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A spatially explicit individual-based controlled random walk model to determine exposure levels and risks of environmental contaminants for terrestrial organisms in river floodplains

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Abstract

An understanding of the complexity of cumulative risks is a prerequisite for the development of more efficient guidelines to provide data for future regulation of chemicals. For this reason it is important that we improve our understanding of complex exposure situations and develop adequate tools for risk assessment. Current approaches to environmental risk assessment usually do not allow for site-specific and other spatially detailed evaluations, yet taking into account spatial variability is increasingly being recognised as a further and essential step in sound exposure and risk assessment.

The present study developed a spatially explicit model that estimates exposure of higher terrestrial organisms to contamination, taking into account spatial variation in contaminant concentrations and habitat characteristics, and food-web relations. This model was parameterised for the heavy metal cadmium and applied to estimate exposure concentrations for 10 characteristic floodplain species in the study area ‘Afferdensche en Deestsche Waarden’, an embanked floodplain along the river Waal, the Netherlands.

Model results showed that the simulation of spatially explicit behaviour, governed by spatial variation in habitat characteristics, yielded intra-specific variation in exposure whereby four habitat characteristics were of influence on predicted exposure concentrations, i.e. soil contaminant concentration, habitat quality, habitat quantity, and food availability. Differences in exposure between different species, however, were governed by variations in diet preferences rather than spatial variation in environmental factors. Food chains based on terrestrial invertebrates resulted in considerably higher exposure estimates than food chains based on diet items of plant origin. Location-specific comparison of predicted and measured internal cadmium concentrations for five mammal species revealed that differences are generally confined to an average factor of 4. Accounting for spatially explicit behaviour and variation in age covers 29% of the variation in internal concentrations observed in the field.

It was concluded that the model provides a valuable tool to generate spatially explicit exposure estimates that include intra-specific variation specifically resulting from spatially explicit behaviour. In addition, this model approach seems especially suitable for exposure assessment to cumulative stressors, because, when dealing with multiple stressors, approaching exposure assessment in a spatially explicit manner is particularly appropriate. Besides employing the model for cumulative exposure assessment, it will be extended in a more flexible object-oriented programming environment that supports the inclusion of relevant ecological processes at population level. In this way more insight can be gained in population survival related to exposure concentrations.
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1. Introduction

Although it is generally acknowledged that chemical, biological, and other physical stressors can cause a variety of effects on human and ecological health, assessing the risks associated with them is, both methodologically and computationally, considerably more complex than current risk assessment practices. An understanding of the complexity of cumulative risks (i.e. risk to mixtures of multiple stressors) is a prerequisite for the development of more efficient guidelines to provide data for future regulation of chemicals. For this reason it is important that we improve our understanding of complex exposure situations and develop adequate tools for risk assessment (NoMiracle, 2006).

A major shortcoming of current approaches to environmental risk assessment is that they usually do not allow for site-specific and other spatially detailed evaluations. Many scientists (e.g. Marinussen and Van der Zee 1996; Hope 2000; Korre et al. 2002; Linkov et al. 2002; Gaines et al. 2005; Makropoulos and Butler 2006) generally acknowledge that exposure and hence risk is strongly influenced by the spatial positions of both receptors and stressors. Exposure to contaminants involves spatially complex situations due to the heterogeneity of contaminant distributions and other environmental characteristics. Thus, taking into account spatial variability is increasingly being recognised as a further and essential step in sound exposure and risk assessment.

This is especially important when focussing on cumulative risk. In a truly cumulative approach it is realised that human and ecological receptors are not exposed to individual substances in a relatively homogeneous environment, but to toxic mixtures in a heterogeneous environment. Single substances entail spatially variable environmental concentrations and variation in the combinations of these substances only increases the spatial variability of exposure and risk. A spatially explicit approach to cumulative exposure assessment might therefore generate more accurate exposure and risk estimates. Distinction can be made between risk assessment approaches in which spatial data and processes are modeled mechanistically (e.g. Kooistra et al. 2001, 2005) and approaches in which spatial data are related using fuzzy statistical techniques (e.g. Makropoulos and Butler 2006). The present study focuses on mechanistic modeling of spatial processes.

Kooistra et al. (2001, 2005) investigated the impact of territory size and spatial variability in cadmium (Cd), copper (Cu) and zinc (Zn) contamination on risk estimates for the little owl (Athene noctua) in an embanked Dutch river floodplain. They used a GIS (Geographical Information System) to both quantify spatial variability in metal contamination and delineate the little owl’s territories, and subsequently linked this to an exposure and effect model. Territories were delineated by superimposing a grid with regularly spaced circular foraging areas on a contamination map. For each foraging area, exposure concentrations were determined by calculating the area-weighted average soil concentrations in suitable habitat. This average concentration was used as input for a simple food web-based exposure model. Such an approach assumes that animals spend equal amounts of time in all suitable habitats within a specific foraging range. However, the proportion of time that a mobile animal spends per unit area can be expected to be spatially variable (Matthiapolous 2002), as it is governed by a.o. spatial variation in habitat quality and species-specific foraging behaviour. Since spatial variability in time spent per unit area can be expected to have profound influence on the duration and hence the level of exposure to a certain stressor, exposure estimates are expected to improve if this factor is incorporated in the assessment procedure. Hope (2000; 2001; 2005) developed an exposure modelling procedure in which an individual receptor moves over a multi-celled landscape, thereby encountering and accumulating spatially variable amounts of contamination. In this procedure, movement can either be random or governed by “rules of movement” that represent a receptor-specific way of responding to variations in the landscape. Such an approach not only facilitates the incorporation of species-specific foraging behaviour in a risk assessment procedure, but can also be applied to account for spatial variability in the duration of exposure, or the presence of multiple contaminants and their respective spatial variability.

