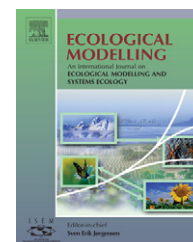


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Use of habitat-contamination spatial correlation to determine when to perform a spatially explicit ecological risk assessment

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ABSTRACT

Anthropogenic contamination is typically distributed heterogeneously through space. This spatial structure can have different effects on the cumulative doses of wildlife exposed to contamination within the environment. These effects are accentuated when individual organisms pursue different movement strategies, and movement strategies can be affected by how individual organisms and species value habitat. Habitat quality is often neglected when ecological risk assessments are performed, despite evidence that inclusion of a quantitative habitat measure can have a significant effect on the overall exposure estimate. We couple an exposure model with habitat data to examine the interactions between habitat preferences, the spatial distribution of contamination, and the resulting impact on dose estimates. Dose distributions are constructed for pronghorn (*Antilocapra americana*) exposed to fluoride when foraging on desert sagebrush. The results show the magnitude of the difference between simulated doses when foraging concentrations are positively or negatively correlated with different spatial distributions of habitat preferences. Mean estimated exposures obtained from non-spatial versus spatial methods can vary by a factor greater than two, and variation within the movement model, due to different habitat preferences, can vary by an order of magnitude. Such differences in calculated exposures can change a remediation decision from no-action to remediation, or vice-versa, and impact the remedial design when cleanup is required. In addition, information concerning which endpoint species are more or less likely to be exposed to chemical contamination in a given spatial setting can be used by stakeholders in the endpoint selection process. Results presented here are generally applicable to other situations where terrestrial wildlife is exposed to chemical contaminants. These simple model results demonstrate that examining the strength of the spatial correlation between habitat preference and contaminant data can be quickly used to determine when the implementation of a spatially explicit ecological risk assessment is useful.

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1. Introduction

The magnitude and effect of contaminant exposure on populations are influenced by the spatial distribution of contaminants, exposed organisms, and habitat (Bell et al., 1993; Clifford et al., 1995). Even so, the use of non-spatial approaches is still common when characterizing exposures and effects of contaminant stresses. Many current ecological risk assessment methodologies assume that habitat is homogeneous and of high quality, with the expectation that this results in conservative estimates of exposure. However, the presence of spatial autocorrelation in available habitat is known to affect population dynamics and extinction risk (Gonzalez-Megias et al., 2005). Higher amounts of spatial environmental autocorrelation can increase the spatial synchrony in the population leading to an increased risk of local extinction (Engen et al., 2002). This trend can either be exaggerated or ameliorated by high positive or negative correlations between habitat quality and contaminant concentrations.

The incorporation of landscape features into the ecological risk assessment process holds promise for increasing the accuracy of exposure assessments and, ultimately, for supporting more informed management decisions (Kapustka, 2003; Linkov et al., 2002; Topping and Odderskær, 2004). Screening estimates of exposures to measured contaminant concentrations requires that multiple data points, measured over space and time, be reduced to a single exposure concentration. The most common approach used in ecological risk assessments for determining an exposure concentration in an area involves using a summary statistic (e.g., mean, percentile, confidence limit). Clearly, the use of a summary statistic does not address the potential for variable exposure due to spatial and/or temporal differences among individual organisms over time and, while appropriate for the purposes of screening-level ecological risk assessments, may not capture bias in exposures that are due to non-random use of habitat. Risks to wildlife are partly a function of this variability, in addition to differences in the foraging behavior of organisms being exposed and uncertainties in toxic effects at the individual organism and population level. Species and individual organisms with foraging areas of different sizes and locations will experience different exposure levels, even at the same contaminated site. While this may be a well-known factor in determining exposure (Suter, 1993), methods that account for this uncertainty are seldom incorporated into risk assessments (Freshman and Menzie, 1996).

Geographical information systems (GIS) are being coupled more regularly with traditional ecological exposure techniques to incorporate spatial variability and landscape features into ecological risk assessments. GIS tools make it more feasible to conduct spatially explicit modeling (Akçakaya, 2001). The additional inclusion of movement models that simulate foraging and other behaviors allows for more comprehensive assessments of population exposures and risks (Gaines et al., 2005a; Kooistra et al., 2005; Topping et al., 2005), although they are accompanied by increased complexity and difficulties in parameterization (Sibly et al., 2005). Inter- or intra-species differences in movement strategies and habitat valuation can have substantial effects on

cumulative exposures, even when receptors share a common range. Movement models conducted at an appropriate scale allow important receptor information, such as foraging area/home range, relative desirability of habitat areas, contaminant distribution, and individual organism behavior, to be captured more realistically in the assessment, and for their effects on the calculated cumulative exposure distribution to be explored.

The majority of direct terrestrial exposures to contamination in soil occur via foraging activities (USEPA, 2005). There is already an extensive literature concerning the methods and applications of different foraging strategies, so the incorporation of contaminant exposures into existing foraging models does not require substantial theoretical development. Successive implementations of a foraging model that accounts for the movement of an individual organism across an underlying soil contaminant concentration grid and tracks its unique cumulative exposures, allows one to build a distribution of the potential population level exposure doses at a contaminated site. This can be combined with forage quality preference information to establish the likelihood of feeding at a particular location to reflect more accurately the movement and feeding activities of wildlife.

Habitat is defined as areas that provide resources necessary for survival and reproduction of a species. Forage quality information can be estimated using habitat preference variables that can be species-specific and also age-dependent. Different species are preferentially drawn to some habitat features due to greater food availability, better cover for hiding, or improved temperature regulation. The resulting process where individual organisms use available habitats in a non-random manner is termed habitat selection (Morris, 2003). The foraging area is where the species most often finds food resources. Since the majority of exposure from chemical contaminants in terrestrial systems comes from ingestion (for non-volatile contaminants and non-burrowing receptors) (USEPA, 2005), sub-areas with high browse quality for the pronghorn are the areas most likely to contribute the majority of total dose if exposure concentrations are equivalent. Underestimating the time that an individual organism spends in these preferred foraging areas can result in an under- or over-estimation of dose and risk depending on whether the soil and sagebrush concentrations in these preferred areas are high or low, relative to the overall average chemical contaminant concentrations for the habitat.

