estuaries, the Great Lakes, and state or national parks) and of quality and quantity of water supplies for local and regional populations.

Although evaluating fishery conditions for an individual water body has value, regional assessments are even more valuable for resource managers concerned with evaluating or forecasting the status and trends of fisheries exposed to regional stressors such as changing precipitation and temperature patterns, regional water management (e.g., interbasin water transfers, reservoir management, and municipal water withdrawals), land use change, atmospheric transport and deposition of contaminants (e.g., Hg), and river basin-wide contaminated sediments (e.g., polychlorinated biphenyls [PCBs] and legacy organochlorine pesticides). Although the utility of regional monitoring data to assess current conditions of fisheries should not be underestimated, such data often have serious shortcomings for assessing fishery trends and expected responses to changing regional stressors. Two factors, which depend on available financial and staff resources, contribute to this assertion. First, multiple intrayear sampling of multiple fisheries over successive years is the exception, not the rule. Second, is the inability to monitor adequately all of the most important biological and physical factors that affect regional fisheries. Fortunately, many important fishery trends can be assessed using simulation models that are initialized and corroborated by monitoring data. After such models are developed and validated, researchers and resource managers can forecast expected regional trends not only from existing conditions but also under different future scenarios that could include regional climate change, habitat restoration activities, projected land use changes, pesticide use, or toxic chemical discharges.

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In this study, we use the Bioaccumulation and Aquatic System Simulator (BASS) simulation model (Barber 2008a, 2012) to demonstrate how a fish simulation model can be integrated with field monitoring data to forecast average annual fish biomasses and population densities, annual fish productions, and expected patterns of methylmercury (MeHg) and legacy PCBs bioaccumulation in Mid-Atlantic wadeable streams. These metrics, which were selected based on their direct and obvious connection to important ecosystem services provided by the region's wadeable streams, are also compared to other appropriate field studies. Using forecasted fish biomasses, population densities, and production values, we also develop a methodology to assess the proportion the region's wadeable streams that would be expected to support healthy fish communities. We then demonstrate how regional fish biomasses might be expected to respond to maximal habitat restoration activities. Last, we demonstrate how our simulated bioaccumulation factors can be used to back-calculate unmonitored Hg water concentrations from monitored concentrations in small nongame fish. Using these water concentrations, we then estimate the proportion of game fish and subsistence fishing species expected to exceed an acceptable human consumption criterion, given that such fish inhabit streams whose nongame fish have detectable whole-body concentrations of Hg.

MATERIALS AND METHODS

The Mid-Atlantic Study Region—description

This case study focuses on the Mid-Atlantic Region (MAR) that encompasses all of the states of Delaware, Maryland, Pennsylvania, Virginia, and West Virginia (i.e., the US Environmental Protection Agency's [USEPA] Region 3) and the portions of New Jersey containing the Delaware River basin, of New York containing the Susquehanna and Allegheny River basins, and of North Carolina containing the Chowan-Roanoke and Neuse-Pamlico basins (Figure 1). This region has a total land area of approximately 393 000 km^2 and a resident population of more than 30 million people.

Using Indices of Biological Integrity (IBIs) and data collected by its Environmental Monitoring and Assessment Program (EMAP), the USEPA concluded that of the 94% of Mid-Atlantic wadeable streams that had detectable and/or catchable fish, 22% had fish communities in good condition, 45% had fish communities in marginal condition, and 33% had fish communities in poor condition (USEPA 2006). Because MAR fish communities are exposed to numerous stressors that include sedimentation due to logging, mining, agriculture, and road construction; stream acidification; contamination by heavy metals and persistent legacy organic pollutants; and water quality degradation due to agriculture fertilizers and pesticides in both overland and subsurface flows (USEPA 2000, 2006), the result of this assessment is not particularly surprising. Although these stressors rarely cause acute fish mortality, they can alter long-term survival, reproduction, and bioenergetics of individual fish and their populations that, in turn, can lead to significant changes in the structure and function of fish communities at large.

Using a subset of the EMAP MAR streams, Lazorchak et al. (2003) estimated the percent of the region's stream lengths expected to harbor nongame fish with whole-body concentrations of Hg, PCBs, or legacy organochlorine pesticides exceeding EMAP's detection limits (i.e., 0.025 μg/g wet wt for Hg and 0.002 μg/g wet wt for pesticides and PCBs) and the percent of stream lengths expected to represent a dietary exposure threat to piscivorous wildlife. Based on these data, Lazorchak et al. (2003) estimated that 78.2% to 84.4% of the MAR wadeable stream lengths held nongame fish with detectable whole-body concentrations of Hg. Applying an approach described in the USEPA Great Lakes Water Quality Initiative (USEPA 1995), Lazorchak et al. (2003) also estimated maximum exposure concentrations (MEC) of Hg in nongame fish that would still support viable kingfisher *Ceryle alcyon*, mink *Mustela vison*, and otter *Lutra canadensis* populations. Using these MECs, they then estimated that 71.6%, 24.7%, and 11.2% of the MAR stream lengths possessed nongame fish whose whole-body Hg concentrations exceeded MECs for kingfishers, minks, and otters, respectively.

The BASS bioaccumulation and community model—description

BASS is a generalized Fortran 95 simulation model that predicts chemical bioaccumulation and individual and population growth dynamics of an age-structured fish community using the temporal and spatial resolution of a day and a hectare, respectively. Each species in the community interest is represented by series of cohorts (i.e., fish that are recruited in the community at the same time or date). The community's food web is specified by defining one or more foraging classes for each fish species based on their body weight, body length, or age and time of year. The dietary composition of each foraging class is then specified as a combination of benthos, incidental terrestrial insects, periphyton, phytoplankton, zooplankton, and/or one or more fish species, including its own. For piscivorous cohorts, the consumption of forage fishes is assumed to be generally size-dependent (Mittelbach and Persson 1998; Juanes 2003). Competition for available food is modeled using guild-specific foraging queues that schedule the sequential feeding of cohorts based on their body sizes. Cohorts that are classified as being primarily piscivores, benthivores, or insectivores are queued in descending order of their lengths; thus, large-bodied cohorts feed before small-bodied ones. Cohorts that are classified as being primarily planktivores are queued in ascending order of their lengths that results in small-bodied cohorts feeding before large-bodied ones. Because BASS also allows for piscivores to switch to benthos and terrestrial insects and for benthivores to switch to zooplankton and terrestrial insects when their preferred prey is unavailable, the planktivore queue feeds before the benthivore queue that feeds before the piscivore queue. As each cohort feeds, the available food remaining for the remaining cohorts in the queue is reduced, which in turn potentially reduces their realized consumption. Cohorts also compete with one another for space via a biomass-based community carrying-capacity algorithm. In addition to simulating the bioaccumulation of chemical pollutants, BASS can also simulate growth and population dynamics of fish assemblages exposed to non-chemical stressors such as habitat degradation due to watershed land-use modifications or changing in-stream physical habitats.

BASS simulates the biomass, population, production, and bioaccumulation dynamics of a user-specified fish community by simultaneously solving the following system of differential equations for all cohorts of all species:

