Effects of Plutonium in Animals

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I would first like to make a few general comments about the reasons why we study the effects of plutonium in animals and about the uses to which our results can be put. This may seem obvious as I tell it, but it is a perspective which is easily lost sight of. We study the effects of plutonium in animals so that we may be able to predict these effects in man. We have essentially *no* knowledge of plutonium effects in man except for that which we infer from the results of animal experiments, and I am sure we all hope that this situation does not change. Avoiding first-hand experience with plutonium effects in man is our ultimate objective.

So animal experiments with plutonium are useful to the extent that they help us in predicting the hazard to man. Now --what kinds of hazard are we concerned with? There are two very different kinds, I think, which require essentially different experimental approaches in their evaluation. There is the hazard from occupational exposure and the hazard from exposure of large populations.

The first of these, the occupational-exposure problem, is one that is concerned with relatively small numbers of people, and with the potential for exposure to relatively large amounts of plutonium. This is a problem that one may hope to directly simulate in an animal experiment--- with a comparable number of subjects, comparable levels of exposure, materials comparable to those encountered in human exposure, and with the expectation of observing unmistakable effects in statistically significant numbers of animals.

The problem of exposure of very large numbers of people - world populations---to very low levels of plutonium is a very different sort of problem. We are concerned here with levels of exposure and effect that we cannot hope to directly simulate in an animal experiment. Our only hope is to learn to understand the mechanisms relating exposure to effect and thus be able to confidently predict what we are unable to measure.

This distinction between occupational and population hazards is, of course, not unique to plutonium or to radionuclides. It applies to any potentially toxic pollutant. It is perhaps only in the radionuclide field that we are really facing up to some of the problems involved in these kinds of predictions.

Aside from the statistical problem of numbers, and the associated necessity for understanding basic mechanisms, there is the problem of species differences. To what extent can you apply results obtained in rats to the prediction of effects in man? Are data from dogs, pigs, and baboons any better? Again it is a problem of numbers and a problem of understanding. If you get the same kind of result from a number of different animal species, you have some basis for assuming that man may behave similarly, but, to have real confidence in this assumption, you need to understand the processes involved in the development of these effects and how these basic processes vary between species.

I would like to make just one more point of a general nature before we get into detailed effects.

The effects we observe result from a destructive release of energy within living tissue. The nature and extent of this destructive effect and its secondary consequences to the welfare of the animal are what we are concerned with here. These effects may be considered to reflect the "radiosensitivity" of the particular tissue involved. But we must also keep in mind that exactly which tissues are irradiated will be determined by where the plutonium is deposited within the animal, which is determined, in turn, by the route by which that plutonium entered the body and the chemical and physical state of the plutonium. In other words, the

SPATIAL SIMULATION OF SMALLMOUTH BASS IN STREAMS[1]

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ABSTRACT

The hydropower industry and its regulators are hampered by the inability
to predict the relationship between alternative flow regimes and fish population
response. We have developed a spatially explicit, individual-based model of
populations of smallmouth bass in streams as part of the Compensatory
Mechanisms in Fish Populations Program (see Sale and Otto 1991). In the
model, the profitability of alternative stream locations varies in response to
habitat depth and velocity through changes in the frequency of prey encounters
and the metabolic costs experienced by fish.

We conducted an evaluation of our hydraulic simulation at the scale of
individual stream cells. The potential error in predictions for individual cell
velocities suggests that larger-scale model predictions for the representative
reach are most appropriate. At this scale, the model appears to produce

realistic patterns in the growth and dispersal of young-of-year smallmouth bass. This verification step allows us to proceed with greater confidence in evaluating the original question of how smallmouth bass populations respond to alternative flow regimes.

INTRODUCTION

The use of habitat-based models to predict fish numbers is adequate only when biological feedbacks are unimportant. The U.S. Fish and Wildlife Service's continually evolving Physical Habitat Simulation (PHABSIM) methodology is the principal quantitative tool currently used in the regulation of instream flows. PHABSIM relies on the assumption that the number of fish of a particular lifestage is set by the total amount of "suitable" habitat, which depends only upon streamflow. PHABSIM predictions of the amount of suitable habitat respond instantaneously to changes in flow. The method assumes that fish densities track changes in habitat as they might a time-variable carrying capacity. It is not clear how densities in the field relate to these habitat-based predictions -- is there a point in time when the habitat-based predictions should correspond to actual fish densities? Although suitable habitat is predicted for each different lifestage, the habitat-based methods do not consider biological feedbacks between and within lifestages.