2. Exposure model development

The specific focus of this paper concerns the modeling of pronghorn exposures via foraging in the vicinity of a fluoride manufacturing plant in the western United States. Pronghorn exposures to fluoride in sagebrush and soil are due to long-term aerial deposition from the manufacturing plant and bioaccumulation from soil into sagebrush. A simple movement model is implemented to estimate pronghorn exposures on the contaminated landscape. Dose sensitivity is examined by varying the spatial habitat quality distribution while the spatial distribution of contamination is held constant. The model does not address intra-individual variability other

Table 1 – Pronghorn exposure variables

Variable	Description	Lower	Default	Upper	Units	Reference
Dose _i	Average dose for individual <i>i</i>	–	–	–	(mg fluoride/kg BW)/day	Calculated
T	Number of days	–	90	–	Day	Length of summer
C _t	Fluoride concentration in forage at time <i>t</i>	6000	–	162000	mg/kg	Data
I _f	Daily forage ingestion rate	0.76	0.85	0.97	kg dry forage/day	Severson et al., 1968
I _s	Daily soil ingestion rate	0.0215	0.0487	0.084	kg soil/day	Arthur and Gates, 1988
B _v	Soil–plant concentration factor	0.024	0.045	0.056	(mg/kg dry plant)/(mg/kg soil)	Rope et al., 1988
BW	Female body weight	34	40	48	kg	Nowak, 1991
A	Absorption factor	0.44	0.54	0.63	Unitless	Welch et al., 1983

than foraging behavior, so more complex individual-based dynamics, such as bio-energetic considerations (Kooijman, 2000; Nisbet et al., 2000) or the response of sagebrush to foraging pressure, are not addressed.

An agent-based model is implemented for this ecotoxicological assessment application and the parameter of interest is the simulated population distribution of the daily dose for a mobile receptor. Elements needed to conduct the analysis include habitat quality information, a wildlife exposure model that includes a movement algorithm, and a spatial distribution of chemical contaminant concentrations so that exposures can be calculated for all portions of the site.

2.1. Exposure model

This study considers uncertainty in habitat selection as a primary contributor to uncertainty in estimated population dose. Therefore, probability distributions were used to parameterize the exposure and effects model to compare sensitivity in these inputs versus habitat selection. As mentioned earlier, of the common terrestrial exposure pathways, soil and food ingestion are dominant (USEPA, 2005). The simple terrestrial exposure equation used herein sums the contribution from the ingestion of forage vegetation and soil ingestion for each individual pronghorn (Eq. (1)) based on measured forage concentrations. Table 1 defines and summarizes the exposure variable distributions used in Eq. (1).

$$\overline{\text{Dose}}_i = \sum_{t=1}^T \frac{(C_t I_f + (C_t/B_v) I_s) A}{T} \quad (1)$$

Pronghorn prefer browse and forb species as year-round forage items (Hoover, 1966), and do not seem to be limited by food availability during the summer months (Smith and Malechek, 1974). Browse such as sagebrush can vary from 40% (Hoover, 1966) to over 90% (Severson et al., 1968) of the pronghorn diet. A body weight of 40 kg is used here as representative of a typical adult pronghorn (Nowak, 1991). Severson et al. (1968) estimated an average daily forage intake of 0.85 kg dry weight/day for pronghorn. For a body weight of 40 kg, this is a food ingestion rate of 0.021 kg dry matter/kg body weight/day. The pronghorn soil ingestion rate is based on an annual mean soil ingestion rate of 48.7 grams/day, approximately 5.4% of the total daily dry matter intake (Arthur and

Gates, 1988). Welch et al. (1983) estimate dry matter digestibility for pronghorn at 54%. This latter value is used as an estimate of the gut absorption rate for the contaminant.

The mammalian toxicity reference value (TRV) commonly used for fluoride is 52.8 mg/kg/day; this is the low observed adverse effects level (LOAEL) reported by Aulerich et al. (1987) based on dietary studies of mink. The soil cleanup concentration applied at the study site is less conservative, 30,000 mg/kg (Mattice et al., 1998). This soil concentration was converted to a TRV of 760 mg/kg/day using the exposure assumptions and parameter values for pronghorn embodied in Eq. (1) and presented in Table 1. This 760 mg/kg/day value is used here as a dose-based cleanup standard for determining whether remedial action is necessary at the study site under different habitat quality distribution scenarios. A distribution for the fluoride TRV is not defined for the sensitivity analysis since we are assessing the uncertainties in pronghorn exposure to fluoride, although uncertainty in soil screening levels and toxicity can be a significant contributor for estimating effects (Regan et al., 2002).

2.2. Habitat delineation

Habitat suitability index (HSI) models provide species-specific habitat information that can be used for exposure assessment, impact assessment and habitat management. HSI models synthesize available information on habitat quality and are scaled so that each location is assigned a value between 0 for unsuitable habitat and 1 for optimal habitat (Allen et al., 1984). Habitat areas with index values closer to 1 are likely to indicate higher rates of survival, growth, and/or reproduction for a given species and may therefore have a higher carrying capacity or species occupation rate, while areas with index values closer to 0 reflect low quality habitat that likely reflect reduced or no carrying capacity for that species. There are many instances where strong positive or negative correlations between contaminant distributions and habitat quality (as measured by HSI) are present. Obviously, there can be strong negative correlations between areas of optimum habitat and contaminant concentrations as a result of anthropogenic disturbance. Indeed, foraging habitat may be less desirable for the pronghorn at some locations compared to others due to invasive plant species, human presence/disturbance, and pesticide use (Maurer and Holt, 1996), in addition to environmental contamination. On the other hand, some wildlife

species may thrive under the same conditions of human disturbance; for these species one would expect to have positive correlations between high environmental contaminant concentrations and desirable habitat due to contamination being present in disturbed areas preferred by the species.

