Spatially-explicit wildlife exposure modeling tools for use in human health and ecological risk assessment: SEEM and FISHRAND-migration

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Abstract

This paper presents two wildlife exposure models that incorporate the influence of chemical distribution in the environment, habitat suitability relative to that chemical distribution, and foraging behaviors of the modeled species. Spatially-explicit wildlife exposure models provide more realistic exposure estimates for use in human health and ecological risk assessments, and provide a means for evaluating the impact of different remedial alternatives by identifying and focusing on areas where habitat use and chemical contamination intersect. The Spatially Explicit Exposure Model (SEEM) is being developed for the US Army to improve the realism of terrestrial wildlife exposure modeling. The aquatic model, FISHRAND-Migration (FR), is a mechanistic, time-varying bioaccumulation model. This second-order probabilistic model incorporates both sediment and water sources to predict the uptake of organic chemicals based on prey consumption and food web dynamics. The Monte Carlo probabilistic approach allows users to distinguish between sources of uncertainty and variability in predicted fish body burdens. Both models offer assessors the tools necessary for advanced exploration of risk drivers and identification of site areas where habitat overlaps with chemical concentrations (and conversely areas where chemicals are present, but habitat is limited).

Keywords: risk assessment, wildlife exposure assessment, spatial modelling, probabilistic, uncertainty, ARAMS.
1 Introduction

Chemical contamination in the environment is not typically homogeneously distributed. This condition, together with variation in biology attributable to the life history of the species being evaluated, leads to more complex exposures than are typically assumed in risk assessment. Many risk assessments use various correction factors with little justification, such as a “site use factor,” or “migration factor” to mathematically reduce the amount of time that a receptor spends at a particular site or area within the site. The development of the models described in this paper is an attempt to overcome some of the limitations inherent in the single correction factor approach.

Wildlife behaviourists and fish ecologists have an expanding understanding of the life history, foraging strategies, habitat requirements, and migratory strategies of species that are the focus of risk assessments. Both laboratory (e.g., diet, ingestion rates) and field studies (e.g., tagging studies, mark-recapture) provide data with which to characterize animal movements, dietary requirements, behaviours and other life history strategies. The models presented here provide a method for evaluating the potential impact of changes in habitat suitability, contaminant distribution, and foraging strategies of the individual species in terms of predicted risks in order to inform the decision-making process and allow for a comparison of “what if” scenarios.

The next section describes the terrestrial model, SEEM, and provides examples of model outputs. The following section describes FR-Migration, and provides examples of model outputs. Finally, the last section provides recommendations for future research.

2 Spatially Explicit Exposure Model (SEEM)

SEEM is an extension of the earlier work of Freshman and Menzie [1] and Hope [2, 3] in which individual exposures are tracked as wildlife receptors move across the landscape. In SEEM, all individuals in a population range across the landscape with the probability of moving to or nesting in any area proportional to the habitat suitability of that area. A Markov Chain Monte Carlo approach is used to generate movement and foraging locations.

Two foraging strategies are available for each species or life stage – free-range foraging (guided by habitat suitability) or static home range foraging. The daily foraging area is constrained within a user-defined foraging radius and actual exposure occurs during the number of user-defined exposure events. The probability of foraging at any particular point in time is proportional to local habitat suitability. Exposure each subsequent day (with the exception of the static home range submodel in which the foraging area/radius does not move) begins at a location within the foraging radius from the previous day weighted by habitat suitability. Users can defined chemical and habitat suitability landscapes through polygons superimposed on an imported base map. The user also selects the local population size and the number of foraging events that occur each day.
Figure 1: Free ranging population EHQ results.

Figure 2: Static home range population EHQ results.

for each individual. SEEM then tracks exposures for all individuals in the population and generates percent population affected curves. SEEM will be incorporated into the Army Risk Assessment Modeling System (ARAMS) and will have the ability to draw upon the comprehensive databases (e.g. toxicity reference values, bioaccumulation factors, life history data), and a habitat suitability evaluation tool to provide an integrated approach to quantifying potential risks to terrestrial ecological receptors [4].