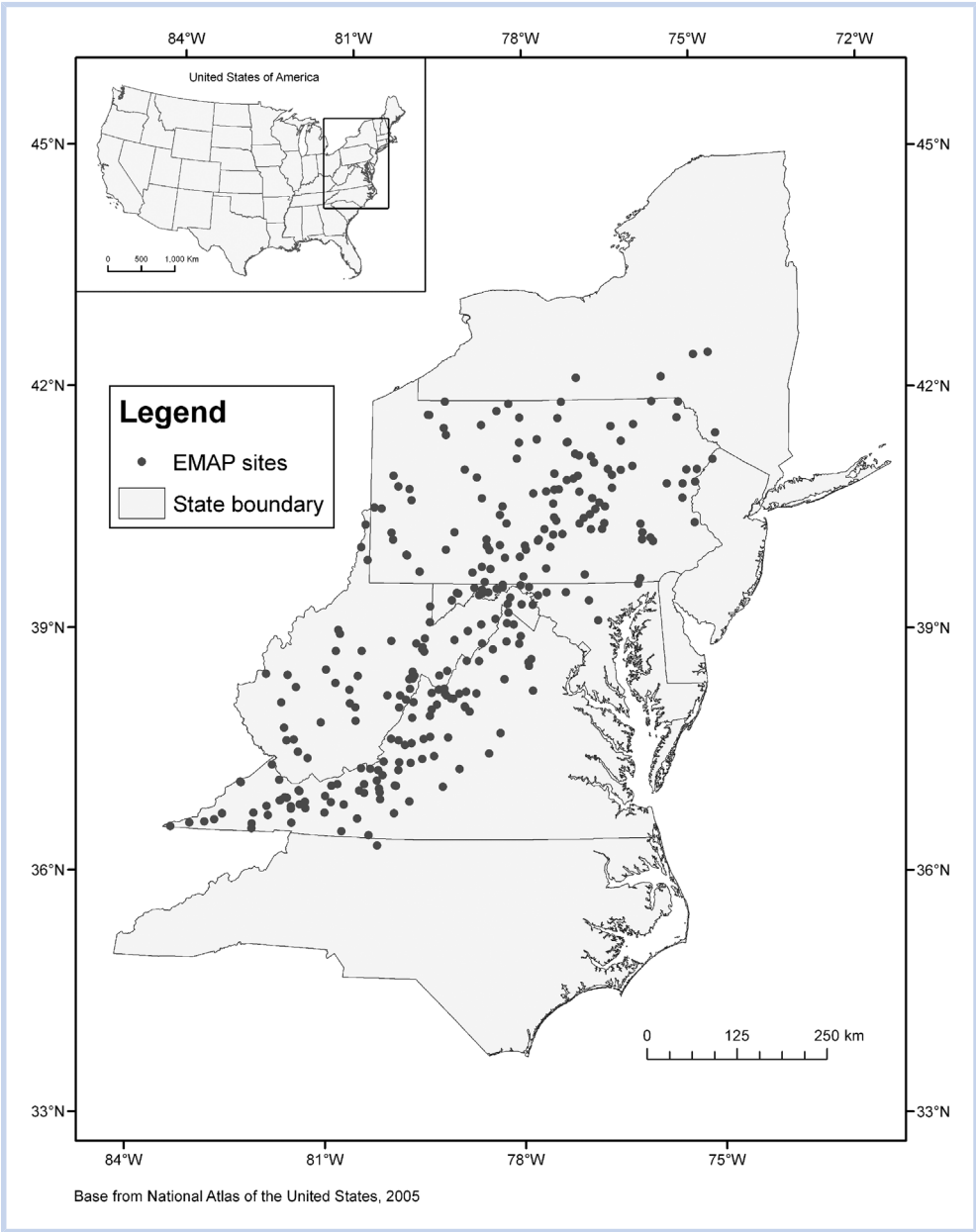

Figure 1. Map of the Mid-Atlantic Region (MAR) study area. Dots locate the EMAP wadeable stream sites analyzed herein.

$$\frac{dB_f}{dt} = U_g + U_i - X_g - X_i - Y_m, \qquad \text{(Eqn. 1)}$$

$$\frac{dW_d}{dt} = F - E - R - \mathrm{EX} - \mathrm{SDA}, \text{ and} \qquad \text{(Eqn. 2)}$$

$$\frac{dN}{dt} = -M_b - M_{cc} - M_p. \qquad \text{(Eqn. 3)}$$

In these equations, B_f and W_d denote the contaminant body burden (μg/fish) and dry body weight (g dry wt/fish) of the cohort's average individual, respectively, and N denotes the cohort's population density (fish/ha). In Equation 1, U_g and U_i denote the gross chemical uptake across the fish's gills from the water and across its intestine from food, respectively; X_g and X_i denote the chemical excretion across its gills to the interlamellar water and across its intestine to the feces, respectively; and Y_m denotes the chemical's biotransformation or metabolism. The cohort's whole-body concentration C_f (μg/g wet wt), which is used to formulate the fluxes on the right-hand side of Equation 1 using well-established thermodynamic principles, is calculated algebraically as the ratio of the fish's body burden to its wet body weight $W_w = W_d/f_d$ where f_d is the fraction of the fish's live weight that is dry organic matter and ash. In Equation 2, F, E, R, EX, and SDA denote the fish's feeding, egestion, routine respiration, excretion, and specific dynamic action (i.e., the additional respiratory expenditure in excess of R required to assimilate food), respectively, in units of g dry wt/d. Although many physiologically based models simulate fish growth in terms of energy content (kcal/fish) and fluxes (kcal/d) (Ney 1993; Chipps and Wahl 2008), Equation 2 is analogous to these models because energy densities of fish depend on their dry weight (Hartman and Brandt 1995; Schreckenbach et al. 2001). Finally, in Equation 3, M_b is the cohort's baseline self-thinning mortality that includes both

physiological mortality and emigration, M_{cc} is the cohort's carrying capacity mortality due to competition for space, and M_p the cohort's predatory mortality. Because the influence of discrete (i.e., noncontinuous) demographic processes (e.g., recruitment and mortalities due to a cohort attaining its maximum age, critical body burden, or minimum condition factor [i.e., the ratio of the cohort's actual weight to its expected weight based its body length that can decrease due to insufficient consumption or excessive metabolic demands]) on population dynamics are accounted for by directly adjusting the cohort's population density at the start of the next day of simulation following the event of concern, terms for these processes do not appear on the right-hand side of Equation 3. BASS simulates each species' recruitment using a spawners' abundance model. All cohorts that attain their user-specified length-at-maturation by the start of their user-specified spawning period (e.g., May–June) spawn and contribute to the creation of a new young-of-year cohort. The initial population density of this cohort is calculated to be fraction (ρ) of the total biomass of the species spawning cohorts divided by the average body weight ($\widehat{W}_w$ g wet wt/fish) of new recruits. Although BASS assumes by default that $\rho = 0.2$ and that $\widehat{W}_w = 0.25$, users can specify these parameters as needed. Even though immigration can be a significant process in determining population sizes, it is not explicitly modeled in BASS. Readers interested in reviewing how these equations are formulated and parameterized in BASS should consult the model's user manuals (Barber 2008a, 2012). Readers interested in a detailed analysis of how BASS's bioconcentration and biomagnification algorithms compare to those used by other bioaccumulation models should consult the review articles by Barber (2003, 2008b).

BASS inputs: Fish physiological and ecological parameters

An extensive database supplement has been compiled for BASS in concert with its code development and applications (Barber 2006). Using this compilation, an auxiliary parameterization program was developed to estimate the bioenergetic, ecological, and morphometric parameters required by BASS using species, genus, or family-specific data (Barber 2008a, 2012). When these taxonomic levels of data are unavailable, however, this parameterization software uses interspecific averages calculated from BASS's database supplement. A significant feature of this program is its ability to estimate long-term specific growth rates [$\gamma = W_w^{-1}(dW_w/dt)$] using observed species- or genus-specific life history data, to calibrate those rates for assumed temperature dependencies and reproductive losses, and to back-calculate expected feeding rates [i.e., $\widehat{F} = \varphi_1 W_w^{\varphi_2} \exp(\varphi_3 T)$ where T is the ambient water temperature in Celsius] using a modification of the method outlined by Barber (2003). The details of these procedures are summarized in our Supplemental Data. We used this program to assign all bioenergetic, ecological, and morphometric parameters required by BASS to simulate the MAR fish communities considered herein. Additional MAR-specific data required by BASS (e.g., fish lipid fractions, habitat suitability indices, etc.) are also described in our Supplemental Data. All BASS input files used for our study can be obtained from the corresponding author by request or downloaded from the USEPA's Center for Exposure Assessment Modeling (CEAM) Web site (http://www2.epa.gov/exposure-assessment-models/bass).

BASS inputs: Fish initial conditions and nonfish biomass

From 1993 to 1998, EMAP compiled extensive MAR data sets on the fish abundance of 670 stream reaches, on the benthic macroinvertebrate (BMI) densities of 644 stream reaches, and on periphyton standing stocks of 468 MAR stream reaches. The methods used to compile these data sets are summarized in our Supplemental Data. We used these data to estimate not only the initial conditions for Equations 2 and 3 but also the biomasses of BMI and periphyton on which MAR stream fishes feed. To accomplish this, we had to address 3 interrelated data issues. First, how can a complete complement of fish, BMI, and periphyton data be estimated for sites having only partial data? Second, what criteria can be used to ensure, for modeling purposes, that all data types—observed or estimated—are ecologically and quantitatively consistent? Third, given a complete complement of measured or estimated biological data, what is the availability of physical stream data (e.g., habitat metrics and monthly water depths and temperatures) needed by BASS?

To address these questions, EMAP fish abundance data were first converted into densities (fish/ha) using reported mean stream widths and reach lengths, and then converted into live biomasses (g wet wt/ha) using an algorithm based on the assumptions that annual fish recruitment is constant (or fluctuating around a long-term mean) and that all cohorts and/or age classes of fish exhibit self-thinning (i.e., $\bar{N} \propto \bar{W}_w^{-b}$ where $\bar{N}$ and $\bar{W}_w$ denote the annual mean population density and wet body weight of a cohort, respectively); see Rashleigh et al. (2004) for details. Observed BMI densities were converted to dry biomasses (g dry wt/m^2) using the taxonomic specific conversion factors reported by Rashleigh et al. (2004). Missing BMI and periphyton biomasses were estimated using the BMI–fish and periphyton–BMI biomass ratios described next.