The present study is carried out within the framework of the NoMiracle work package 4.2, The explicit modelling of exposure and risk in space and time, and contributes directly to NoMiracle objective III – to improve our understanding of complex exposure situations and develop adequate tools for sound exposure assessment – and indirectly to objectives I and VI (see Appendix I). The main aim is to develop a generic model for exposure and risk assessment that addresses the spatial heterogeneity for both ecological and human receptors. The derived aim is to tailor and apply such a
model to a case study. Therefore a floodplain was selected along the river Waal, the main distributary of the river Rhine in the Netherlands, which is contaminated with a.o. the heavy metal cadmium. A novel spatially explicit and receptor-oriented model has therefore been developed assessing the exposure of ecological receptors to stressors. This model improves our understanding of complex and cumulative exposure situations and can be used to more accurately assess complex exposure situations in which the spatial positions of stressors and receptors are relevant. The model is a first step towards modelling of exposure to multiple stressors.

This report describes the model in detail. A conceptual model approach (Hope 2000; 2001; 2005) was transformed into an operable program, using specific software and structuring the code into several modules (Chapter 2). The model has been parameterised for the case study area. Chapter 3 discusses the study area and its specific input data. The model has been analysed by varying the levels of spatial detail and validated with field data of internal cadmium concentrations obtained from several floodplain species (Chapter 4). Chapter 5 shows the results for the case study and discusses the analysis and validation of the model. Chapter 6 is a discussion of the model itself and Chapter 7 concludes with possible applications of the model and proposes future model improvements.
2. Modelling principle

2.1 Introduction

A conceptual and general exposure modelling procedure was adopted that has been developed by Hope (2000; 2001; 2005). In this procedure, an individual receptor moves over a multi-celled landscape, whereby it encounters and accumulates spatially variable amounts of contamination. Movement can either be random or governed by “rules of movement”, representing a receptor-specific way of responding to variations in the landscape. Such an approach not only facilitates the incorporation of species-specific foraging behaviour in a risk assessment procedure, but can also be applied to account for spatial variability in the duration of exposure or the presence of multiple contaminants and their respective spatial variabilities.

The present model extended the procedure of Hope (2000; 2001; 2005) by incorporation of a food web module, thus accounting for feeding relationships between species. A food web-based model is considered a particularly useful tool to estimate exposure of higher trophic level species, both because the intake of contaminated food is the main exposure route for most vertebrate species (Ma et al. 1991; Shore & Douben 1994) and because these higher trophic species are generally unavailable for tissue sampling (Hope 1999). Furthermore, whereas Hope (2000; 2001; 2005) constructed a hypothetical landscape to examine his procedure, we applied our model to a specific study area (i.e. ’Afferdensche en Deestsche Waarden’; ADW study area) and compared the model results with internal body concentrations measured in several animal species being found in this area. This enabled us to test the performance of the model.

2.2 Model approach

The model, schematically illustrated in Figure 1, simulates the entire life spans of organisms that make up a food web of endpoint target species in a spatially explicit manner – through the simulation of foraging behaviour – in a polluted area, whereby these organisms are exposed to varying levels of contamination. Corresponding levels of exposure are calculated using species-specific exposure routes and taking into account environmental factors that determine to which levels of exposure organisms are exposed.

The simulation is performed in a landscape divided into a regular grid. Each grid cell contains information on environmental variables such as contaminant concentration in the soil, ecotope type, and, for this specific floodplain study area, distance to flood-free terrain. Ecotopes are spatial units that are homogeneous with respect to vegetation structure, succession stage, and main abiotic factors, as defined according to the Dutch river ecotope classification system (Rademakers & Wolfert 1994). They are used to determine the species-specific habitat quality for each cell.

The predicted environmental concentrations (PECs), i.e. the environmental concentrations to which the organisms are exposed, are calculated by spatially linking the foraging path to the cell-specific exposure concentrations. These PECs are finally compared with the predicted no effect concentrations (PNECs) for each species to establish their level of risk.

Two types of organisms are distinguished based on their trophic level in the food web, namely: basic (1st level) and higher level (2nd and 3rd level) organisms. The basic level organisms are considered sessile; they do not move between the cells. The higher level organisms are considered mobile; they move through the landscape, in a manner corresponding to their specific foraging behaviour within an area that represents their home range. This behaviour is mainly directed by species-specific spatial variation in habitat quality, which determines the likelihood of an organism to visit this specific habitat. By simulating the movements of the organism a foraging path is constructed, which is assumed to represent the individual’s foraging behaviour throughout its life span.