Our model predictions of the number and growth of young-of-year smallmouth bass derive from simulation of the daily activities of individual fish responding to changes in a heterogeneous stream habitat. We borrow the hydraulic modeling component of PHABSIM and superimpose on it a mechanistic model of smallmouth bass reproduction and young-of-year dynamics. The biological model is individual-based and the physical model is spatially explicit (Jager et al., submitted). Abiotic influences on reproduction and growth are modeled through the spatial variation in habitat quality in response to temperature and flow. Biological feedbacks in the model include: (1) the effect of the number of reproductive adults on young-of-year densities. (2) the effect of competition among young-of-year fish for space and food on growth and survival, (3) the effect of prey densities on growth and survival, (4) and the effect of size-dependent predation on the size distribution and number of young-of-year fish that recruit to the first year class.

SIMULATION METHODS

The model is currently being applied to the North Anna River in Virginia. A workstation analysis and visualization environment (PV/WAVE) is used to display the results of hydraulic simulation, the time series of weighted usable area, and the predictions generated by our fish model. These include temporal and spatial patterns in the density, movement, and habitat preferences of simulated fish.

Simulation of Stream Habitat. The daily foraging, growth, survival, and movement of individual smallmouth bass are simulated in a heterogeneous stream habitat that is defined by water temperature, depth, and velocity. Like the habitat-based models, we rely on a representative reach to describe the status of young-of-year smallmouth bass in the stream system of interest. We partition a representative stream reach into spatial cells such that each cell contains one or more measurement stations used in a PHABSIM survey of the reach. These cells provide a fixed spatial reference system for the duration of the simulation. The habitat simulation predicts the spatial distribution of depth and velocity as a function of average daily flow. Local (within-cell) velocity predictions depend on several cell-specific hydraulic parameters that are estimated by PHABSIM, including two parameters of a power function developed between velocity and flow and estimates of Manning's n at each calibration flow. The details of how we predict depth and velocity from flow are given in Jager et al. (submitted).

Simulation of Fish Growth and Survival. The representative reach can be thought of as a collection of cells that vary in growth potential for fish of different sizes. Growth of each individual smallmouth bass is modeled using a standard bioenergetics model (DeAngelis et al. 1991) that subtracts the energetic costs incurred by each fish from its assimilated foraging intake on a daily basis. Both components, prey intake and energetic costs, depend on flow (Jager et al., submitted). Two examples are: (1) prey densities in the model are limited by a habitat-dependent carrying capacity that varies in time and space as the habitat suitability indices (HSI) for prey taxa respond to flow; and (2) the energetic cost of spending time in a particular cell increases with local velocity. These and other relationships that we simulate between the growth and survival of individual fish and habitat are described in greater detail in Jager et al. (submitted).

Simulation of Fish Movement. We assume that fish inhabit one cell per day. Departure from the current day's cell is initiated either by degradation of the local habitat caused by extreme flows (HSI = 0.0) or by insufficient daily growth of the fish. The movement and habitat utilization of model fish can be observed with the help of our PV/WAVE visualization program.