To determine these biomass ratios, we first calculated the expected annual production (g dry wt $\times$ m^{-2} $\times$ y^{-1}) of fish and BMI for the 408 EMAP sites that had a complete complement of observed fish, BMI, and periphyton data using regressions reported by Plante and Downing (1989) and Randall et al. (1995). Sites having predicted BMI-to-fish production ratios greater than 0.5 were then assumed to be appropriate for determining the required biomass ratios. This selection criterion is based on the bioenergetic assumption that a stream's combined estimated production for BMI and periphyton should be at least greater than its estimated fish production. For simplicity, however, we assumed that streams having estimated BMI-to-fish production ratios greater than 0.5 also had fish, BMI, and periphyton biomasses that were logically consistent with each other from an ecological production perspective. Whereas calculated BMI-to-fish biomass ratios at these sites ranged from 1.73×10^{-3} to 37.0 g dry wt BMI/g wet wt fish (mean [$\bar{x}$] = 0.428; median [$\tilde{x}$] = 0.0476; standard deviation [SD] = 2.29; sample size [n] = 324), the calculated periphyton-to-BMI biomass ratios ranged from 3.47 to 9.55×10^4 g dry wt periphyton/g dry wt BMI ($\bar{x} = 1610$; $\tilde{x} = 203$; SD = 6970; $n = 324$). Because of the large coefficients of variation associated with these ratios, we assumed that median BMI–fish and periphyton–BMI biomass ratios would better predict missing BMI and periphyton than their means, and estimated such biomasses accordingly. Because we assumed that the biomasses of zooplankton and phytoplankton in MAR streams were insignificant in comparison to those of benthos and periphyton, respectively, we

assigned zero biomasses to both zooplankton and phytoplankton. We also assumed that the biomass of incidental terrestrial insects in all MAR streams was approximately 3% of their benthos biomass. Although BASS has the flexibility to simulate the biomasses of benthos, periphyton, phytoplankton, and zooplankton, for this study, we used BASS's alternative mode of simulation that treats these nonfish biomasses as external forcing functions. In this mode, BASS uses user-specified nonfish biomasses and the simulated biomasses of all fish cohorts that can serve as forage fish to set daily upper limits to the realized consumption rates of the all fish cohorts within the community of concern.

The initial conditions for Equations 2 and 3 were estimated using the aforementioned auxiliary BASS software that converts a species' total biomass into cohort body weights and population densities using an algorithm described in BASS user manuals (Barber 2008a, 2012).

BASS inputs: Assumed MeHg and PCB exposures

For this study, we assumed that each selected fish community was exposed to a constant, freely dissolved MeHg concentration equal to 0.1 ng/L and to a constant, freely-dissolved total PCB concentration equal to 0.1 ng/L treated as an Arochlor 1254 mixture (i.e., 11% tetra-CB, 49% penta-CB, 34% hexa-CB, and 6% hepta-CB). These exposures were assumed to estimate expected achievable bioaccumulation factors (BAF) and biomagnification factors (BMF) rather than actual whole-body concentrations for MAR stream fishes, because BAFs and BMFs are independent of water concentrations, provided they are constant (Barber 2008b). Exposure concentrations in BMI, drifting macroinvertebrates, and periphyton were calculated using empirical or quantitative structure activity relationship (QSAR) BAFs. In particular, MeHg BAFs were estimated using data reported by Loftus et al. (1998), and BAFs for the PCB homologues were estimated using QSAR regressions reported by Arnot and Gobas (2006), assuming average $\log_{10}$ transformed octanol–water partition coefficients (i.e., $\log_{10} K_{OW}$) equal to 5.91, 6.34, 6.75, and 7.19 for tetra-CB, penta-CB, hexa-CB, and hepta-CB, respectively. We also assumed that the PCBs of concern were not metabolized by any MAR fish species.

BASS: Selection of EMAP streams for study

Using the aforementioned median biomass ratios to estimate missing BMI and periphyton biomasses and requiring that all study sites have estimated BMI–fish production ratios greater than 0.5, we obtained a potential simulation set of 462 EMAP stream reaches. Of these sites, 377 sites had the necessary fish habitat and physical water data needed to parameterize and execute BASS. Of this subset, 352 sites attained dynamic steady-state biomasses (i.e., repeating annual biomass cycles as illustrated by Supplemental Data Figures S1, S2, and S3) by the end of our 25-year spin-up simulations that were designed to eliminate transient dynamics and to reflect long-term, community dynamics. We used BASS outputs for the last year of simulation of these 352 sites to estimate the MAR's annual mean fish biomasses and population densities, annual fish production, and annual mean fish bioaccumulation potentials for methylmercury and legacy PCBs. Table S1 summarizes the 144 fish species found in these streams, and Table S2 summarizes salient features of these streams reported by EMAP.

BASS: Selection of outputs for analysis

Auxiliary subroutines were added to BASS to generate annual means and integrals of selected primary and secondary simulation variables that were sampled daily for the last year of all simulations. Simulation variables selected to assess each stream's ecological structure and function included each cohort's population density (N), dry and wet weight biomasses ($B_{dc} = N \times W_d$ and $B_{wc} = N \times W_w$, respectively), dry weight consumption ($F_c = N \times F$), and dry and wet weight production ($P_{dc} = N \times [dW_d/dt]$ and $P_{wc} = N \times [dW_w/dt]$, respectively). Each cohort's individual-based dry weight consumption (F), specific growth rate ($\gamma = W_d^{-1} \times [dW_d/dt] = W_w^{-1} \times [dW_w/dt]$), and trophic position (TP), which was simulated using a model similar to that proposed by Hesslein et al. (1993) (see Barber [2012], Section 2.8. Modeling stable isotopes and trophic position), were also analyzed. Using these data, mean biomasses, mean population densities, annual consumption, and annual production were then calculated for each species and total fish.

The bioaccumulation potentials of MeHg and PCBs in MAR fish were assessed using BASS's predicted cohort bioaccumulation factors ($BAF_f = C_f/C_w$ where C_w is the freely dissolved water concentration of the chemicals of concern) and cohort biomagnification factors ($BMF_f = C_f/C_p$ where C_p is the diet-weighted average chemical concentration in the cohort's prey).

Although basic statistics (e.g., mean, median, SD, etc.) were calculated for all selected variables, a subset of them that were expected to have strong functional dependencies on fish body weight, biomass, or trophic position or on $\log_{10} K_{OW}$ were also summarized using simple and multiple linear regressions. Table 1 summarizes these regressions that are referenced by their indicated ID number (e.g., Regression 1, etc.).

BASS: Sensitivity analysis of fishery outputs

The long-term specific growth rates of the 144 species of fish considered in this study are arguably some of BASS's most critical input parameters. These rates not only determine the baseline or self-thinning mortality rates of cohorts (Peterson and Wroblewski 1984; McGurk 1993, 1999) but also are used by BASS's parameterization software to back-calculate expected feeding rates for BASS's allometric feeding model. Changing a species' long-term specific growth rates will therefore impact not only the population dynamics of all of its cohorts but also realized rates of ingestion and growth by those cohorts. Altered realized growth rates, in turn, impact the size-dependent competition between cohorts for available prey, the predatory mortalities of forage fish cohorts, and species reproduction because only cohorts that have attained their minimum length at maturity during their designated spawning period are allowed to reproduce. As previously mentioned, our Supplemental Data summarizes the procedure used by BASS's parameterization program to estimate long-term specific growth rates using observed life history data and to back-calculate expected feeding rates using user-specified annual temperature profiles. Because this procedure appears to be most sensitive to specifying a species' maximum body weight at its maximum age (i.e., see Eqn. S15), we analyzed BASS's sensitivity to species' long-term specific growth rates by changing their assumed maximum body weights by plus and minus 33%.

Table 1. Regressions calculated using BASS model outputs for MAR stream fishes

Regression ID	Regression equation	*n*	r^2_{adj}	SE
1	$\log_{10} B_{dc} = -0.671 + 0.998 \log_{10} B_{wc}$	16 579	0.998	0.0449
2	$\log_{10} B_{ds} = -0.674 + 1.00 \log_{10} B_{ws}$	2584	0.999	0.0358
3	$\log_{10} B_{dt} = -0.682 + 1.01 \log_{10} B_{wt}$	352	0.998	0.0281
4a	$\log_{10} \mathrm{BAF}_{\mathrm{MeHg}} = 4.48 + 0.0860 \log_{10} W_{wc} + 0.516\mathrm{TP}_c$	16 579	0.662	0.183
4b	$\log_{10} \mathrm{BAF}_{\mathrm{MeHg}} = 4.46 + 0.0910 \log_{10} W_{wc} + 0.527\mathrm{TP}_c$	16 330	0.812	0.127
5a	$\log_{10} \mathrm{BAF}_{\mathrm{PCB}} = -1.63 + 0.0434 \log_{10} W_{wc} + 0.599\mathrm{TP}_c + 0.851 \log_{10} K_{ow}$	66 316	0.893	0.169
5b	$\log_{10} \mathrm{BAF}_{\mathrm{PCB}} = -1.72 + 0.0498 \log_{10} W_{wc} + 0.610\mathrm{TP}_c + 0.861 \log_{10} K_{ow}$	65 320	0.964	0.0956
6	$\log_{10} F_i = 0.0893 + 0.893 \log_{10} W_{wc}$	16 578	0.845	0.354
7	$\log_{10} F_c = 0.158 + 1.02 \log_{10} B_{wc}$	16 578	0.977	0.176
8	$\log_{10} F_s = 0.168 + 1.01 \log_{10} B_{ws}$	2584	0.991	0.103
9	$\log_{10} F_t = 0.179 + 1.01 \log_{10} B_{wt}$	352	0.990	0.0648
10	$\log_{10} N_c = 1.68 - 1.07 \log_{10} W_{wc}$	16 579	0.435	1.13
11	$\log_{10} N_s = 2.29 - 0.626 \log_{10} W_{ws}$	2584	0.137	1.03
12	$\log_{10} N_t = 3.69 - 0.374 \log_{10} W_{wt}$	352	0.0753	0.605
13	$\log_{10} P_{wc} = 0.179 + 1.01 \log_{10} B_{wc} - 0.198 \log_{10} W_{wc}$	16 576	0.962	0.231
14	$\log_{10} P_{ws} = -0.00248 + 1.00 \log_{10} B_{ws}$	2584	0.990	0.106
15	$\log_{10} P_{wt} = -0.0135 + 1.00 \log_{10} B_{wt}$	352	0.986	0.0758
16	$\log_{10} W_{dc} = -0.725 + 1.05 \log_{10} W_{wc}$	16 578	1.00	0.0118
17	$\log_{10} W_{ds} = -0.717 + 1.05 \log_{10} W_{ws}$	2584	1.00	0.0103
18	$\log_{10} W_{dt} = -0.713 + 1.06 \log_{10} W_{wt}$	352	0.999	0.0142
19	$\log_{10} \gamma = -2.39 - 0.202 \log_{10} W_{wc}$	16 576	0.375	0.241