HSI models, as originally developed, assume that there is a positive relationship between the quality of the habitat (as measured by the quantitative index) and habitat carrying capacity or likelihood of species presence. Data that support the determination of the probability of movement to each available habitat location would have greater value for implementing a movement model. Some forms of HSI may be inappropriate as the basis of a foraging model if they are based on regressions to variables that are not important to foraging. For example, if the majority of time for a species is spent sheltering from predators or from adverse weather, indices based on these values and used as the basis for a foraging model may inaccurately represent the actual foraging behavior of the species.

The pronghorn has a variable range, dependent upon habitat, season, sex, and age (Yoakum, 1978); their normal range is reasonably large compared to the area of the study site. Pronghorn form large, mixed herds of up to 1000 individuals in the fall and winter, breaking into smaller sex-segregated groups during the spring and summer. Foraging pronghorn can be expected to cover the full study area during a summer season. Daily movements depend on availability of resources; Yoakum (1978) has reported movements of 0.1–0.8 km per day in spring and summer, and 2–9.7 km per day in fall and winter. For the purposes of this modeling effort, a grid with nodes every 0.5 km was defined for the site covering approximately 310 square kilometers. In the movement model, each pronghorn feeds at one grid location per day and is then assumed to move and feed at any of eight adjacent patches on the subsequent day, depending upon the relative desirability of these eight patches. The use of an eight square (versus nine square) movement model forces average movements of 0.5 km per day due to the selected grid resolution. This daily movement is consistent with female pronghorn use of the area during the summer and also prevents simulated individual pronghorn from inhabiting the same square for long periods of time, thereby degrading habitat quality. Therefore, habitat quality is assumed to be constant over the course of the simulation, independent of foraging pressure. The simulation is run for a 90-day period to simulate the length of the summer season. Individual pronghorn are randomly placed on the grid, as the initial condition, and the simulation run for one year prior to the 90-day exposure period so that pronghorn start in suitable habitat according to the available habitat quality. A distribution of simulated population exposures was generated by iterating each exposure scenario for 1000 individuals, representing the exposed population. A random start location is used for each pronghorn and there is no restriction on the number of pronghorn per grid cell. Summer is the breeding season and males over 3 years of age become territorial as the summer progresses while females and younger males travel freely. The movement model implemented is more representative of female movement patterns during the summer season; males will sometimes cover more ground during the summer and have established territories by the fall. The vari-

ables important for habitat quality and preference shift in late fall and winter, and a different HSI would need to be used to account for a higher valuation of habitat with more topographic relief as shelter from the elements and cover from predators.

2.3. Foraging and movement model

Spatially explicit foraging models have been developed and implemented for ecological risk assessment and management purposes (Freshman and Menzie, 1996; Hope, 2005; Linkov et al., 2002; Woodbury, 2003). A number of ecological mechanisms and processes are incorporated into these foraging models. Habitat resource distribution is commonly incorporated into ecological risk assessments (Gaines et al., 2005b; Chow et al., 2005) and is incorporated for the model application in this paper. Other ecological mechanisms (not addressed by this model) can influence the use of habitat resources, and resulting estimates of population dose when used in an ecological risk assessment context, include interspecific interactions (Connell, 1961; Rosenzweig, 1981), intraspecific variability and competition (Gill and Wolf, 1975), spatial scale (Morris, 1992; Pulliam and Danielson, 1991), and density-dependence (Bellows, 1981).

Additional considerations relevant for agent-based implementations include how to incorporate aspects of individual organism behavior into the movement model. Uncorrelated random walk models are the simplest for animal locomotion. These assume that individual organisms move in “hops” of fixed length and duration. After each hop, the individual is assumed to move in a new, randomly chosen direction. These models vary depending on the number of adjacent grid nodes eligible for movement and whether the grid is square or hexagonal. With a correlated random walk model (Kareiva and Shigesada, 1983), the individual organism is assumed more likely to move in a direction similar to the previous direction (Holmes, 1993) such that the movement direction is correlated to some degree between daily movements. However, use of uncorrelated or correlated random walk models, in the absence of other ecological mechanisms, are not expected to change the summary statistics significantly for exposure estimates in the ecological risk assessment process and, therefore, should not have an impact on remediation decisions resulting from their implementation. This is because random foraging strategies are reasonably approximated by the mean and confidence limit summary statistics commonly used in risk assessments where individual organism behavior is not modeled.

To the contrary, non-random movement can significantly impact exposure estimates used for an ecological risk assessment. An additional constraint in agent-based movement models is the selection of areas to move to, either through the use of prior knowledge concerning foraging area productivity or by evaluating suitability of habitat from a distance (Pulliam and Danielson, 1991). This selective use of habitat, in conjunction with positive or negative spatial correlation between habitat quality and contaminant concentrations, can impact the exposure portion of an ecological risk assessment and resulting risk management decisions. Incorporating this selective behavior allows for more realistic simulation of for-

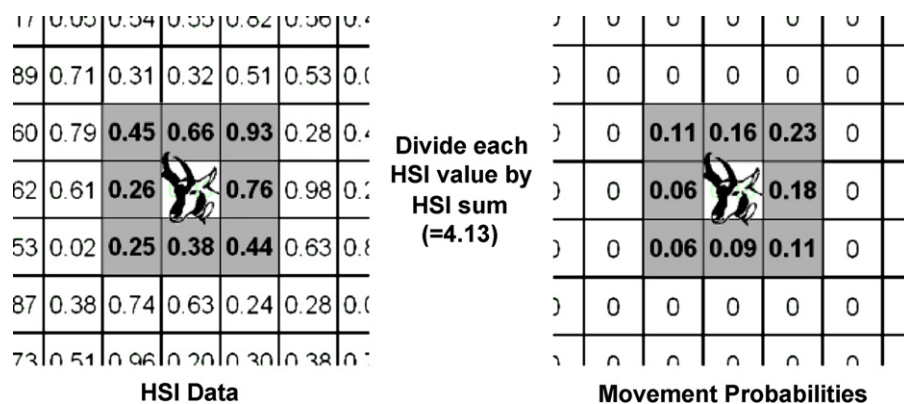


Fig. 1 – Visual description of habitat-based movement model described by Eq. (2). Pronghorn is eligible to move to one of eight adjacent grid cells each time step. Movement probabilities for each cell are determined by dividing the HSI value for that cell by the sum of the HSI values for the eight cells available for movement.