RESULTS AND DISCUSSION

Simulation of Stream Habitat. Predicted velocities are shown for stream cells in a representative reach of the North Anna River for the low calibration flow (1.4 m³/s) in Figure 1a and for the high calibration flow (8.8 m³/s) in Figure 1b. The maps in Figure 1 show an overhead view of the stream. Each cell is characterized by velocities predicted at 5 measurement stations that lie within the cell. The measured velocities are shown for comparison in Figures 1c and 1d. Figure 2a compares predicted and observed velocities for these cells over
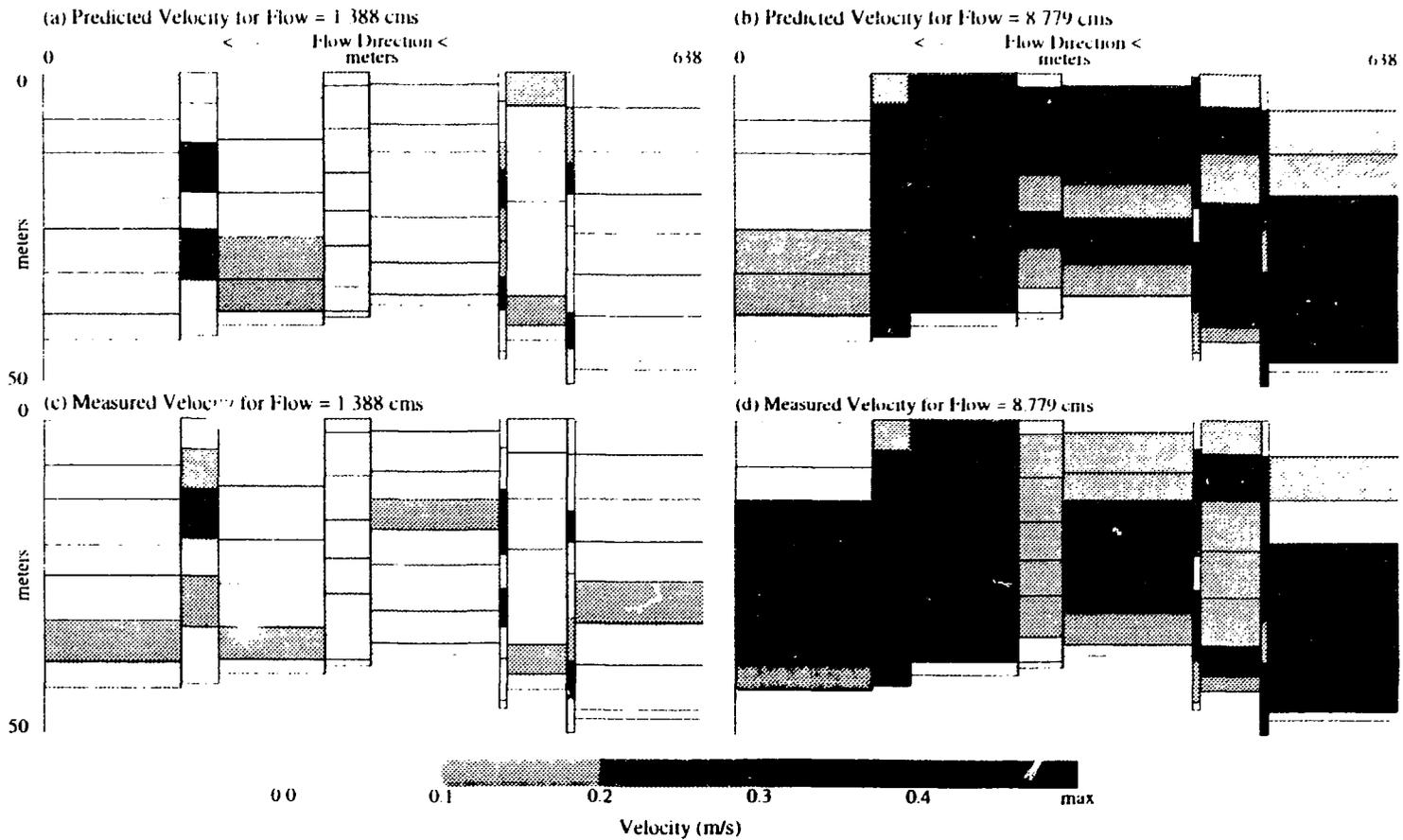
(a) Predicted Velocity for Flow = 1 388 cms

0   <   Flow Direction <   638
               meters

0

meters

50

(c) Measured Velocity for Flow = 1 388 cms

0

meters

50

(b) Predicted Velocity for Flow = 8 779 cms

0   <   Flow Direction <   638
               meters

(d) Measured Velocity for Flow = 8.779 cms

0 0   0.1   0.2   0.3   0.4   max

Velocity (m/s)