MAR = Mid-Atlantic Region.
Dependent and independent variable names are defined following the table. All regression coefficients are significant for $p < 10^{-6}$.
Dependent variables are:
1. The annual mean dry biomass (kg dry wt/ha) of a cohort (B_{dc}), of a species (B_{ds}), or of total fish (B_{dt}).
2. A cohort's annual mean BAFs (L/kg wet wt) for methylmercury ($\mathrm{BAF}_{\mathrm{MeHg}}$) and PCBs ($\mathrm{BAF}_{\mathrm{PCB}}$).
3. The annual consumption of an individual (F_i g dry wt/y), of a cohort (F_c g dry w $\times$ ha^{-1} $\times$ y^{-1}), of a species (F_s g dry wt $\times$ ha^{-1} $\times$ y^{-1}), or of total fish (F_t g dry wt $\times$ ha^{-1} $\times$ y^{-1}).
4. The annual mean population density (fish/ha) of a cohort (N_c), of a species (N_s), or of total fish (N_t).
5. The annual production (kg wet wt $\times$ ha^{-1} $\times$ y^{-1}) of a cohort (P_{wc}), of a species (P_{ws}), or of total fish (P_{wt}).
6. The annual mean dry body weights (g dry wt/fish) of a cohort (W_{dc}), of a species (W_{ds}), or of total fish (W_{dt}).
7. An individual's annual mean specific growth rate [γ (g dry wt growth) $\times$ (g dry wt) $^{-1}$ $\times$ d^{-1}].
Independent variables are:
1. The annual mean wet biomass (kg wet wt/ha) of a cohort (B_{wc}), of a species (B_{ws}), or of total fish (B_{wt}).
2. The $\log_{10} K_{OW}$ of a PCB homologue.
3. The annual mean trophic position (unitless) of a cohort (TP_c).
4. The annual mean wet body weights (g wet wt/fish) of a cohort (W_{wc}), of a species (W_{ws}), or of total fish (W_{wt}).
Note that the data sets used for BAF regressions 4a and 4b differ by including or excluding, respectively, cohorts that feed entirely on nonaquatic insects that were assumed to be uncontaminated, and similarly for BAF regressions 5a and 5b.

Corroboration of BASS outputs and functionality

Traditional approaches used for model corroboration and validation, (i.e., comparing time series of simulated model outputs [e.g., fish body sizes, population densities, biomasses, productions, BAFs, and BMFs] to time series of those outputs measured independently in the field over multiple years) could not be performed in this study because such field data simply does not exists. However, we did compare BASS's mean annual biomasses, population densities, and production estimates with those observed by Stauffer and Ferreri (2002) for 91 impacted and reference streams in the mountain-top mining and valley fill regions of Kentucky and West Virginia (KY-WV). We also compared BASS's predicted annual production and consumption rates, BAFs, and BMFs with those predicted by other field-based studies (Ney 1990, 1993; Randall et al. 1995; USEPA 2001; Liao et al. 2005; Arnot and Gobas 2006; Sanborn and Brodberg 2006; Alpers et al. 2008) to corroborate important aspects of BASS's internal structure and function.

Assessing the condition of MAR fisheries

To estimate the proportion of MAR streams that can be considered to be in good fishery condition, we sorted our total fish mean biomasses (B_{wt}), total fish mean densities (N_t), and total fish annual productions (P_{wt}) estimated for each stream into 3 descending lists. From each of these lists, we then constructed 2 additional lists; the first contained the original list's partial averages [i.e., $\bar{V}_k = \left(\sum_{i=1}^{k} V_i\right)/k$ where V_i is the total fish mean biomass, mean density, or annual production of the i-th stream], and the second contained the original list's partial medians [i.e., $\tilde{V}_k = \mathrm{MEDIAN}(V_1, \cdots, V_k)$]. From these 6 lists, we then determined the largest k indices whose associated values were greater than or equal to comparable values that we estimated for other field studies, described below, which we assumed to support healthy fisheries. The mean of these k indices was assumed to be a reasonable estimate of the number of MAR streams in good fishery condition.

We identified 3 field studies that can be reasonably assumed to support healthy fisheries; these were studies by Radwell (2000) for 10 rivers and streams in the Boston Mountain ecoregion (BME) of Arkansas, by Baldigo and Lawrence (2000) for 14 rivers and streams in Neversink River Basin (NRB) of New York, and by Habera et al. (2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009) for 21 eastern Tennessee wild trout (TWT) rivers and tributaries. The BME study was considered to support healthy fisheries because 6 of its 10 rivers and streams are listed under the Wild and Scenic Rivers Act of 1968 (PL 90-542) passed by the US Congress to preserve free-flowing rivers with outstanding natural and cultural values. The NRB study was considered to support healthy fisheries because it is located entirely within New York's Catskill State Park that contains the Catskill Forest Preserve created by the New York State Legislature in 1885 that now encompasses almost 300 000 acres. Last, the TWT study was considered to support healthy fisheries because its mean trout biomasses are comparable to biomass targets set for wild trout waters by the Pennsylvania Fish and Boat Commission (http://fishandboat.com/pafish/trout/trout_plan/troutplan2010.pdf).

Assessing potential human dietary exposures to Hg

Using EMAP's nongame fish data for Hg and BASS's predicted BAFs, we estimated the percent of MAR fish cohorts typically eaten by people that could be expected to exceed human consumption criteria for Hg. Fish species of concern included not only those identified as game fish (i.e., brook trout *Salvelinus fontinalis*, brown trout *Salmo trutta*, rainbow trout *Oncorhynchus mykiss*, all *Lepomis* sunfish, all *Micropterus* bass, rockbass *Ambloplites rupestris*, crappie *Pomoxis* spp., chain pickerel *Esox niger*, sauger *Sander canadensis*, and yellow perch *Perca flavescens*) but also those potentially targeted for subsistence fishing (i.e., carp *Cyprinus carpio*, channel catfish *Ictalurus punctatus*, fallfish *Semotilus corporalis*, freshwater drum *Aplodinotus grunniens*, and white sucker *Catostomus commersoni*). To make these estimates, we back-calculated expected MeHg water concentrations for MAR wadeable streams using the aforementioned fish data and MeHg BAFs calculated by Regression 4a (Table 1), using our estimated mean species body weights and trophic positions for each fish species represented in the EMAP residue data set. In particular, we calculated expected freely dissolved water concentrations (C_{wi} ng/L) of MeHg using the equation

$$C_{wi} = C_{fi} BAF_{fi}^{-1}, \qquad \text{(Eqn. 4)}$$

where C_{fi} is the whole-body MeHg concentration (ng/kg wet wt) of the i-th fish in the EMAP residue database, and BAF_{fi} is that fish's estimated BAF calculated by Regression 4a. Using only the whole-body fish concentrations that exceeded EMAP's MeHg detection limit, we estimated an average MeHg water concentration for MAR wadeable streams to be 0.131 ng/L ($\tilde{x} = 0.0992$; SD = 0.117; $n = 223$). Using this mean water concentration and our BASS-estimated BAFs, we then calculated whole-body concentrations for all cohorts of the 24 fish species that we identified as game or subsistence fishing species. Table S6 summarizes our estimated whole-body MeHg concentrations (μg/g wet wt) of these fish species.

RESULTS AND DISCUSSION

Total fish biomasses and population densities

Table 2 summarizes the average annual total fish biomasses and total fish population densities that we forecasted for the MAR, and Regression 12 describes the expected self-thinning pattern of MAR total fish densities (i.e., how fish densities vary as a function of mean body weight). These estimates are based on the nonzero biomasses and densities of 2833 persistent species–stream combinations representing 18 447 cohorts. Another 821 species–stream combinations, however, were predicted to become "extinct" by the end of our 25-y baseline simulations, and 8 of the 144 species sampled by the EMAP field monitoring were predicted to become "extinct" in all sites where they occurred (see Table S1). These simulated "extinctions," however, should not be interpreted as real events but rather as indicators of the importance of microhabitats in sustaining populations of rare species within large stream reaches. It is also important to note that 249 of the 2833 persistent species–stream combinations, representing a total of 1868 cohorts and all cohorts of 12 other species, had predicted annual mean biomasses less than 1 g wet wt/ha. For our species- and cohort-level of analyses, we ignored all 20 of these "extinct and rare" species.