Cell-specific exposure concentrations are calculated, using formulas that express the various routes of contaminant uptake and depend on food web relations. The exposure of basic level organisms is governed by direct contact with the soil (e.g. through soil ingestion or dermal uptake). The higher level organisms are assumed to be indirectly exposed to contaminants through the intake of contaminated food.
2.3 Software

The exposure model was constructed in MS Excel® with the MS Visual Basic Application® (VBA). MS Excel® worksheets were used to store input and output data. The model is grid-based, i.e. the environmental variables constituting the model landscape are "mapped" into cells within spreadsheets, in the same relative spatial locations as in the actual landscape. Species-specific data of the individuals modelled and their food web relationships between the species are also available in MS Excel worksheets. The model is implemented in a VBA program to manipulate the data; it reads the values presented in the worksheets to perform the necessary calculations and prints results to worksheets. Maps were visualised using ArcGIS software.

Arrays are used throughout the model: in the construction of virtual habitat quality maps, in the run-time storage of food web and species-specific data from worksheets, and in the storage of several run-time generated temporary data, etc. The landscape characteristics are stored in a two-dimensional array, one dimension for the longitude, the other for the latitude.

2.4 Model structure

The program code contains several modules to calculate species-specific exposure, of which the most important are (1) a landscape module, (2) a foraging path module, and (3) an exposure and risk module (Figure 1 & 2). The landscape module tailors the spatial input data for the foraging path and the exposure and risk modules. Each cell of the landscape grid contains information on contaminant concentrations and on environmental parameters influencing foraging behaviour. The receptors are represented by sets of algorithms that describe the processes relevant to exposure, which can generally be classified into moving and uptake algorithms. In the foraging path module, movement algorithms allow individual receptors to move from grid cell to grid cell, thereby obeying species-specific movement rules. Movement continues until the total area foraged (i.e. the sum of the area of the grid...
cells visited) equals the receptor-specific foraging area within its home range. Subsequently, the exposure and risk module calculates exposure for each cell of the foraging path established in the previous module, and for the entire foraging path established. The time basis for the internal concentration calculation is an organism’s life-span, represented by its complete foraging path and hence a single individual is simulated with one foraging path. The exposure and risk calculations are based on concentration in food and have no explicit time basis. The entire program can be repeated \( n \) times in order to simulate exposure for a population of \( n \) individual receptors. It should be noted that inter- or intra-specific interactions between individuals have not yet been incorporated; only one individual can be simulated at a time. For each simulation the risk per species is calculated. The whole program is controlled from a so-called main module, which sequentially calls each of the other modules for execution (refer to Appendix IIa for the VBA source code). A print module is used to print the results from the virtual arrays to spreadsheets. Table 1 provides an overview of the principle parameters of the model.

**Landscape Module**

**Habitat Quality Maps**

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</table>

HQ – Habitat Quality Value

**Cell-specific Exposure Maps**

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</tbody>
</table>

C – Potential Exposure Value

**Foraging Path Module**

**Exposure & Risk Module**

**Exposure and Risk Indicator**

Calculations

\[
\text{Exposure} = C_1 + c_2 + C_3 + c_4
\]

Figure 2. Simplified presentation of the principal modules of the model and their coherence.

### 2.4.1 Landscape module

The landscape is divided into a regular grid, of which each cell contains information on environmental characteristics and with which organisms can interact. This paragraph outlines the method used to generate species-specific habitat maps. Please refer to the section Environmental Data in paragraph 3.2 for the description of the input data specific to the study site.

Habitat quality refers to the ability of the environment to provide conditions appropriate for individual and population persistence. In general, the concept of creating species-specific maps of habitat quality, relates measurable environmental variables to the suitability of a site for a species. Hall et al. (1997) suggested that habitat quality should be considered a continuous variable, ranging from low to medium to high, based on resources (such as food, water and cover) available for survival, reproduction, and population persistence, respectively. Other models (USFWS, 1996; Burgman et al., 2001) provide a numerical index of habitat suitability on a 0.0 (non-habitat) to 1.0 (optimal habitat) scale, based on the assumption that there is a positive relationship between the index and habitat carrying capacity (U.S. Fish and Wildlife Service 1981).
## Table 1. Overview of the model parameters