Figure 1. Comparison of predicted and measured velocities for each cell of our representative reach.
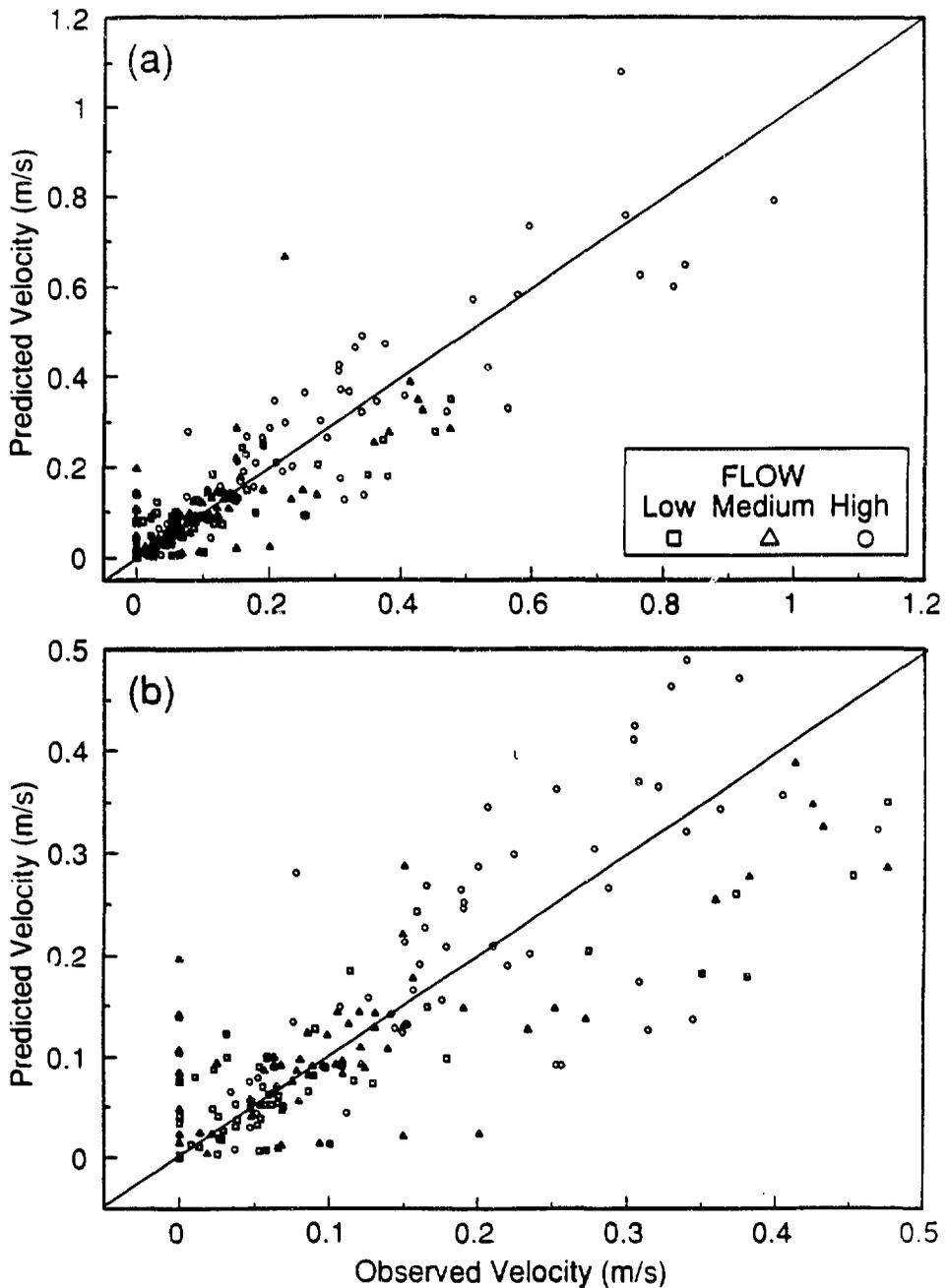
Figure 2. A comparison of predicted and measured velocities based on a PHABSIM survey and analysis of a representative reach of the North Anna River, Virginia. The comparison is made for three flows: 1.4 m³/s, 2.8 m³/s. and 8.8 m³/s for (a) the full range of measured velocities and (b) excluding measured velocities greater than 0.5 m/s.