Table 2 also summarizes our calculated descriptive statistics of total fish biomasses and population densities using data reported for other eastern US stream studies whose species composition is similar to that of the MAR; these include our assumed validation study by Stauffer and Ferreri (2002) for the KY-WV and the 3 reference studies that we assumed to represent fisheries in good condition (i.e., the BME study by Radwell [2000], the NRB study by Baldigo and Lawrence [2000], and the TWT study by Habera et al. [2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009]). Whereas our simulated total population densities agree with those observed for the KY-WV, NRB, and the TWT studies, they are significantly lower than those observed for the BME study (Figure 2). Similarly, although our simulated total fish biomasses compare well to those observed for the KY-WV study, they are significantly lower than those observed in the BME, NRB, and TWT studies (Figure 3).

Species biomasses and population densities

Our simulated average annual species-specific biomasses and population densities ranged from 1.02×10^{-3} to 672 kg wet

Table 2. Summary of total fish biomasses, population densities, and production of MAR wadeable streams and of other eastern US field studies having species compositions similar to that of the MAR

Variable study	Mean	Median	SD	Minimum	Maximum
Total fish biomass (kg wet wt/ha)					
MAR ($n = 352$)	32.1	10.3	66.4	0.183	706
KY-WV ($n = 91$)	32.3	22.1	48.5	0	350
NRB ($n = 14$)	52.0	50.0	37.3	8	150
TWT ($n = 174$)	73.3	56.1	51.9	6.71	323
BME ($n = 10$)	118	121	51.6	26.8	203
Total fish density (fish/ha)					
MAR ($n = 352$)	6.85×10^3	2.08×10^3	1.37×10^4	15	1.37×10^5
KY-WV ($n = 91$)	6.05×10^3	3.63×10^3	6.52×10^3	0	3.10×10^4
NRB ($n = 14$)	5.58×10^3	4.50×10^3	5.38×10^3	500	1.70×10^4
TWT ($n = 174$)	7.58×10^3	5.18×10^3	6.96×10^3	289	5.06×10^4
BME ($n = 10$)	2.23×10^4	1.81×10^4	1.15×10^4	8.68×10^3	4.62×10^4
Total fish production (kg wet wt/ha/y)					
MAR ($n = 352$)	32.1	9.79	65.1	0.221	620
[a]KY-WV ($n = 91$)	37.7	28.8	33.1	0.362	158
[a]NRB ($n = 14$)	47.4	45.4	33.1	8.30	134
[a]TWT ($n = 174$)	65.3	51.7	43.9	8.74	235
[a]BME ($n = 10$)	126	137	46.1	41.1	201

BME = Boston Mountain Ecoregion; KY-WV = Kentucky and West Virginia; MAR = Mid-Atlantic Region; NRB = Neversink River Basin; SD = standard deviation; TWT = Tennessee wild trout.
These studies are for streams in the mountain-top mining and valley fill regions of KY-WV (Stauffer and Ferreri 2002), for rivers/streams in NRB of New York (Baldigo and Lawrence 2000), for TWT rivers/streams (Habera et al. 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009), and for BME rivers/streams (Radwell 2000). All MAR values are based on the ending year of 25 y baseline BASS simulations.
[a]Annual fish production estimated using Equation 6.

wt/ha ($\bar{x} = 4.38$; $\tilde{x} = 0.309$; SD = 23.0; $n = 2584$) and from 3.31×10^{-3} to 9.85×10^4 fish/ha ($\bar{x} = 933$; $\tilde{x} = 86.1$; SD = 4410; $n = 2584$), respectively. Regression 11 describes the expected pattern of self-thinning exhibited by MAR fish species. Table S3 presents a complete summary of our estimated species-specific mean biomasses and population densities for MAR wadeable streams.

The pattern of relative biomasses predicted by BASS for the dominant species in MAR is surprisingly consistent with those in the BME and TWT field studies. In particular, when

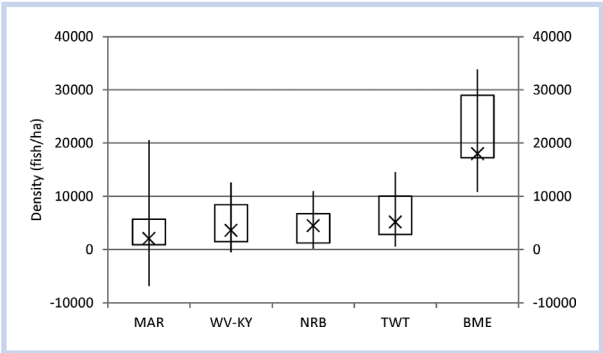

Figure 2. Whisker-box plots of total fish densities (fish/ha) in the Mid-Atlantic Region (MAR), the mountain-top mining and valley fill regions of Kentucky and West Virginia (KY-WV), the Neversink River Basin (NRB) of New York, Tennessee wild trout (TWT) rivers and tributaries, and rivers and streams in the Boston Mountain ecoregion (BME) of Arkansas. Whiskers represent the mean ± 1 SD; the median is identified by "X."

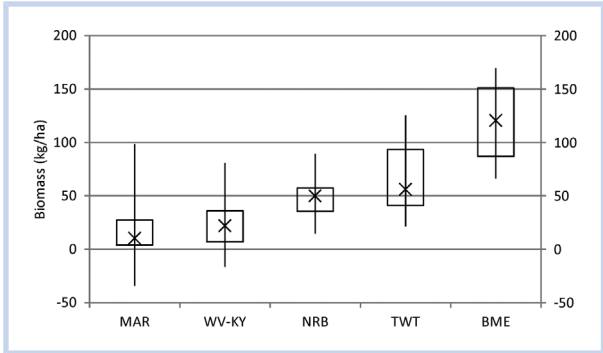

Figure 3. Whisker-box plots of total fish biomass (kg wet wt/ha) in the Mid-Atlantic Region (MAR), the mountain-top mining and valley fill regions of Kentucky and West Virginia (KY-WV), the Neversink River Basin (NRB) of New York, Tennessee wild trout (TWT) rivers and tributaries, and rivers and streams in the Boston Mountain ecoregion (BME) of Arkansas. Whiskers represent the mean ± 1 SD; the median is identified by "X."

Table 3. Summary of simulated and observed relative biomasses of the top six ranked species in MAR wadeable streams, TWT rivers and/or streams[a], and BME rivers and/or streams[b]

Rank	MAR	TWT	BME
1	0.669 (0.244; 352)	0.609 (0.226; 174)	0.479 (0.162; 10)
2	0.185 (0.112; 311)	0.208 (0.108; 174)	0.200 (0.093; 10)
3	0.0879 (0.0634; 284)	0.109 (0.061; 134)	0.125 (0.065; 10)
4	0.0511 (0.0418; 265)	0.0702 (0.0413; 111)	0.0626 (0.0284; 10)
5	0.0317 (0.0286; 240)	0.0480 (0.0358; 87)	0.0347 (0.0194; 10)
6	0.0217 (0.0206; 212)	0.0266 (0.0187; 78)	0.0257 (0.0162; 10)

BME = Boston Mountain Ecoregion; MAR = Mid-Atlantic Region; SD = standard deviation; TWT = Tennessee wild trout.
Parenthetic values denote, from left to right, the variable's SD and the number of streams used for the estimate. Note that for MAR and TWT rivers and/or streams, brook trout, brown trout, and rainbow trout were summed and treated as a single species due to their sport fish status.
[a]Habera et al. 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009.
[b]Radwell 2000.

the relative species biomasses of each stream and/or river in these studies are calculated and rank ordered, one sees that the sum of the mean relative biomasses of the 6 top-ranked species ranges from 0.927 to 1.07 (Table 3). Thus, on average, more than 90% of the total fish biomass in these 3 studies can be expected to be attributable to, at most, 6 fish species. Moreover, assuming that the distribution of our simulated BASS relative biomasses represents a theoretical expectation for those of other lotic fish communities in the eastern United States, we can straightforwardly test whether the relative biomasses summarized in Table 3 are significantly different from each other. In particular, when these relative biomasses are normalized to their respective sums and converted to percentages, Pearson's χ^2 tests indicate that the relative biomasses of the BME ($\chi^2 = 7.43$; degrees of freedom [df] = 5; $p = 0.191$) and the TWT ($\chi^2 = 2.64$; $df = 5$; $p = 0.755$) are not significantly different from those of our BASS simulations.