<table>
<thead>
<tr>
<th>Symbol</th>
<th>Description</th>
<th>Units</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Required parameters</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>( N )</td>
<td>number of individuals modelled</td>
<td>unitless</td>
</tr>
<tr>
<td><strong>Environmental variables</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>( \text{HQ}_{i,e} )</td>
<td>habitat quality of model cell ( i ) in terms of vegetation structure and main abiotic factors</td>
<td>dimensionless</td>
</tr>
<tr>
<td>( E_i )</td>
<td>Ecotope type in cell ( i )</td>
<td>dimensionless</td>
</tr>
<tr>
<td>( C_{i,\text{soil}} )</td>
<td>contaminant concentration in soil in model cell ( i )</td>
<td>mg·kg(^{-1}), dry wt</td>
</tr>
<tr>
<td>( D_{F_i} )</td>
<td>distance to higher area that will not be flooded at a certain discharge</td>
<td>m</td>
</tr>
<tr>
<td>( \text{DMC} )</td>
<td>dry matter content as fraction of fresh weight</td>
<td>dimensionless</td>
</tr>
<tr>
<td><strong>Species traits</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>( \text{HR} )</td>
<td>home range size</td>
<td>m(^2)</td>
</tr>
<tr>
<td>( \text{HQ}_{\text{threshold value}} )</td>
<td>threshold value of ( \text{HQ} ) that is assumed to be sufficient for supporting an organism</td>
<td>dimensionless</td>
</tr>
<tr>
<td>( f_{\text{suitable habitat}} )</td>
<td>Minimum suitable habitat fraction</td>
<td>dimensionless</td>
</tr>
<tr>
<td>( \text{CD}_{sp} )</td>
<td>Species-specific colonisation distance</td>
<td>m</td>
</tr>
<tr>
<td>( \text{LE} )</td>
<td>life expectancy</td>
<td>days</td>
</tr>
<tr>
<td>( \text{FR} )</td>
<td>feeding rate</td>
<td>g·day(^{-1})</td>
</tr>
<tr>
<td>( \text{BW} )</td>
<td>body weight</td>
<td>g</td>
</tr>
<tr>
<td><strong>Food web</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>( f_j )</td>
<td>fraction of prey item ( j ) in diet</td>
<td>dimensionless</td>
</tr>
<tr>
<td>( f_{i,,j} )</td>
<td>fraction of prey item ( j ) in diet present in model cell ( i )</td>
<td>dimensionless</td>
</tr>
<tr>
<td><strong>Ecotoxicological variables</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>( \text{BAF} )</td>
<td>bioaccumulation factor</td>
<td>dimensionless</td>
</tr>
<tr>
<td>( a,b )</td>
<td>regression coefficients</td>
<td>dimensionless</td>
</tr>
<tr>
<td>( \text{CAE}_j )</td>
<td>contaminant assimilation efficiency of contaminant from prey item ( j )</td>
<td>dimensionless</td>
</tr>
<tr>
<td>( \text{GCF}_j )</td>
<td>gut content correction factor for prey item ( j )</td>
<td>dimensionless</td>
</tr>
<tr>
<td>( \text{PNEC}_{sp} )</td>
<td>species-specific predicted no effect concentration in food</td>
<td>mg·kg(^{-1}) food(^{-1})</td>
</tr>
<tr>
<td>( \text{NOEC}_{\text{food}} )</td>
<td>no effect concentration in food</td>
<td>mg·kg(^{-1}) food(^{-1})</td>
</tr>
<tr>
<td><strong>Bioenergetics</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>( \text{EMR} )</td>
<td>existence metabolic rate</td>
<td>kJ·day(^{-1})</td>
</tr>
<tr>
<td>( \text{FMR} )</td>
<td>field metabolic rate</td>
<td>kJ·day(^{-1})</td>
</tr>
<tr>
<td>( \text{FCC} )</td>
<td>food caloric content</td>
<td>kJ·g(^{-1})</td>
</tr>
<tr>
<td>( \text{FAE} )</td>
<td>food assimilation efficiency</td>
<td>dimensionless</td>
</tr>
<tr>
<td><strong>Generated parameters</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>( A_{i,,j} )</td>
<td>age of prey item ( j ) in model cell ( i ) as fraction of its life expectancy</td>
<td>dimensionless</td>
</tr>
<tr>
<td>( \text{HQ}_i )</td>
<td>habitat quality of model cell ( i )</td>
<td>dimensionless</td>
</tr>
<tr>
<td>( \text{HQ}_{i,f} )</td>
<td>habitat quality of model cell ( i ) in terms of food availability</td>
<td>dimensionless</td>
</tr>
<tr>
<td>( \text{TAF} )</td>
<td>total area foraged</td>
<td>m(^2)</td>
</tr>
<tr>
<td>( \text{FA} )</td>
<td>foraging area</td>
<td>m(^2)</td>
</tr>
<tr>
<td>( \text{PEC} )</td>
<td>predicted environmental concentration</td>
<td>mg·kg(^{-1}) food(^{-1})</td>
</tr>
<tr>
<td>( \text{RI} )</td>
<td>risk indicator</td>
<td>dimensionless</td>
</tr>
</tbody>
</table>
The spatially explicit habitat maps in this study are created by discretising a landscape into subunits (raster cells or polygons) and calculating a habitat quality value for each unit. This concept is comparable to the habitat suitability index (HSI) model described by the USFWS (1996) & Burgman et al. (2001). The suitability of a site for a species are related to vegetation structure and main abiotic factors (represented by ecotopes) and to food availability. Species-specific habitat quality values were assigned to each model grid cell that is part of the study area and are calculated according to equation 1:

\[ HQ_{i} = HQ_{i,e} \cdot HQ_{i,f} \]  

\( HQ_{i} \) = habitat quality of model cell i (dimensionless)  
\( HQ_{i,e} \) = habitat quality of model cell i in terms of vegetation structure and main abiotic factors (dimensionless)  
\( HQ_{i,f} \) = habitat quality of model cell i in terms of food availability (dimensionless)

\( HQ_{i,e} \) was determined by linking an ecotope map to a species-ecotope matrix, in which each ecotope type was assigned a species-specific habitat quality value based on literature and expert knowledge. \( HQ_{i,f} \) represents the availability of the main resources food and cover.