the complete range of measured velocities. We are mainly interested in predicting the velocities accurately over the range shown in Figure 2b, since even velocities of 0.2 m/s are considered extreme enough to destroy smallmouth bass nests. Regression analysis over the full range of measured velocities shows reasonable agreement between the predicted and observed velocities ($r^2 = 0.73$, predicted $= 0.83 \cdot$ observed $+ 0.03$). In general, the predictions improve at higher calibration flows, with slopes increasing toward the expected slope of 1.0. For the low flow, the slope is 0.47 ($r^2 = 0.30$); for the middle flow, the slope is 0.68 ($r^2 = 0.51$), and for the high flow, the slope is 0.88 ($r^2 = 0.79$).

These results help us to define the appropriate spatial scale of our predictions and guide us in the use of velocity as a habitat variable in the model. It is clear from these results that the modeling capabilities afforded by PHABSIM, combined with the expense of collecting field measurements with a suitably small cell size, may place serious limitations on our ability to predict effects of flow on a small spatial scale. This suggests, for example, that we can expect to have trouble predicting the velocities to which nests in particular sites are exposed. Research is needed to identify alternative hydraulic simulation techniques with modest requirements for field data that can be used at this scale.

In the absence of these improvements, we must restrict our modeling goal to predicting the effect of flow on smallmouth bass in a theoretical reach that shares the statistical habitat properties of our representative reach. We can treat cell depths and velocities in the model as stochastic values generated from a distribution with the PHABSIM predictions as an average. The simulated variation around the cell average can be designed to mimic the differences in the average velocity experienced by individual fish within a cell, or even between multiple cells visited on a given day. In this context, model predictions of fish growth, survival, and reproduction apply to the representative reach and not to individual cells. An important step in verifying the predictions is to ensure that the velocity and depth predictions for the reach are not biased and that they provide a reasonable representation of habitat conditions available to fish in the reach under different flow conditions.