aging in that individual organisms use available habitat in a nonrandom manner based on habitat preferences (Morris, 2003). The model we chose herein to represent pronghorn movement is a nonrandom walk model (8-square) that incorporates the relative value of different habitat patches through an HSI value assigned to each grid node. At each movement step, the pronghorn proceeds to one of the eight adjoining patch locations. The probability of moving to any one adjacent patch is given by dividing the index value of the prospective patch by the sum of the indices of the corresponding eight adjacent patches available for movement. The process is illustrated in Fig. 1. Eq. (2) shows the general formula for estimating the probability (p_{ij}) of moving from an original grid location i to each of the neighboring grid locations j for k number of potential movement squares.

$$p_{ij} = \frac{HSI_j}{\sum_{j=1}^k HSI_j} \quad (2)$$

This approach is reasonable for simulating non-territorial movement; therefore, it is representative for female pronghorn and younger males that spend the summer months searching for high quality foraging patches, as well as for more mature males in early summer before they become territorial (Yoakum, 1980). This approach is not relevant for males during the breeding season when they defend defined territories. However, females are our receptor of interest because the toxicity values for fluoride are based on reproductive effects in mammals at dose levels similar to those calculated for in the model at our study site. This approach can be implemented in a Monte Carlo framework, where individual organisms are allowed to move over the landscape based on their valuations of nearby habitat. Since the individual valuation of habitat and movement does not incorporate density-dependence or other interactions, individual organisms can be modeled separately. Summary statistics of the resulting population dose distribution of the individual organisms modeled for an area can then be assessed for risk management purposes by comparison to a toxicity reference value.

In the modeling efforts conducted for this paper, the grid of habitat values was varied for each set of Monte Carlo simulations, corresponding to different correlation strengths between habitat quality and exposure concentration. While HSI values for each grid node range from 0 to 1, the different habitat scenarios were designed to have different correlation strengths between estimated habitat quality and analytical fluoride concentrations from sampled locations. The habitat data for the different scenarios in this paper are therefore hypothetical, but they are tied into the actual spatial distribution of fluoride using the desired correlation strength. The scenarios represent the full range of possible bivariate spatial correlations and are chosen to maximize variability in spatial foraging at the site when the model is implemented. Eight different sets of HSI data were generated, with a range of correlation values (0.75, 0.5, 0.25, 0, −0.25, −0.5, −0.75), as discussed in the next section.

2.4. Spatial distribution of contamination and habitat

The distribution of the contaminant in space is another important feature of the landscape, and rarely are there enough resources available to collect and analyze soil and biota exhaustively for the entire site being considered. For these situations, and in order to support the underlying movement model of the receptor species, it may be necessary to implement interpolation methods to estimate contaminant concentrations in areas where data are not available.

The contamination data used for estimating exposure at the site consisted of regularly spaced samples of desert sagebrush analyzed for fluoride, collected for several years in the early 1990s over a 400-km² area. A histogram of data is presented in Fig. 2. The desert sagebrush fluoride concentrations used here are as reported in Mattice et al. (1998) and are above expected concentrations in non-contaminated sagebrush; derived soil concentrations are also above reference concentrations of soil for the 200–500 mg/kg area (Rope et al., 1988). The data in Fig. 2 fail Lilliefors test for normality, Lilliefors test for lognormality, and the Anderson–Darling and Kolmogorov–Smirnov tests for a gamma distribution; therefore, non-parametric statistical data assessment techniques

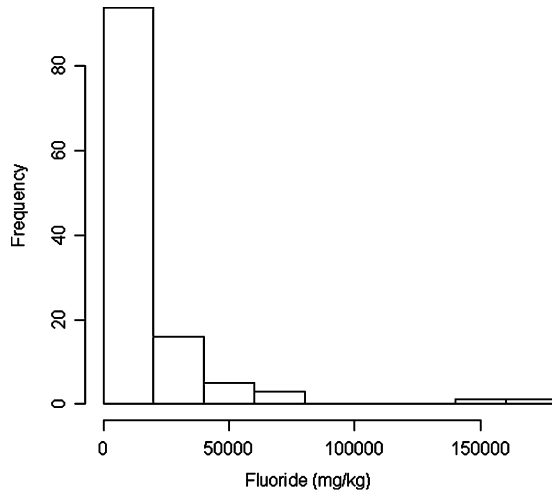


Fig. 2 – Histogram of fluoride sagebrush concentrations in mg/kg. Data fail parametric tests and non-parametric methods are used for confidence limit.

were used. For conducting non-spatial risk assessments (and ignoring any possible auto-correlation), current USEPA guidance recommends using a Chebyshev upper confidence limit (UCL) on the mean value exposure concentration determined from non-parametric data sets (USEPA, 2002).

The fluoride data set was used to indirectly produce the eight simulated habitat data sets for the pronghorn movement model. These data sets introduce strong positive, strong negative, and neutral correlations between habitat quality and contaminant concentrations to evaluate simulated exposures for a range of conditions. A non-linear transformation of the measured fluoride concentrations C at all locations u_i , with a uniformly distributed random element ε , was implemented for all of the N locations where fluoride data were collected. This is shown in Eq. (3):

$$HSI(u_i) = (\alpha + \varepsilon)C(u_i)^{\beta+\varepsilon} \quad \text{for } i = 1 \dots N \text{ s.t. } r = x \quad (3)$$

Values of α and β were determined by trial and error until the desired correlation strengths, r , for the range of correlations from $x = 0.75$ to $x = -0.75$ were achieved to represent each habitat scenario. The values were then scaled by the maximum observed HSI value so that all the habitat values ranged from 0 to 1. This approach maximizes the entropy of the habitat variable among the different scenarios with respect to the fluoride contamination distribution. This non-linear (versus linear) transformation of the concentration data is required to construct a habitat preference distribution that generates habitats with desired negative correlations. However, it also requires that a different spatial correlation function used in kriging the original fluoride forage concentration data set (discussed next paragraph) be used to interpolate the data for each habitat scenario. Therefore, a different interpolation method is necessary to interpolate habitat data sets so that there are HSI values for all u_i . An inverse distance relationship with a power of 2 was used to spatially model the different HSI grids for each of the correlation strengths.