Figure 1 provides example output which shows the impact of foraging strategy on potential exposures. In both cases, all model assumptions are exactly the same except for the foraging strategy. In Figure 1, the population is free ranging while in Figure 2, the population has a static home range. The population distribution presented in Figure 1 shows that 80% of the population has an estimated ecological hazard quotient greater than one, while in Figure 2, 40% of the population has an estimated ecological hazard quotient greater than one.
The model takes into account the habitat suitability of each of the defined polygons. The impact of this can be seen in Figures 3 and 4. The underlying assumption in this set of runs is that there is a single hotspot of contamination with either low or high habitat suitability. The results in Figure 3 show that 20% of the population has an estimated ecological hazard quotient greater than one. However, if the area of contamination is also known to have higher habitat suitability, then the results presented in Figure 4 show that the fraction of the population potentially affected increases, as expected, in this case to 75%.
2.1 Remedial decision-making with SEEM

Risk managers and remedial engineers face the challenge of balancing the intensity of remedial activities (and possible loss of viable habitat) with the reduction in risk to potential receptors. While the capping or removal of all soil at a site may eliminate all exposure pathways, it may unnecessarily destroy the framework of a functioning ecosystem. Traditional risk management methodologies attempt to derive remedial goals from site-wide statistics or apply a site-specific preliminary remediation goal (PRG) to an entire site. From an ecological perspective, habitat suitability is a primary determinant of the potential for exposure. While chemical concentrations may be elevated in a gravel parking lot, the potential for exposure of a small mammal that requires a diverse herbaceous understory and closed canopy forest cover is very low in this instance.

Because SEEM incorporates habitat suitability into the exposure assessment in addition to tracking the exposure of all individuals in a local population, remedial activities that are derived with data from SEEM will balance habitat suitability with risk reduction from chemical removal. Further examples of applications and additional details are provided in Wickwire et al. [5].

3 FISHRAND-migration

Several earlier papers have explored development of a spatially explicit model for a population of winter flounder [6, 7]. Current model enhancements include offering the option of defining contaminant distributions through the use of a polygon tool and defining input parameters as “uncertain” or “variable” in a two-dimensional analysis. The sediment and water concentrations of contaminants to which aquatic organisms are exposed in areas of localized contamination are a function of spatial factors together with species biology. Species with overlapping foraging areas may experience significantly different contaminant exposures from the same site due to local variability in species behavior and contaminant distribution. Predicted exposure estimates and subsequent human health and ecological risk projections typically assume static exposures of receptors to contaminant concentrations characterized by descriptive statistics such as a mean or maximum. The level of health protection is unknown, and the results may not be representative of actual exposures experienced by aquatic organisms in a dynamic system. In addition, these static exposures do not account for uncertainty and variability in the underlying input parameters.

3.1 Uncertainty and variability

There is “true” uncertainty (e.g., lack of knowledge) in the estimated concentrations of sediment and water to which aquatic organisms are exposed and also variability in parameters contributing to contaminant bioaccumulation. Uncertainty and variability should be viewed separately in risk assessment because they have different implications to regulators and decision makers [8].
Variability is a population measure, and provides a context for a deterministic point estimate (e.g., average or reasonable maximum exposure). Variability typically cannot be reduced, only better characterized and understood. In contrast, uncertainty represents unknown but often measurable quantities. Typically, uncertainty can be reduced by obtaining additional measurements of the uncertain quantity. Quantitatively separating uncertainty and variability allows an analyst to determine the fractile of the population for which a specified risk occurs and the uncertainty bounds or confidence interval around that predicted risk. If uncertainty is large relative to variability (i.e., it is the primary contributor to the range of risk estimates) and if the differences in cost among management alternatives are high, additional collection and evaluation of information can be recommended before making management decisions for contaminated sediments. On the other hand, including variability in risk estimates allows decision makers to quantitatively evaluate the likelihood of risks both above and below selected reference values or conditions (for example, average risks as compared to 95th percentile risks).