\( HQ_{i,f} \) was introduced with regard to the assumption that a predator prefers a site with high chances of encountering a prey above less favourable sites. Food availability (\( HQ_{i,f} \)) for a certain species X depends on the sum of all habitat quality (\( HQ_{i} \)) values for its respective prey species. Hereby the \( HQ_{i} \) value of each diet species is weighted according to the fraction it represents in the diet of species X, according to equation 2. Consequently, if no prey species are available in a given cell, \( HQ_{i,f} \) for this cell is 0 and an organism is assumed to only forage in habitat with available food resources.

\[ HQ_{i,f} = \sum_{j=1}^{n} (f_j \cdot HQ_{i,j}) \]  

\( f_j \) = fraction of prey item j in diet (dimensionless)  
\( HQ_{i,j} \) = habitat quality of model cell i for prey item j (dimensionless)  
\( n \) = number of prey items

Areas beyond a species-specific Colonisation Distance (CD_{sp}) from flood-free areas are assumed to be unavailable for small mammal species. These areas are assigned a value of \( HQ_{i} = 0 \), irrespective of \( HQ_{i,e} \) and \( HQ_{i,f} \) values. The resulting species-specific habitat quality maps are used for defining the foraging path. Refer to Appendix IIb for the VBA source code of the Landscape module.

2.4.2 Foraging behaviour module
The Foraging behaviour module consists of three parts, which are described below: 1) the selection of a starting position, 2) the movement algorithm and 3) a stopping criterion. The foraging path module is only applied to mobile organisms (2nd and 3rd food web level species).

Starting position selection
The starting position is considered as an individual’s nest from which it starts to forage. For every cell in the study area, the model establishes whether the cell is a possible starting position. A possible starting position must meet the following general criteria:

1. The habitat in the cell should be classified as suitable, i.e. habitat quality in terms of vegetation structure and main abiotic factors should have the maximum value available in the study area (i.e. \( HQ_{i,e} = 1 \)). It is assumed that an organism will most likely nest in habitat that provides shelter and it is further assumed that habitat quality (\( HQ_{i,e} \)) with value 1 will provide this shelter;
2. The starting position should lie in an area that is colonisable for the species of concern. Specifically for the study area, a floodplain that suffers the effects of periodical flooding, this criterion intends to deal with species-specific capabilities in selecting nesting areas. The species available in the ADW study area show different abilities in colonising periodically flooded areas in the floodplain; some are restricted to nest in flood-free terrain, others are restricted to nest in the areas that lie within the species-specific Colonisation Distance (CD\textsubscript{sp}), i.e. the maximum distance a species can disperse, for colonisation purposes, from flood-free terrain in a period between two successive floodings (set at 9 months). The varying colonising abilities are reflected by a custom probability distribution: cells in non-flooded area have a probability of 1 and cells in periodically flooded areas have a probability that linearly decreases from 1 to zero when the distance to flood-free terrain (DF\textsubscript{i}) increases from zero to the species-specific Colonisation Distance. This probability is given by equation 3.

\[
CP_i = 0 \rightarrow \left( -\infty , 0 \right) \cap \left[ CD_{sp} , \infty \right) \\
CP_i = 1 - \frac{DF_i}{CD_{sp}} \rightarrow \left[ CD_{sp} \right]
\] (3)

\( CP_i \) = Colonisation Probability of cell \( i \) (dimensionless)
\( DF_i \) = Distance to flood-free terrain in cell \( i \) (meters)
\( CD_{sp} \) = Species-specific maximum colonisation distance (meters)

The final probability of a cell to be chosen as a starting position (\( P_i \)) is calculated by dividing each cell-specific colonisation probability by the cumulative colonisation probability of all the possible starting positions (equation 4).

\[
P_{i,sc} = \frac{CP_i}{\sum_{p=1}^{n} CP_p}
\] (4)

\( P_{i,sc} \) = Probability of cell \( i \) to be selected as starting position (dimensionless)
\( CP_i \) = Colonisation Probability of cell \( i \) (dimensionless)
\( CP_p \) = Colonisation Probability of \( p^{th} \) possible starting positions (dimensionless)
\( n \) = number of suitable starting positions;