A number of interpolation methods can quantitatively describe the spatial distribution of a contaminant, though care must be taken not to overreach with inadequate data sets (Woodbury, 2003). Various geostatistical methods are available, including various forms of kriging (Rossi et al., 1992; Goovaerts, 1997) and geometric interpolants such as natural neighbor (Watson, 1995) and inverse distance (Shepard, 1968). These methods rely on an assumption of spatial continuity; i.e., two sample locations close together are more likely to be similar in concentration than two samples farther apart.

Ordinary kriging was used to estimate forage fluoride concentrations for all grid locations at the site. A Gaussian semivariogram with 14 lags was implemented, with a range of 7000 m, and a nugget and sill fitted using iteratively reweighted least squares (Cressie, 1985). Interpolation was performed using Spatial Analysis and Decision Assistance (SADA) software (Stewart and Purucker, 2006). Ordinary kriging output for the sagebrush fluoride concentrations and the inverse distance interpolation of the habitat preference data sets for the different correlation strengths with the fluoride data are presented in Fig. 3. A uniform habitat data set for a random walk scenario is also included in the figure.

3. Model results

The simple, discrete-time, habitat selection exposure model was run with the same grid of fluoride sagebrush exposure concentrations and seven different sets of habitat suitability index data, corresponding to spatial correlation strengths of 0.75, 0.5, 0.25, 0, -0.25, -0.5, -0.75 between the habitat index values and fluoride concentrations at sampled locations. In addition, results from a simulated random walk model and non-spatial assessment using the mean and UCL95 of the sample data are presented. Model code was developed in Visual Basic, and used that software's pseudo-random number generator for the Monte Carlo runs. Summary statistics for each set of 1000 Monte Carlo simulations are presented in Table 2.

3.1. Pronghorn exposure model results

The results given are average daily exposure fluoride doses of pronghorn for 1000 simulations of a 90-day period; the averages are directly comparable to the fluoride site-specific toxicity reference value of 760 mg/kg/day. The mean fluoride concentration in sagebrush was 16500 mg/kg and the Chebyshev UCL is 25700 mg/kg, resulting in doses of 417 mg/kg/day and 649 mg/kg/day, respectively. The calculated dose results for the summary statistics are below our dose-based standard of 760 mg/kg/day. For the simulation results, exposure cumulative distribution functions were used to estimate the percent of simulated doses above that action level. The population exposure exceedance percentages for no correlation (17%) and the random walk scenario (18%) are both below the 20% that is often used in the US as a remedial action trigger (Suter et al., 1995; Hope and Peterson, 2000). However, the three habitat scenarios with positive correlation produced increases in the percent of population that exceeded the 20% threshold trigger; the +0.25 correlation scenario produced a