Simulation of Fish Growth and Survival. The flows during this year were low and stable compared with other years. Habitat suitability criteria were developed in this river for young-of-year smallmouth bass (Sabo, in preparation), juvenile smallmouth bass (Groshens, 1992), and for spawning (Joe Lukas, Virginia Polytechnic Institute, personal communication, 1992). The weighted usable area for spawning, larval and juvenile smallmouth bass in this representative reach of the North Anna River in Virginia fluctuates over the growing season in response to flow (Figure 3). In contrast, the numbers of larval and juvenile smallmouth bass predicted by our simulation model increase as a result of reproduction in late spring and early summer, and then decline as a result of attrition through the rest of the model growing season.
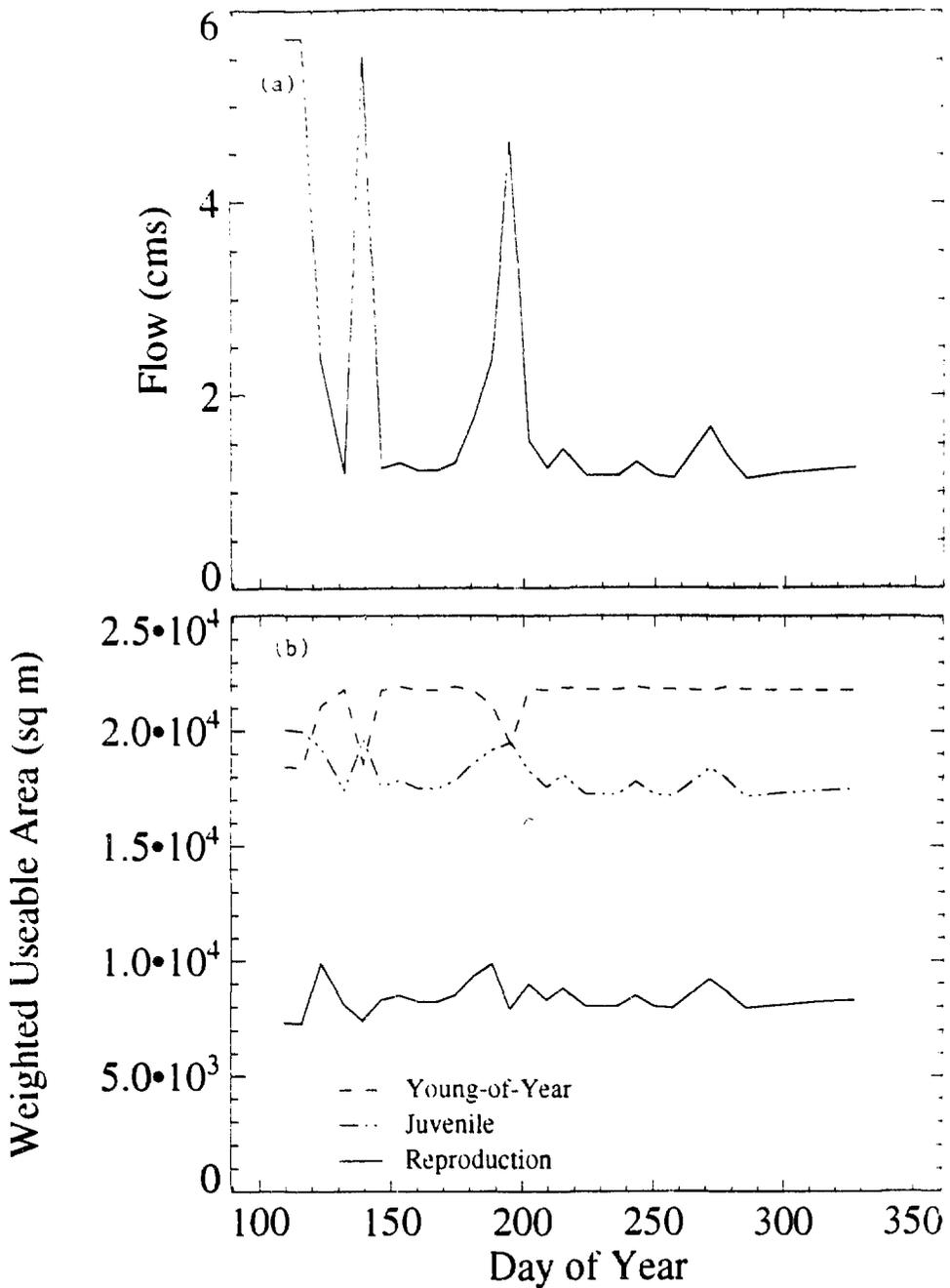
Figure 3. Seasonal patterns in 1991 for (a) measured stream flow and (b) weighted usable area available for three lifestages (spawning adults, fry, and juveniles < 200 mm in total length) of smallmouth bass in a representative reach of the North Anna River in Virginia.

Simulation of Fish Movement. Dispersal of juvenile smallmouth bass from the nests in the model occurs at roughly the same time as dispersal is observed in the field — 15 to 20 days after larvae reach the swimup stage. Model fish are dispersed throughout the representative reach by the time the last juveniles leave the nest, approximately 30 days after nesting commences.

Habitat utilization by model juveniles can be visualized by comparing maps of the representative reach for velocity, depth, and the numbers of fish in each cell. Figure 4 shows maps of this type for the peak flow on a simulation date in mid July (see Figure 3a, day 195). The population on the day shown by the map consists of 390 model fish that range in size from 55.7 to 88.6 mm. On this particular day, the highest density occurs in a moderately deep riffle cell. Figure 4 is presented here to illustrate the types of model results and visualization capabilities available.

CONCLUSIONS

We determined that our model predictions for individual cells would benefit from improvements in the hydraulic simulation component and welcome suggestions for improving velocity prediction at a small spatial scale. Reach-scale predictions can be improved by enhancing our ability to generate theoretical stream habitats with realistic statistical properties and physical constraints. The basic problem is to develop a statistical model to allocate flow among the cells in a transect with the predictions conditioned on local information (e.g., cell depth, Manning's n estimates at each flow). In addition, we anticipate a need for a statistical model to generate realistic theoretical streams without conditioning on local information in situations where the cost of collecting those data is not justified.