3. The starting position is the centre cell of the home range. It should be possible to define a suitable home range surrounding the starting position. Burt (1943) described a home range as: “... that area traversed by an individual in its normal activities of food gathering, mating, and caring for the young.” In order to realistically simulate the individual’s foraging behaviour the movements are confined to the area that makes up its home range. This is considered to be the area in which the individual moves during its entire life and its size is species-specific. In the model, the home range area is represented by a group of cells in a square that surround the starting position. If the starting position specified makes the home range area to extend out of the floodplain boundaries, then the floodplain boundaries will be considered to be the home range area limits of that individual. The home range should provide sufficient resources for an animal to survive, so an individual requires a minimum area of suitable habitat within its home range. Cells within the home range are considered suitable for foraging when the HQ is greater than a user-defined habitat quality threshold value (HQ\textsubscript{threshold value}). This threshold value is set at zero, since not sufficient data was found in literature indicating a specific value for this threshold. The model tests whether sufficient suitable habitat area is available in a home range by comparing the fraction suitable habitat cells with a threshold value, according to equation 5. This threshold value, the minimum suitable
habitat fraction \( f_{\text{suitable\_habitat}} \) is the species-specific minimal suitable \((HQ_i > HQ_{\text{threshold\_value}})\) fraction of the home range that the species needs in order to survive. For the calculation of \( f_{\text{suitable\_habitat}} \) refer to Chapter 3.

\[
\frac{HR_{\text{cells}}(HQ_i > HQ_{\text{threshold\_value}})}{HR_{\text{cells}}} > f_{\text{suitable\_habitat}} \quad (5)
\]

\( HR_{\text{cells}}(HQ_i > HQ_{\text{threshold\_value}}) \) = number of cells within the home range with a higher habitat quality than the habitat quality threshold value

\( HR_{\text{cells}} \) = total number of cells within the home range

\( f_{\text{suitable\_habitat}} \) = species-specific minimum fraction of suitable habitat within the home range that the species needs in order to survive (dimensionless).

Once a set of all the possible starting positions is established, one starting position is chosen randomly from this set in accordance with the colonisation probability distribution. For the VBA source code refer to Appendix IIC, section starting position.

**Movement algorithms**

Movement of the mobile individuals is determined by habitat requirements and a random element and confined to a set of selectable destination cells within the home range area. The set of selectable cells depends on:

1. **Habitat quality**
   Cells should have a habitat quality \((HQ_i)\) higher than the habitat quality threshold value \((HQ_{\text{threshold}})\);

2. **Energy status**
   The model assumes that food (comprising the location-specific preys available) is available where \( HQ_i \) is greater than zero. However, it is not very realistic to assume that food is illimitably available: the natural resources need to be restored. Therefore, a rule is applied that excludes the last three cells that were visited from being selected as next positions of the foraging path. This implementation prevents the organism from moving to and fro a limited number of cells, which is considered unrealistic. It also, indirectly, introduces a form of directional persistence (i.e. the degree of correlation with previous direction in the random walk), because the organism can not move backwards;

3. **Moving abilities of receptor (flying, walking)**
   Differences between terrestrial and flying organisms are made explicit in the movement algorithm. The group of cells that can consecutively be selected for foraging differs topologically between the two classes.
   Since terrestrial organisms moving from one location to the other have to actually travel across and interact with the terrain in between, algorithms are introduced that make terrestrial animals scrutinise only adjacent cells in the cell selection process, following the *Neighbouring Cell* rule (Figure 3). If no adjacent habitat-containing cells are found, the search radius is enlarged. Search radius enlargement increases at intervals of one cell length until cell selection criteria are met (i.e. the above mentioned criteria *habitat quality* and *energy status* are fulfilled). This rule results in the destination cell being the nearest suitable and precludes that an organism gets trapped in a cell.
Are any of the neighbouring cells within the search radius possible destinations?

Yes
No

The initial search radius comprises the directly neighbouring cells.

The search radius is enlarged. One of them is selected randomly according to a probability distribution (based on Habitat Quality).

Figure 3. Possible destination cells for ground moving animals defined by the Neighbouring Cell rule.

Contrastingly, flying organisms are assumed capable of moving from one habitat-containing cell to any other habitat-containing cell within their home range, without interacting with the terrain in between. This is applied in the model by enabling all the suitable cells within this home range to be possible destination cells; the flying organisms are not restricted to scrutinise only adjacent cells.

Once the set of selectable cells is defined, cell selection takes place. It is assumed that the habitat quality $HQ_i$ (equation 1) influences the foraging behaviour – the consumer will spend more time in higher profitability areas – following the reasoning of the optimal foraging theory (MacArthur & Pianka, 1966; Charnov, 1976). A forager will have a preference for habitats where it is more likely to encounter food, and thus for habitats where the food availability is higher and hence where $HQ_i$ and $HQ_f$ is higher. In the model, cells with higher $HQ_i$ will have a higher chance of being selected as a destination cell in the foraging path. A custom distribution with visiting probabilities is calculated for the range of possible cells based on the $HQ_i$ of these cells. Cells that have an $HQ_i$ equal to zero get a probability of zero and can hence not be selected during foraging. The cell-specific probability value ($P_i$) is calculated by dividing the $HQ_i$ for this cell by the total habitat quality for all cells in the range of possible next cells, according to equation 6.

$$P_{i,fp} = \frac{HQ_i}{\sum_{i=1}^{n} HQ_i}$$

(6)

$P_{i,fp}$ = Probability of cell i to be selected as foraging path cell (dimensionless)

$HQ_i$ = habitat quality of model cell i (dimensionless)

n = number of cells in foraging path

When the probabilities are calculated, one of the cells is selected randomly from the set of selectable cells according to the distribution defined.