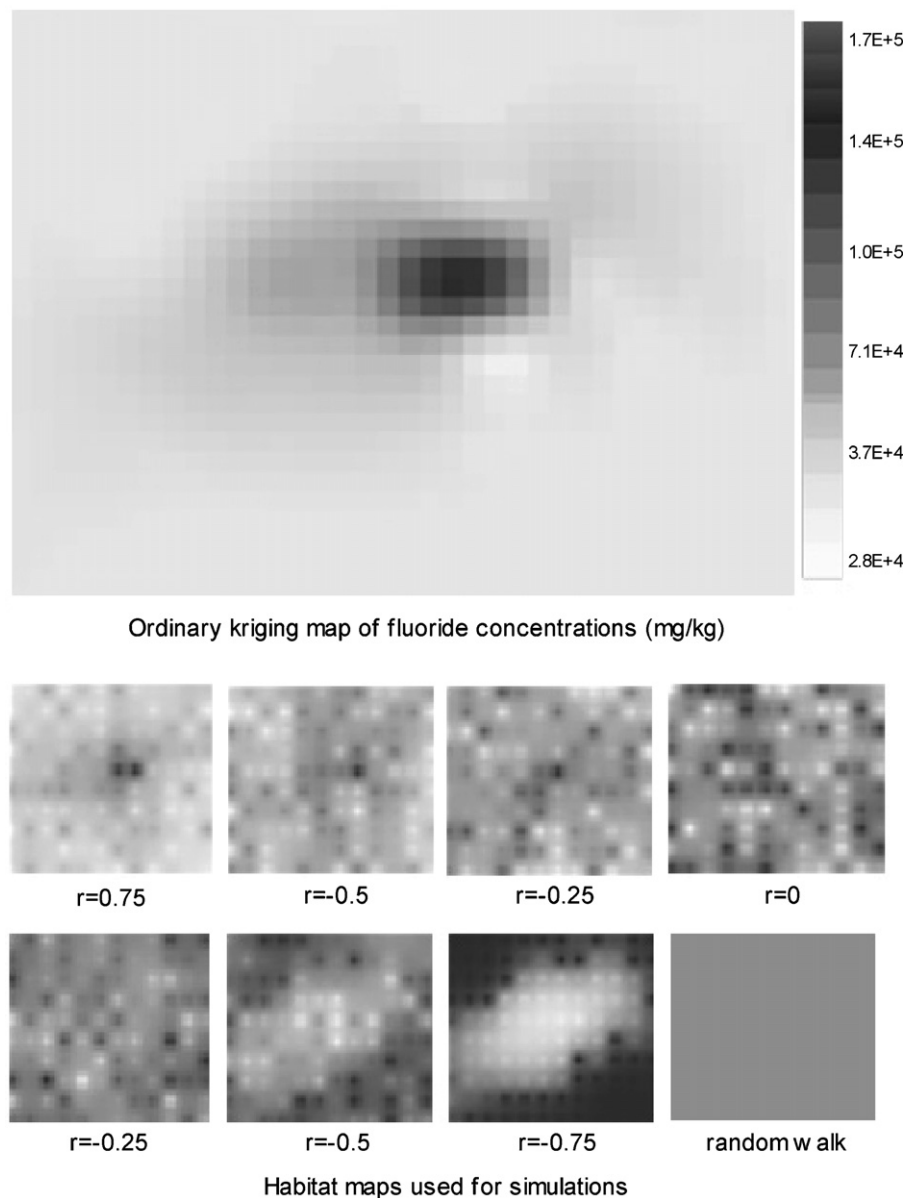


Fig. 3 – Ordinary kriging results for fluoride concentrations in sagebrush. Smaller figures are simulated HSI data sets with different degrees of correlation to the fluoride data set. The random walk habitat data set has uniform habitat quality.

Table 2 – Descriptive statistics for fluoride exposures (mg/kg/day) for different correlation strengths between habitat and fluoride concentrations

Scenario	Median	Mean	Standard deviation	Coefficient of variation	%Exceeding dose standard
$r=0.75$	664	958	811	0.85	46
$r=0.5$	381	621	558	0.90	29
$r=0.25$	319	543	521	0.96	23
$r=0$	230	424	408	0.96	17
$r=-0.25$	221	379	371	0.98	12
$r=-0.5$	177	251	221	0.88	3.4
$r=-0.75$	166	194	86	0.44	0.5
Random walk	275	439	389	0.89	18
Mean concentration	–	417	–	–	–
Chebyshev UCL	–	649	–	–	–

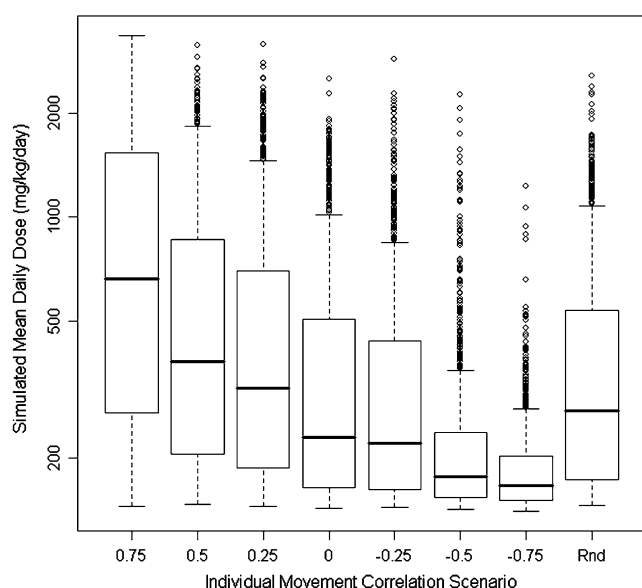


Fig. 4 – The population dose distributions are presented as box plots for each exposure/movement scenario. Population doses decrease as the degree of correlation between habitat suitability and contamination levels decreases from 0.75 to -0.75 . The random walk exposure box plot, used for comparison purposes to the correlation scenarios, is similar to the exposures for 0 correlation.

population exceedance rate of 23%, the $+0.5$ correlation rate 29%, and the high correlation scenario a 46% exceedance rate. The negative correlation scenarios produced a declining trend; the -0.25 correlation population exceedance rate was 12%, the -0.5 correlation rate 3.4%, and the -0.75 correlation scenario exceeded the state standard for only 0.5% of the exposed population. This trend in the simulated exposure dose for the different correlation scenarios, when compared to non-spatial methods and uncorrelated habitat data, demonstrates that the presence of spatial autocorrelation between habitat suitability and contaminant concentration distributions can potentially change the remedial decision that will be made at the site. Results for each habitat scenario are further illustrated in the box plots in Fig. 4.

Sensitivity analyses were also performed for other variables in the exposure model to compare the variability in the simulated doses for the different habitat scenarios. The one-at-a-time (OAT) design method (Daniel, 1973; Campolongo et al., 2000) is a simple, efficient sensitivity analysis method that was used to vary each model input variable one at a time from the standard default value. Reasonable lower and upper values were selected for the daily forage ingestion rate, daily soil ingestion rate, soil-forage concentration factor, body weight, and absorption factor variables to examine the effect of the entire range of the input variable on the population dose output. These effects can then be compared to the calculated population dose results for the full range of correlated habitat suitability-contaminant concentration strengths to determine the relative importance of these variables. Our sensitivity analysis results (summarized in Appendix A, Tables A.1–A.5) indicated that none of the model exposure variables individ-

ually contributed as much variation in the model output as did varying the sets of habitat suitability data, based on the different correlation strength scenarios.

For the pronghorn-fluoride contamination site model developed here, the movement rules for female pronghorn allowed them to utilize the whole site, but in general, to be attracted to higher quality foraging areas. Exposure distributions for male pronghorn would likely be quite different during periods of territoriality, since they partition the site into discrete, defended areas. In this instance, the dose distributions of the sexes could differ significantly.

3.2. Remedial design implications

Implementing an efficient remedial design strategy at a site strongly depends on understanding the spatial distribution of contamination. Therefore, risk methods that explicitly factor in spatially distributed properties have great potential for assisting in efficient remedial design (Freshman and Menzie, 1996). The inclusion of methods that use habitat information can improve the quality of terrestrial ecological exposure assessments by adding both a spatial and temporal component. Typically, in remedial design, the goal is to determine specific areas of a contaminated site that require remediation in order to minimize the amount of soil treatment necessary to meet cleanup criteria for the sake of cost efficiency. Exposure, dose, and risk models can therefore be used to optimize the remedial design by incorporating spatial information into the assessment. To illustrate this capability, two different approaches are examined: an iterative hot spot removal design with modifications based on conservative foraging assumptions; and a dose-based spatial remedial design.