Although our mean total fish biomass predicted for MAR wadeable streams is significantly lower than those observed in either the BME or TWT studies, the average species biomasses across the species that these studies share are not statistically different. Table S4 summarizes the mean biomasses for the 30 species shared by the MAR and the TWT and for the 20 species shared by the MAR and the BME. When these biomasses are log-transformed and their means tested for equality using 2-tailed, paired sample t tests, average species biomasses estimated for the MAR were not significantly different from those reported for the TWT ($t = 0.200$; $df = 29$; $p = 0.843$) or for the BME ($t = -0.811$; $df = 19$; $p = 0.427$). Although these results may seem counterintuitive, they can be explained by acknowledging that whereas mean biomasses of the species shared by these studies may not be statistically different, their expected relative biomasses can be very different. To illustrate this situation, consider the expected total fish biomasses in 2 randomly selected MAR and TWT streams that contain fantail darters *Etheostoma flabellare*. Although MAR fantail darters have an average biomass of 2.87 kg wet wt/ha and an average relative biomass of 0.130, TWT fantail darters have an average biomass of 2.92 kg wet wt/ha and an average relative biomass of 0.0304. Consequently, one would predict the total fish biomasses of these MAR and TWT streams to be 22.1 and 96.1 kg wet wt/ha, respectively.

Interestingly, the average species biomass predicted by BASS for MAR streams is also not statistical significantly different from that predicted for streams in Michigan's Lower Peninsula (MLP) using multiple linear regression models developed by Zorn et al. (2004) for 68 fish species using a database of observed biomasses, in-stream physical habitat parameters, and catchment-scale variables for 263 MPL streams sampled from 1982 to 1995. The biomasses predicted by these 2 approaches for the 42 species shared by these studies are summarized in Table S5. Using the same analysis procedure to compare the MAR, TWT, and BME fish biomasses, the average species biomass predicted by BASS is not statistically different from that predicted by the regression models developed by Zorn et al. (2004) ($t = -0.432$; $df = 41$; $p = 0.668$).

Total fish and species-specific productions

Table 2 summarizes our simulated total fish productions of MAR streams, and Figure 4 displays how these values compare to those estimated for the WV-KY, NRB, TWT, and BME field studies. Table S3 summarizes our species-specific production values that ranged from 6.05×10^{-4} to 584 kg wet wt $\times$ ha^{-1} $\times$ y^{-1} ($\bar{x} = 4.38$; $\tilde{x} = 0.301$; SD = 22.3; $n = 2584$). Annual production functions for individual species and total fish are described in Table 1 by Regressions 14 and 15, respectively. Although there are few comparable species-specific production functions in the literature, we compared our predicted total fish production values to those predicted by the classic work of Randall et al. (1995) who developed the following production regressions for lake and riverine fish communities

$$\log_{10} P_{\mathrm{wt,Randall\ 1}} = -0.16 + 0.97 \log_{10} B_{\mathrm{wt}} + 0.38\mathrm{ID} \quad \text{(Eqn. 5)}$$

($r^2 = 0.82$; $n = 73$) and

$$\log_{10} P_{\mathrm{wt,Randall\ 2}} = 0.28 - 0.35 \log_{10} \bar{W}_{\mathrm{wt}} + 0.90 \log_{10} B_{\mathrm{wt}} + 0.22\mathrm{ID}, \quad \text{(Eqn. 6)}$$

($r^2 = 0.89$; $n = 53$). In these regressions, $P_{\mathrm{wt,Randall\ 1}}$ and $P_{\mathrm{wt,Randall\ 2}}$ are the community's total annual wet weight productions (kg wet wt $\times$ ha^{-1} $\times$ y^{-1}); B_{wt} is the community's annual mean wet biomass (kg wet wt/ha); $\bar{W}_{\mathrm{wt}}$ is the annual mean wet body weight (g wet wt/fish) of individuals within the community; and ID is a classification variable assuming values of 0 or 1 for lakes or rivers, respectively. When we evaluated

Equation 5 for riverine communities (i.e., ID = 1) with our predicted total fish biomasses and regressed the results on our predicted production values, we obtained the following regression

$$\log_{10}P_{\mathrm{wt,Randall\ 1}} = 0.247 + 0.952\log_{10}P_{\mathrm{wt,BASS}}, \quad \text{(Eqn. 7)}$$

($r^2_{\mathrm{adj}} = 0.986$; standard error [SE] = 0.0727; $n = 352$). This regression suggests that our BASS annual production estimates are essentially proportional to those predicted by Equation 5. Assuming this to be true, the mean of the logarithmic ratios $\log_{10}(P_{\mathrm{wt,Randall\ 1}}/P_{\mathrm{wt,BASS}})$ would estimate the proportionality constant between them. Thus, we can reasonably assume that

$$P_{\mathrm{wt,Randall\ 1}} \approx 1.58P_{\mathrm{wt,BASS}}. \quad \text{(Eqn. 8)}$$

Because the total production of any fish population of concern can be expressed as

$$P_{\mathrm{wt}} = \gamma\bar{W}_{\mathrm{wt}}N_t = \gamma B_{\mathrm{wt}}, \quad \text{(Eqn. 9)}$$

where γ is the specific growth rate of the population's average individual, whose body weight is $\bar{W}_{\mathrm{wt}}$, it follows that the intercepts of Equation 5 and Regression 15 correspond to $\log_{10}\gamma_{\mathrm{Randall}}$ and $\log_{10}\gamma_{\mathrm{MAR}}$, respectively, and that the proportionality constant in Equation 8 represents the ratio of these specific growth rates. Assuming that the average specific growth rate underling Equation 5 is adequately described by Regression 19, we would expect that

$$\frac{P_{\mathrm{wt,Randall\ 1}}}{P_{\mathrm{wt,BASS}}} = \frac{\gamma_{\mathrm{Randall}}}{\gamma_{\mathrm{MAR}}} = \left(\frac{\widehat{W}_{\mathrm{w,Randall}}}{\widehat{W}_{w,\mathrm{MAR}}}\right)^{-0.202} = \left(\frac{4.1}{7.86}\right)^{-0.202} = 1.14, \quad \text{(Eqn.10)}$$

where $\widehat{W}_{\mathrm{w,Randall}}$ and $\widehat{W}_{\mathrm{w,MAR}}$ are the average fish body weights of the data sets associated with Equation 5 and Regression 15, respectively. Our predicted production values are therefore within 14% of those predicted by the Randall et al. (1995) regression when adjusted for differing mean body weights.

Because accurate production estimates for individual cohorts and species depend on accurate cohort and species consumption estimates, we indirectly corroborated our predicted cohort and species production values by demonstrating that our predicted cohort and species consumption values agreed well with those predicted by regressions developed by other researchers (Ney 1990, 1993; Liao et al. 2005). Readers should consult our Supplemental Data for details and results.

Sensitivity analysis of simulated fishery variables

When each species' maximum body weight is increased by 33% and their calibrated allometric functions for specific growth rate are evaluated for the mean fish body size (i.e., 7.86 g wet wt/fish) and mean water temperature (i.e., 12.9 °C) of our baseline simulations, long-term growth rates range from 1.05 to 1.64 ($\bar{x} = 1.18$; $\tilde{x} = 1.17$; SD = 0.108; $n = 144$) when expressed as the ratio of their baseline values Under the same conditions, expected feeding rates range from 1.01 to 1.30 ($\bar{x} = 1.05$; $\tilde{x} = 1.04$; SD = 0.0447; $n = 144$) of their baseline values. When each species' maximum body weight is decreased by 33%, and their calibrated allometric functions for specific growth rate are again evaluated for the mean body size of fish across all species from our baseline simulations, growth rates range from 0.200 to 0.792 ($\bar{x} = 0.527$; $\tilde{x} = 0.489$; SD = 0.142; $n = 144$) of their baseline values. Similarly, expected feeding rates range from 0.577 to 1.04 ($\bar{x} = 0.868$; $\tilde{x} = 0.913$; SD = 0.0927; $n = 144$) of their baseline values.

Table 4 summarizes our parameter sensitivity analysis of BASS's species and total fish mean annual biomasses, population densities, and individual body weight and of BASS's species and total fish annual productions when each species maximum body weight is increased and decreased by 33%. Results are expressed as the percent changes in the ratios of the indicated perturbed output variable to its unperturbed value. The central tendency of these percentages is summarized by their medians, and their variation is characterized by their first and third quartiles. The most sensitive variables, as measured by the absolute value of the reported median percent changes, were species and total fish average body weights, total fish production, species production for a 33% decrease in maximum body weight, and total fish biomass for a 33% decrease in maximum body weight. The absolute values of the median percent change for these variables ranged from 9.53% to 23.7%.