**Stopping criterion**

The consecutive selection of new positions that constitute the foraging path (i.e. the moving/foraging of the organism) stops when a stopping criterion is met, depending on the area visited (equation 7).

$$TAF = FA$$

(7)
TAF = total area foraged (Sum of the areas of the cells which belong to the foraging path)
FA = species-specific foraging area (area of all habitat-containing cells in the home range area)

As stated before, the entire foraging path represents an organism’s life-span and the amount of time spent per cell visited thus depends on the length of the foraging path (as well as the habitat quality of that cell).

Please refer to Appendix IIc, section Foraging path for the VBA source code of the movement algorithms and stopping criterion.

2.4.3 Exposure and Risk module

Exposure and risk estimates, which are derived from life-time exposure concentrations and risk indicators respectively, are determined for higher level species only and are based on contaminant concentrations in their diet. The exposure is calculated consistently with the major routes channelling the fate of the contaminant through the food web. Hereby, the organism is exposed to the contaminant concentrations specific for the cells that form its foraging path. First, internal concentrations in lower level (1st level) organisms are calculated. They are directly exposed to the cell-specific contaminant concentration in soil of the cell they live in. Secondly, cell specific internal concentrations in higher level (2nd and 3rd level) organisms are calculated; they are indirectly exposed to contaminants through the intake of contaminated food. From the internal concentrations of lower level organisms, the exposure concentrations in food of higher level organisms are calculated. A more detailed description of the calculations involved in the exposure and risk assessment is given below. Note that for all equations described in this section, weight units refer to fresh weight unless indicated otherwise.

**Internal concentration in 1st level organisms**

For 1st level, soil-dwelling and plant organisms internal metal concentrations are directly derived from soil concentrations, through the application of so-called bioaccumulation factors (BAFs) or by means of regression equations. BAFs are empirically determined ratios of contaminant concentrations in organisms to those in soil and their application is based on the assumption that the concentration of chemicals in organisms is a linear, no-threshold function of concentrations in soil (Sample et al. 1998). However, several studies indicate that this assumption does not hold true for heavy metals, as BAFs for heavy metal concentrations in invertebrates tend to decrease with increasing soil concentrations (e.g. Gräff et al. 1997, Lock & Janssen 2001, Van Straalen et al. 2001). Log-linear regression equations are therefore likely to give more accurate results for these types of contaminants (Sample et al. 1998) and if sufficient data are available this approach should be preferred. General equations for both approaches are given below (equations 8 and 9). Both approaches yield internal concentrations in 1st level organisms on a dry-weight basis. Because other equations applied in the exposure module are based on fresh weight, values derived from equations 8 and 9 are converted to fresh weight concentrations by multiplication with species-specific values for dry matter content (DMC) as fraction of total body weight (10).

\[
C_{DW,i,j} = C_{i,soil} \cdot BAF
\]  
\[
^a \log C_{DW,i,j} = a + b \cdot ^a \log(C_{i,soil})
\]

\[
C_{i,j} = C_{DW,i,j} \cdot DMC
\]

\(C_{DW,i,j}\) = contaminant concentration in prey item j in model cell i (mg·kg\(^{-1}\) dw)
\(C_{i,soil}\) = contaminant concentration in soil in model cell i (mg·kg\(^{-1}\) dw)
BAF = bioaccumulation factor (dimensionless)
a,b = regression coefficients (dimensionless)
$C_{i,j}$ = contaminant concentration in prey item j in model cell i (mg·kg$^{-1}$)

DMC = dry matter content as fraction of fresh weight (dimensionless)

It should be noted that the application of bioaccumulation factors and regression equations to determine internal concentrations of chemicals in organisms is based on the assumption of a stable ratio between a certain concentration in soil and a corresponding internal concentration in the organisms, i.e. it is assumed that the intake of the chemical is balanced by excretion and/or internal regulation mechanisms. Please refer to Appendix IId, section Internal concentrations for the VBA source code.

**Internal concentration in 2nd and 3rd level organisms**

To calculate internal contaminant concentrations of 2nd and 3rd level prey items, a more mechanistic approach was chosen, taking into account processes that are relevant for bioaccumulation. Because the case study focuses on cadmium, excretion mechanisms are assumed to be negligible and are not taken into account.

Basically, the contaminant concentrations of all prey items are added, whereby the contaminant concentration in each prey item k present in a certain cell i ($C_{i,k}$) is weighted by the fraction this item represents in the diet of the receptor. It is assumed that during the foraging procedure diet fractions should always sum up to 100% and therefore the absence of a certain prey item is compensated for by proportionally enlarging the fractions of the prey items that are actually present in the cell. This reflects the assumption that the species modelled exhibit optimistic foraging behaviour.