The iterative hot spot removal remediation design technique is commonly used (Freshman and Menzie, 1996; Schulz and Griffin, 2001). For this method, a model simulates the cleaning of individual contaminated grid areas at a site in descending order of contaminant concentration magnitude. The representative site statistic that is being compared against a decision criterion (e.g., the mean or specified percentile of a soil concentration) is recalculated, as subsequent area blocks of soil are cleaned, and compared to a target, ecologically-based remedial concentration until the decision criterion is reached. This approach is simple to implement, but does not incorporate habitat quality or home range considerations. The successive model outputs can be plotted as a curve of remediated area site versus site post-remediation soil concentration to illustrate the effect of cleaning progressively more of the site. Alternatively, the curve can be plotted as cost of remediation versus site post-remediation soil concentration (Van Meirvenne and Goovaerts, 2001) when cost is a constraint.

This approach can be modified using conservative receptor species foraging assumptions that retain aspects of the spatial distribution of the contamination to provide exposure estimates consistent with the foraging home ranges, without explicitly incorporating habitat information (Freshman and Menzie, 1996). Specifically, based on the home range area of the receptor being assessed, the method assumes that the receptor is exposed to the most contaminated grid cells at the site equivalent to this area, and remediation of these grid cells is conducted until the average concentration of the cells con-

stituting this area is below the cleanup standard. This method for generating an exposure curve can be sufficient for many remedial decisions. However, this method can still under- or over-estimate exposure for receptors in some situations, e.g., the combination of a receptor species that non-randomly uses heterogeneous habitat where there is a fairly significant degree of positive or negative correlation between contaminant concentrations and habitat quality, as modeled in this paper.

Under such circumstances, rather than implementing a post-remedial exposure curve that only cleans areas with the highest concentrations, an optimal remedial design method would target areas of the site where the highest estimated levels of receptor population exposure occur by considering both habitat use and the spatial distribution of contamination. Evaluating the cumulative population exposure at each grid cell has the advantage of incorporating selective use of the habitat in combination with the spatial distribution of contamination. The main drawback is that this approach can be computationally extensive since the set of Monte Carlo simulations has to be run iteratively for each remediated block. However, the cleanup area curves generated are intuitively satisfying, and may differ significantly from cleanup curves that do not account for how the receptor uses habitat.

4. Summary and conclusions

Although it has been suggested that complications introduced into population exposure and risk assessment by accounting for spatial heterogeneity may be unimportant (Emlen, 1989), the spatial structure of contamination and habitat, and their correlation, can have a profound impact on the estimated exposure of a population to contamination, as shown in this work. These impacts can complicate the tasks of understanding, managing, and preventing unacceptable levels of exposure to contamination in terrestrial environments (McLaughlin and Landis, 2000). The use of spatially explicit approaches in ecological risk assessment requires more complexity in model development. However, the resulting models are amenable to scenario-based decision-making often applied in environmental remediation (Baker et al., 2004; Schumaker et al., 2004) and provide a better foundation for ecological approaches in assessing and prioritizing the risks from combinations of multiple stressors, physical sources, and exposed species than is often applied in strict toxicological applications (Relyea and Hoverman, 2006).

A correlation analysis between contaminant concentrations and habitat quality is recommended as a means of determining whether conducting a spatially explicit exposure analysis that incorporates HSI data is informative versus non-spatial implementations. The calculation of correlation between analytical concentration data and habitat quality can be done at the collected sample level, where observations of habitat quality are collected in the field simultaneously with the collection of contaminated media; or at the site grid level, if aerial photos or satellite images are used to quantify habitat quality (e.g., vegetative cover or type) and contaminant

concentrations can be spatially interpolated. If it is deemed necessary to perform a spatially explicit assessment, selective habitat use by potential endpoint species can also be compared to identify those species that have higher correlations of habitat suitability with the measured contaminant concentrations. This information should be made available for endpoint species under consideration by stakeholders and be considered as an important part of the endpoint selection process. When significant correlations are present, it also may be more efficient to incorporate assumptions regarding habitat use into the remedial design process to optimize cleanup of the site. In addition, there are also trophic level considerations that should be in consideration, if, for example, the endpoint selection process selects a higher trophic level species as an endpoint, extensive correlation between habitat use and lower trophic level species that the endpoint depends upon may result in inaccuracies in estimating exposure to the higher trophic level species, so it may be worthwhile to examine correlations between habitat use and species other than selected endpoints if the endpoints utilize them, even if they were not explicitly selected as endpoints (in order to accurately calculate exposure at higher trophic levels).

There is a potential disconnect between the importance of cleaning-up areas that are of high habitat quality for species of concern versus the impacts of remediation on these same areas. This is a problem when contaminant concentrations and habitat quality for a species are positively correlated since a number of remediation technologies result in destruction of habitat, and this, in itself, can cause significant ecological risk to the species of concern (Chapman et al., 2003; Wenning et al., 2006). The decision to remediate and the choice of technology must take into account the local and regional importance of the habitat and the potential for post-remedial recovery. In industrial areas, contamination and habitat quality for a number of typical receptors are often negatively correlated, and endpoint species that are more likely to inhabit these areas may be preferentially considered.

Current ecological risk assessments are more capable of fully considering landscape characteristics and spatial interactions than ever before. However, it is not always clear, for a specific contaminated site, when the implementation of a spatially explicit ecological risk assessment is worth the additional assessment effort. Examining the degree of spatial correlation between contaminant distributions and habitat quality for species of interest at contaminated sites is a simple way to check for possible significance of landscape when conducting an ecological risk assessment.

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Appendix A

see Tables A.1–A.5.