We conclude that our model shows promise for predicting the relationship between alternative flow regimes and smallmouth bass recr "ment. We have plans to validate various aspects of model predictions i   ••
habitat utilization of young-of-year smallmouth bass, the timing of
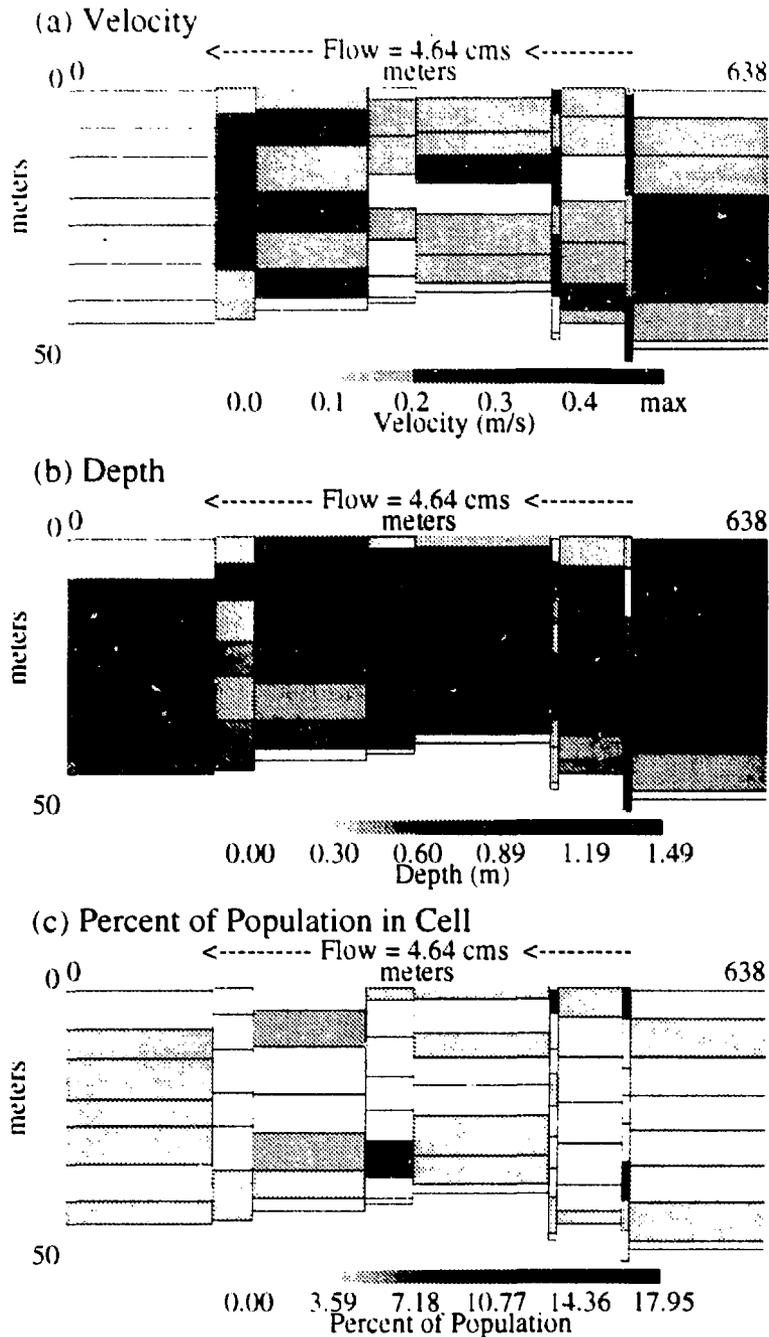activity, the selection of nest locations, and their ultimate succr

Figure 4. Simulated (a) velocity, (b) depth, and (c) the percentage of the smallmouth bass in each model cell of the representative reach on July 14th.

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DISCLAIMER

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