Assessing the condition of MAR fisheries

Using total fish biomasses, densities, and production values of the BME, NRB, and TWT studies that we assumed represented healthy fisheries (Table 2), we estimated a mean fishery condition index k of 147 (SE = 21.1; $n = 18$) implying that approximately 42% of MAR fish communities are in good condition or, conversely, that approximately 58% of these communities are in marginal or poor condition. Although this estimate is larger than EMAP's estimate of 22% of MAR streams being in good condition (USEPA 2006), our estimates are based on entirely different criteria and assumptions. In

Table 4. Parameter sensitivity analysis of BASS's fishery outputs with respect to a 33% increase and decrease in the maximum body weights for each species

Output type/parameter change	Biomass	Density	Production	Body weight
Species/0.67*W_{max}	−5.83 (−22.0, −0.222)	7.51 (−7.97, 15.1)	−14.0 (−30.4, −6.10)	−19.4 (−25.1, −13.9)
Species/1.33*W_{max}	2.25 (−5.69, 10.3)	−8.96 (−16.1, 0.910)	7.30 (−2.36, 19.3)	16.4 (11.0, 23.5)
Total fish/0.67*W_{max}	−12.0 (−20.9, −2.94)	6.67 (−0.889, 15.1)	−19.2 (−29.2, −9.86)	−23.7 (−31.7, −18.0)
Total fish/1.33*W_{max}	4.27 (−0.918, 11.0)	−8.70 (−14.8, −1.87)	9.53 (2.56, 20.4)	18.9 (13.6, 29.5)

Nonparenthetic entries are the medians of the percent changes in the ratios of the indicated perturbed output variable to its unperturbed value (i.e., its forecasted value herein). Parenthetic entries are the first and third quartiles of these percent changes. The sample sizes of the species percent changes are 2566 and 2458 for the maximum body weight increases and decreases, respectively. The sample size of the total fish percent changes is 352.

particular, unlike the IBI approach used by EMAP, our approach makes no a priori assumptions regarding how various taxonomic (e.g., darters–minnows), functional (e.g., insectivore–omnivores), or other categorical (e.g., tolerant–sensitive species) proportions of a fish community contribute to its overall condition via its IBI.

There are at least 3 mechanisms in BASS that could be responsible for these marginal or poor fishery conditions; these include: accelerated habitat-dependent self-thinning (i.e., increased dispersal and nonpredatory mortality), prey-limited consumption, and condition-factor dependent mortality. Accelerated habitat-dependent self-thinning obviously leads to reduced population densities just as prey-limited consumption leads to reduced growth. In BASS, condition-factor mortality is assumed to occur when the ratio of a cohort's actual body weight to its expected body weight (based on its inputted weight-length regression and current body length that is nondecreasing) is less than half. All 3 mechanisms were active in our simulation set of 352 MAR streams. Forty-five MAR streams had 1 or more instances of a species cohort's consumption being less than half of its expected consumption, and 167 streams had 1 or more instances of condition-factor mortality that could result from prey-limited consumption, increased respiratory demands associated with assumed stream temperatures, or a combination of both. To investigate the effects of accelerated habitat-dependent self-thinning on our predicted total fish biomasses, we re-ran our simulation set assuming HSI = 1 for all species in all streams. Although this reparameterization had a minimal effect on the MAR's expected total fish biomass (i.e., 34.9 kg wet wt/ha vs 32.1 kg wet wt/ha), there were significant changes in the mean biomasses of several species of special interest. For example, the following percent biomass increases were observed for regionally important game fish: 460% for rockbass, 416% for pumpkinseed *Lepomis gibbosus*, 321% for largemouth bass *Micropterus salmoides*, 285% for brook trout, 277% for fallfish, 271% for brown trout, 259% for longear sunfish *Lepomis megalotis*, 198% for spotted bass *Micropterus puntulatus*, and 161% for rainbow trout.

Estimated BAFs and BMFs

Table 5 summarizes realized BAFs and BMFs predicted by BASS for PCBs and MeHg in MAR fishes. These metrics, however, are influenced by a number of biological, environmental, and chemical variables. Although important biological variables include fish body size, rates of growth, feeding and respiration, dietary composition, trophic position, lipid content, and reproductive status, important environmental variables include water temperature and factors that determine time-varying water concentrations of the chemicals of concern. For organic chemicals such as PCBs, whose distribution within fish occurs by chemical partitioning to lipid and nonlipid organic matter, the single most important chemical property controlling a contaminant's bioaccumulation is its K_{OW}. Unlike PCBs, however, the distribution of MeHg within fish occurs by covalent binding to protein sulfhydryl groups that makes BAFs of MeHg independent of its K_{OW}. We therefore calculated separate multiple linear BAF regressions for MeHg and PCBs. Whereas the independent variables for our MeHg BAF regression were a cohort's annual mean live body weight and trophic position, the independent variables for our PCB regression included these biological variables and the PCB's assumed $\log_{10} K_{OW}$. Additionally, because we assumed that nonaquatic insects were uncontaminated by either MeHg or PCBs, and because our BASS simulations contained cohorts that were assumed to feed entirely on nonaquatic insects, we calculated our MeHg and PCB regressions by including and excluding these cohorts (see Regressions 4a, 4b, 5a, and 5b).

Recently, Arnot and Gobas (2006) evaluated the quality of 1656 measured BAFs and estimated traditional BAF QSARs for both aquatic invertebrates and fish using data deemed to be of sufficient quality. Their "acceptable" QSAR function 11b for fish was

$$\log_{10}\mathrm{BAF} = 0.12 + 0.86\log_{10} K_{OW}, \qquad \text{(Eqn. 11)}$$

($r^2 = 0.55$; $n = 912$). When our Regressions 5a and 5b are compared to Equation 11, 2 key observations can be made. First is the striking similarity between the $\log_{10} K_{OW}$ slope estimated by Arnot and Gobas (2006) (i.e., 0.86) and by our analysis (i.e., 0.851 and 0.861, respectively). Second, including afish's body weight and trophic position as predictor variables significantly increases the r^2_{adj} of Regressions 5a and 5b over that of Equation 11. Although the low coefficients for $\log_{10} W_w$ in Regressions 5a and 5b might suggest that body weight contributes only marginally to improving Equation 11, that conclusion is unwarranted based on Principal Component Analyses of these regressions' data sets. In particular, the first principal components of Regressions 5a and 5b explain 58.8% and 59.2%, respectively, of their data's total variance, and the largest loading for both components is a fish's body weight. This result, however, is not surprising because the rates of growth, feeding, and respiration are generally allometric functions of a fish's body weight; additionally, long-term mean lipid fractions and those assumed herein are generally allometric functions of a fish's body weight.

Table 5. Summary of bioaccumulation potentials for MAR stream fishes based on annual cohort means for ending year of 25 y baseline simulations

Variable	MeHg	tetra-PCB	penta-PCB	hexa-PCB	hepta-PCB
$\log_{10}$ BAF$_f$	6.01 (0.315; 4.08; 7.24)	5.09 (0.224; 3.93; 5.70)	5.48 (0.293; 3.96; 6.32)	5.82 (0.346; 3.97; 6.81)	6.18 (0.391; 3.98; 7.25)
BMF$_f$	5.30 (1.72; 0.0193; 27.1)	1.78 (0.367; 0.0170; 30.2)	2.02 (0.389; 0.0125; 22.9)	2.14 (0.480; 0.00773; 18.5)	2.18 (0.547; 0.00418; 16.0)

MAR = Mid-Atlantic Region; MeHg = methylmercury; PCB = polychlorinated biphenyls; SD = standard deviation.
Parenthetic values denote, from left to right, the variable's SD, minimum, and maximum. Reported values pertain only to those streams with persistent populations (i.e., streams with simulated species biomasses >1 g wet wt/ha). Whereas the sample sizes for log BAF$_f$ statistics were $n = 16\,579$, for BMF$_f$ statistics variables, $n = 16\,330$ due to the assumption that the cohorts of several species fed entirely on terrestrial insects that were assumed to be uncontaminated (i.e., $C_p = 0$).

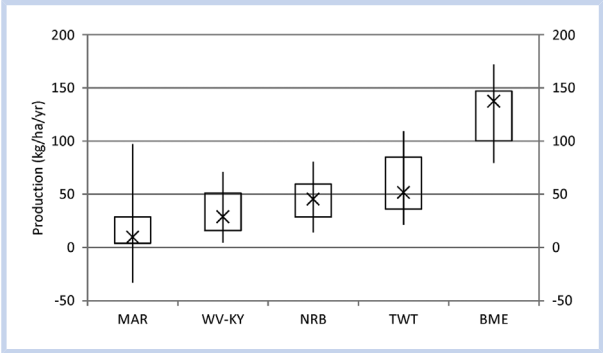

Figure 4. Whisker-box plots of total fish production (kg wet wt/ha/y) in the Mid-Atlantic Region (MAR), the mountain-top mining and valley fill regions of Kentucky and West Virginia (KY-WV), the Neversink River Basin (NRB) of New York, Tennessee wild trout (TWT) rivers and tributaries, and rivers and streams in the Boston Mountain ecoregion (BME) of Arkansas. Whiskers represent the mean ± 1 SD; the median is identified by "X."

Our regressions' coefficients for TP specify how a cohort's $\log_{10}$ BAF changes with a unit change in trophic position, and their antilogs correspond to food-web magnification factors (FWMF) (Fisk et al. 2001); consequently, Regressions 5a and 5b predict that FWMF ranges between 3.97 and 4.07 for PCBs in MAR fishes. This estimate agrees well with the FWMFs equal to 4.2 and 4.4 reported by Kidd (1998) for Lake Ontario and Lake Baikal, respectively, and with the FWMF equal to 4.36 (SD = 2.12; $n = 6$) reported by Mackintosh et al. (2004) for PCBs in a British Columbian marine food web.