Table A.1 – One-at-a-time sensitivity analyses of the daily dose exposure for varying the forage ingestion variable

OAT sensitivity value	Low			Central			High		
Percentile	10%	50%	90%	10%	50%	90%	10%	50%	90%
$r = 0.75$	148	580	1975	162	664	2258	190	877	2441
$r = 0.5$	139	325	1415	159	381	1495	179	456	1833
$r = 0.25$	136	287	1124	151	319	1330	173	353	1561
$r = 0$	134	202	913	151	230	1091	172	263	1210
$r = -0.25$	134	199	848	150	221	854	171	251	975
$r = -0.5$	134	165	388	150	177	402	171	201	459
$r = -0.75$	134	147	237	149	166	268	171	187	291
Random walk	135	225	825	151	275	961	172	290	1016

Low, central, and high parameter values for pronghorn forage ingestion (Table 1) were used to run sets of Monte Carlo simulations and calculate distribution statistics for daily dose exposure (mg/kg/day) for each of the habitat scenario and parameter variable combinations. Three percentile values are presented (10%, 50%, 90%) for each set of Monte Carlo simulations. Variation in the daily dose exposure simulations within a habitat scenario for the full range of the forage ingestion variable is less than the variation amongst different habitat correlation strengths with all exposure input parameters held constant.

Table A.2 – One-at-a-time sensitivity analyses of the daily dose exposure for varying the soil ingestion variable

OAT sensitivity value	Low			Central			High		
Percentile	10%	50%	90%	10%	50%	90%	10%	50%	90%
$r = 0.75$	112	516	1437	162	664	2258	211	942	2965
$r = 0.5$	105	269	1079	159	381	1495	201	477	2024
$r = 0.25$	102	208	919	151	319	1330	201	423	1649
$r = 0$	101	151	745	151	230	1091	198	302	1218
$r = -0.25$	101	149	637	150	221	854	197	292	1245
$r = -0.5$	101	124	292	150	177	402	197	243	869
$r = -0.75$	100	110	178	149	166	268	196	216	348
Random walk	101	169	620	151	275	961	198	331	1212

Low, central, and high parameter values for pronghorn soil ingestion (Table 1) were used to run sets of Monte Carlo simulations and calculate distribution statistics for daily dose exposure (mg/kg/day) for each of the habitat scenario and parameter variable combinations. Three percentile values are presented (10%, 50%, 90%) for each set of Monte Carlo simulations. Variation in the daily dose exposure simulations within a habitat scenario for the full range of the soil ingestion variable is less than the variation amongst different habitat correlation strengths with all exposure input parameters held constant.

Table A.3 – One-at-a-time sensitivity analyses of the daily dose exposure for varying the soil–plant concentration factor variable

OAT sensitivity value	Low			Central			High		
Percentile	10%	50%	90%	10%	50%	90%	10%	50%	90%
$r = 0.75$	93	427	1188	162	664	2258	208	956	2662
$r = 0.5$	87	222	892	159	381	1495	195	498	1999
$r = 0.25$	84	172	760	151	319	1330	189	385	1702
$r = 0$	84	125	616	151	230	1091	187	280	1380
$r = -0.25$	84	124	527	150	221	854	187	277	1180
$r = -0.5$	83	103	241	150	177	402	186	230	540
$r = -0.75$	83	91	147	149	166	268	186	205	329
Random walk	84	140	513	151	275	961	187	314	1149

Low, central, and high parameter values for the fluoride soil–plant concentration factor for sagebrush (Table 1) were used to run sets of Monte Carlo simulations and calculate distribution statistics for daily dose exposure (mg/kg/day) for each of the habitat scenario and parameter variable combinations. Three percentile values are presented (10%, 50%, 90%) for each set of Monte Carlo simulations. Variation in the daily dose exposure simulations within a habitat scenario for the full range of the soil–plant concentration factor variable is less than the variation amongst different habitat correlation strengths with all exposure input parameters held constant.

Table A.4 – One-at-a-time sensitivity analyses of the daily dose exposure for varying the body weight variable

OAT sensitivity value	Low			Central			High		
Percentile	10%	50%	90%	10%	50%	90%	10%	50%	90%
$r = 0.75$	167	768	2139	162	664	2258	166	648	2209
$r = 0.5$	156	400	1606	159	381	1495	155	363	1582
$r = 0.25$	152	309	1367	151	319	1330	152	321	1257
$r = 0$	151	225	1109	151	230	1091	150	226	1021
$r = -0.25$	150	223	844	150	221	854	150	221	854
$r = -0.5$	150	186	487	150	177	402	150	177	402
$r = -0.75$	150	165	253	149	166	268	149	164	255
Random walk	150	254	914	151	275	961	151	254	890

Low, central, and high parameter values for pronghorn body weight (Table 1) were used to run sets of Monte Carlo simulations and calculate distribution statistics for daily dose exposure (mg/kg/day) for each of the habitat scenario and parameter variable combinations. Three percentile values are presented (10%, 50%, 90%) for each set of Monte Carlo simulations. Variation in the daily dose exposure simulations within a habitat scenario for the full range of the body weight variable is less than the variation amongst different habitat correlation strengths with all exposure input parameters held constant.

Table A.5 – One-at-a-time sensitivity analyses of the daily dose exposure for varying the absorption factor variable

OAT sensitivity value	Low			Central			High		
Percentile	10%	50%	90%	10%	50%	90%	10%	50%	90%
$r = 0.75$	136	626	1743	162	664	2258	195	897	2496
$r = 0.5$	127	326	1309	159	381	1495	183	467	1874
$r = 0.25$	124	252	1114	151	319	1330	177	361	1596
$r = 0$	123	184	903	151	230	1091	176	263	1294
$r = -0.25$	123	181	773	150	221	854	175	260	1107
$r = -0.5$	122	151	354	150	177	402	175	216	507
$r = -0.75$	122	134	216	149	166	268	174	192	309
Random walk	123	205	752	151	275	961	175	294	1077

Low, central, and high parameter values for the fluoride absorption factor (Table 1) were used to run sets of Monte Carlo simulations and calculate distribution statistics for daily dose exposure (mg/kg/day) for each of the habitat scenario and parameter variable combinations. Three percentile values are presented (10%, 50%, 90%) for each set of Monte Carlo simulations. Variation in the daily dose exposure simulations within a habitat scenario for the full range of the absorption factor variable is less than the variation amongst different habitat correlation strengths with all exposure input parameters held constant.

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