Quantification of uncertain and/or variable distributions for model parameters requires judgment [9, 10]. Unlike the SEEM model, which reflects population heterogeneity in exposure and potential risk, FishRand-Migration models the influence of both uncertainty and variability to predicted fish concentrations. The model was originally developed as part of the Remedial Investigation/Feasibility Study (RI/FS) for the Hudson River Superfund Site [11]. The conceptual model represents a predominantly sediment-driven food web appropriate for sites with contaminated sediments for which bioaccumulation is the dominant pathway of concern. The mathematical approach has been validated for hydrophobic, lipophilic contaminants such as PCBs [6, 7, 10, 12, 13] and most pesticides known to partition into the organic fraction of the media they reside in (e.g., lipid, total organic carbon). The model is based on a nested Monte Carlo approach (Figure 5). The inner-most “loop” is a spatially explicit foraging sub-model that generates time series sediment and water concentrations that a fish may encounter within its habitat. As with SEEM, the user defines contaminant distributions and fish life history information using a polygon tool over a base map of the area being modeled.

The full mathematical framework for FR-Migration is provided in von Stackelberg et al., [6]. The fundamental equations are based on a “Gobas” modelling framework [6, 7, 10, 12, 13] in which input parameters are characterized by distributions rather than point estimates. The Gobas model itself has been validated using data from several systems, and formed the basis for the development of the Great Lakes Water Quality Criteria [14].

The time-varying predicted fish tissue concentrations serve as inputs into separately developed human health and ecological risk models. FR allows users to incorporate greater realism in modeling exposures by incorporating distributions into risk models. For example, because human and ecological receptors integrate exposures over spatial and temporal scales, they are typically exposed to average predicted biota concentrations and the uncertainty around the average [15]. Alternatively, FR output is appropriate for joint probability
analyses which convolve an exposure distribution with a toxicity distribution in order to predict the probability of exceeding a threshold level or an increasing magnitude of effect (e.g., 20% probability of a 50% decline in fecundity).

Figure 5: Schematic of nested models in FishRand-migration.

3.2 Model results

The model provides predictions of contaminant concentrations in aquatic biota as a function of time as shown in Figure 6.

The abundance assumption determines the uptake pattern throughout the year, as shown in Figure 6. Fish populations with small foraging areas relative to localized contamination will show similar means to fish with larger home ranges, but the population variability will be higher. Uncertainty in sediment and water concentrations is “magnified” the more localized contamination is present because each hotspot (and any contribution from background) is defined by its own probability distribution which combine multiplicatively. Diagnostic runs show that differences in predicted average and 95% upper confidence limits for a given human health risk assessment scenario can range from a factor of two to an order of magnitude depending on different combinations of foraging, abundance, and attraction factor.

Introducing greater realism in modelling behaviours and spatial contamination patterns that influence potential exposure makes calibration and validation more challenging. It is very important for analysts to develop a site conceptual model and a priori modelling framework and hypotheses in order to make the best use of site specific data. All modelling efforts should be informed by site specific data to provide greater confidence in the results.
4 Conclusions

Rather than relying on simple site use or migratory factors, the models presented here incorporate available data to describe home ranges, abundance, and foraging strategies. These tools allow analysts and decision makers to evaluate the influence of species habitat use together with contaminant distributions in the environment. Both models provide population-level predictions of exposure, and, in the case of SEEM, ecological risk. FR explicitly separates uncertain and variable parameters, while SEEM requires iterative runs to quantify uncertainty bounds. The goal is to use the best available science informed by site specific data in order to provide defensible modelling tools to support environmental decision making. In addition, these models offer risk managers additional management options more closely aligned with observed wildlife behaviours. However, calibration and validation of increasingly sophisticated models is required in order to assure the utility of these approaches in describing the potential for risk.

References