To compare our MeHg regressions to other empirically derived MeHg BAFs, we calculated the following regression

$$\log_{10}\mathrm{BAF}_{\mathrm{MeHg}} = 4.27 + 0.535\,\mathrm{TP}, \qquad \text{(Eqn. 12)}$$

($r^2_{\mathrm{adj}} = 0.272$; SE = 0.650; $n = 36$) using data reported by the USEPA (2001), Sanborn and Brodberg (2006), and Alpers et al. (2008) for national and California MeHg exposure assessments. Despite its low r^2_{adj}, this regression is significant for $p < 0.001$ and predicts a MeHg FWMF equal to 3.43 that agrees well with the MeHg FWMFs equal to 3.28 and 3.36, as predicted by Regressions 4a and 4b, respectively.

In this study, BMFs are defined directly by the equation $\mathrm{BMF}_f = \mathrm{C}_f/\mathrm{C}_p$ where C_p is the diet-weighted average chemical concentration in the fish's prey. This definition is not the same as an FWMF that, as noted above, is the antilog of the coefficient of a fish's trophic position for regressions whose independent variable is either the fish's log-transformed whole-body concentration or its $\log_{10}$ BAF (Fisk et al. 2001). Consequently, our annual mean predicted BMFs for PCBs varied from 1.78 to 2.18 (Table 5) whereas our estimated FWMFs for PCBs varied between 3.97 and 4.07. Similarly, our annual mean predicted BMF for MeHg was 5.30 (Table 5) whereas our estimated FWMFs for MeHg varied between 3.28 and 3.36.

Human dietary exposures to MeHg from MAR fishes

The cumulative distribution function (CDF) of our estimated MeHg whole-body concentrations in all cohorts of game fish and subsistent fishing species ($n = 3960$) is presented in Figure 5. To interpret this CDF, we used the whole-body safe human consumption criterion of 0.185 μg/g wet wt proposed by Peterson et al. (2007). This criterion is based on an extensive EMAP study of 626 western US streams and rivers and is consistent with the tissue-based criterion of 0.30 μg/g wet wt fillet proposed by USEPA (2010). Using this benchmark, we estimated that approximately 24% of the game and subsistence fishing cohorts occurring in MAR streams with detectable MeHg concentrations would exceed the acceptable human consumption criterion of 0.185 μg/g wet wt. Because Lazorchak et al. (2003) estimated that 78.2% to 84.4% of the MAR's stream lengths contained fish with detectable Hg concentrations, our results could have significant regional implications for frequent consumers of fish harvested from MAR wadeable streams and rivers.

SUMMARY AND CONCLUSION

The goal of this study was to demonstrate how a dynamic simulation model like BASS could be integrated with field

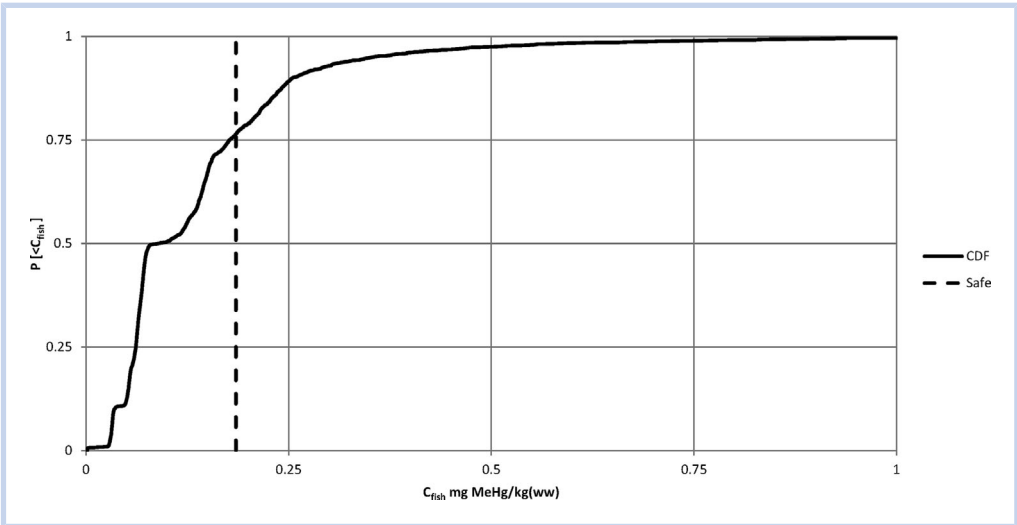

Figure 5. Cumulative distribution function of MeHg whole-body concentrations (mg/kg wet wt) in all cohorts of game fish (i.e., trout, sunfish and black basses, chain pickerel, sauger, and yellow perch) and of potential subsistence fishing species (i.e., carp, channel catfish, fallfish, freshwater drum, and white suckers) assuming a constant aqueous exposure of 0.131 ng/L. The vertical dashed bar represents the whole-body safe human consumption criterion of 0.185 μg/g wet wt proposed by Peterson et al. (2007). This figure represents 24 species and 3960 cohorts.

monitoring data and other data sources to estimate fishery conditions of Mid-Atlantic wadeable streams. Using this approach, we forecasted the region's average annual fish biomasses and population densities, annual fish production, and average annual BAFs and BMFs that can be used to assess MeHg and PCB exposures to humans and piscivorous wildlife. Predicted total fish biomasses and population densities were corroborated by an independent study by Stauffer and Ferreri (2002) for impacted and reference streams in the mountain-top mining and valley fill regions of Kentucky and West Virginia. BASS's predicted annual production values, BAFs, and BMFs were corroborated with those predicted or reported by other field-based studies (Randall et al. 1995; USEPA 2001; Arnot and Gobas 2006; Sanborn and Brodberg 2006; Alpers et al. 2008). In addition to these primary fishery indicators and/or metrics, we also demonstrated that BASS simulates credible patterns of species-specific biomasses; of relative biomasses of dominant fish species; of annual consumption of both individual cohorts and whole species; of PCB BAFs as functions of $\log_{10} K_{OW}$ and of a fish's body weight and expected trophic position; and of MeHg BAFs as functions of a fish's body weight and expected trophic position. Although informative and important in their own right, these secondary fishery indicators and/or metrics also corroborate indirectly BASS's primary fishery indicators that cannot be corroborated directly in a traditional manner (e.g., by comparing a time series of total fish biomasses to one-time or unsynchronized field observations or by comparing simulated fishery productions to independently estimated and/or measured fishery productions year by year). These secondary fishery indicators establish the credibility of our primary indicators by corroborating key processes and relationships that determine them.

In this study, we assumed no significant changes in contaminant loadings (i.e., MeHg or PCBs), habitat suitability, land cover or land conversion (e.g., infrastructure development, mountain-top mining, or urbanization), regional climate, or other regional stressors in order to assess regional baseline fishery conditions. We did, however, investigate how total fish and species-specific biomasses might change if the habitat suitability for all species could be simultaneously maximized (i.e., HSI = 1 for all species). Although it is obviously impossible to maximize the habitat suitability for all species simultaneously (see, for example, the HSI regression functions developed by Rashleigh et al. [2005]), this analysis demonstrates how our baseline BASS simulations could be compared to those of an alternative future environmental scenario (i.e., maximum habitat restoration) to attain an objective and quantitative assessment of the effects of that scenario. Importantly, modeling studies such as this one can be readily adapted to evaluate actual and expected exposure scenarios for an array of physical, chemical, or biological stressors acting alone or in combination. Such model applications would be important steps toward improving regional watershed management and planning that directly or indirectly affect fishery-based ecosystem services (Dalyander and Cerco 2010; Johnston et al. 2011).

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SUPPLEMENTAL DATA

Table S1. List of fish species simulated to evaluate fishery conditions in Mid-Atlantic Region wadeable streams.

Table S2. Summary of biological and physical characteristics of MAR streams selected Q4for simulation based on EMAP monitoring data.

Table S3. Summary of mean species-specific biomass, population density, annual production, annual dry-weight-based production-to-biomass ratio (PBR), relative biomass and population density, and trophic position (with parenthetic values designating the species' minimum and maximum cohort trophic positions) simulated by the BASS for MAR wadeable streams. Reported values pertain only to those streams with persistent populations (i.e., streams with simulated species biomasses greater than 1 g wet wt/ha).

Table S4. Average species biomasses (kg wet wt/ha) predicted for MAR streams using BASS and observed in TWT and BME rivers/streams. NP denotes "not present" and parenthetic numbers indicate sample sizes.

Table S5. Comparison of average species biomasses predicted for MAR streams using BASS and for Michigan Lower Peninsula (MLP) streams using multiple linear regressions developed by Zorn et al. (2004).

Table S6. Summary of estimated whole-body MeHg concentrations (μg/g wet wt) of game fish in MAR streams whose small non-game fish concentrations exceeded the maximum acceptable wildlife exposures reported by Lazorchak et al. (2003). The sample size for all statistic is $n = 236$.

Figure S1. Example transient and steady-state time dynamics of the 2 EMAP streams whose simulated total fish biomass were the highest and the lowest for those streams having 6 persistent species.

Figure S2. Example transient and steady-state time dynamics of the 2 EMAP streams whose simulated total fish biomass were the highest and the lowest for those streams having 7 persistent species.

Figure S3. Example transient and steady-state time dynamics of the 2 EMAP streams whose simulated total fish biomass were the highest and the lowest for those streams having 8 persistent species.

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