Many mammalian and avian predators consume the whole carcass of a prey and hence the contaminant load of the prey’s gut and its contents might be of significance. The gut and contents of mice, for example, have been shown to significantly contribute to the total body burden of cadmium (Walker et al. 2002) and therefore a prey item-specific so-called gut content correction factor (GCF) is incorporated in the exposure calculations.

Further, the internal concentration of a 2nd level species j is dependent on its consumption rate $F_{R_j}$, the assimilation of contamination from the prey items digested (CAE$_k$), and the time span over which accumulation has been taking place. It is assumed that predators do not select prey species according to their age and therefore each 2nd level prey item (3rd level organisms are never preyed upon) in each cell is assigned a randomly determined age $A_{i,j}$ as fraction of its life expectancy $L_{E_j}$. This 2nd level prey item is assumed to have lived its entire life in the cell where it was caught, implicating that its internal concentration is only related to the soil contaminant concentration in this specific cell. Taking all relevant variables into account, for each 2nd level prey item a cell-specific internal concentration is then calculated according to equation 11:

$$C_{i,j} = A_{i,j} \cdot L_{E_j} \cdot \frac{F_{R_j}}{B_{W_j}} \cdot \sum_{k=1}^{n} C_{i,k} \cdot f_{i,k} \cdot G_{C_F_k} \cdot C{AE}_k$$  \hspace{1cm} (11)

$A_{i,j}$ = age of prey item j in model cell i as fraction of its life expectancy (dimensionless)

$L_{E_j}$ = life expectancy of prey item j (days)

$F_{R_j}$ = feeding rate of prey item j (g·day$^{-1}$)

$B_{W_j}$ = body weight of prey item j (g)

$C_{i,k}$ = contaminant concentration in prey item k in model cell i (mg·kg$^{-1}$)

$f_{i,k}$ = fraction of diet item k in diet of prey j in model cell i (dimensionless)

$C{AE}_k$ = contaminant assimilation efficiency of contaminant from prey item k (dimensionless)

$G_{C_F_k}$ = gut content correction factor for prey item k (dimensionless)

$n$ = number of diet items k

Note that, in contrast to prey items, foragers are modelled spatially explicit. This implicates that when a 2nd level species is modelled as a prey it has stayed in one cell its entire life, whereas when the 2nd level species is modelled as a forager it moves between cells and both its predicted exposure concentration and internal concentration are modelled spatially explicit.
Concentration in food
Exposure concentrations per model cell, $C_i$, are determined by calculating cell-specific contaminant concentrations in the diet of the receptor by means of summing the contaminant concentrations of all prey items ($1^{\text{st}}$ and/or $2^{\text{nd}}$ level food web species). The cell-specific contaminant concentrations depend on the composition of its diet expressed in diet fractions $f_{i,j}$, the contaminant concentrations in the respective prey items ($C_{i,j}$) corrected for the amount of contamination present in their guts ($GCF_j$). The cell-specific exposure concentration is thus calculated according to equation 12:

$$C_i = \sum_{j=1}^{n_j} f_{i,j} \cdot C_{i,j} \cdot GCF_j$$

Equation 12

- $f_{i,j}$ = fraction of diet item $j$ in model cell $i$ (dimensionless)
- $C_{i,j}$ = internal contaminant concentration in diet item $j$ in model cell $i$ (mg·kg$^{-1}$)
- $GCF_j$ = gut content correction factor for diet item $j$ (dimensionless)
- $n_j$ = number of diet items

Life-time exposure concentrations
Life-time exposure concentrations are calculated by summing up the cell-specific total contaminant concentration in the diet of the receptor of all cells visited (equation 13). These concentrations are weighted according to the relative amount of time the receptor spent in each specific cell, which is proportionally related to the receptor-specific habitat quality $HQ_i$ and is estimated by dividing $HQ_i$ for this cell by the total habitat quality for all cells visited.

$$PEC = \frac{\sum_{i=1}^{n} HQ_i \cdot C_i}{\sum_{i=1}^{n} HQ_i}$$

Equation 13

- $PEC$ = predicted exposure concentration; life-time averaged concentration in diet (mg·kg$^{-1}$)
- $C_i$ = exposure concentration in model cell $i$ (mg·kg$^{-1}$)
- $HQ_i$ = receptor-specific habitat quality in cell $i$ (dimensionless)
- $n$ = number of cells in foraging path

Risk indicator
Finally, risk indicators are calculated according to equation 14.

$$RI = \frac{PEC}{PNEC}$$

Equation 14

- $PEC$ = predicted exposure concentration; life-time averaged concentration in diet (mg·kg$^{-1}$)
- $RI$ = risk indicator (dimensionless)
- $PNEC$ = predicted no-effect concentration (mg·kg$^{-1}$)

Please refer to Appendix IIId, section Exposure and risk calculation for the VBA source code of the exposure and risk calculations.
3. Case study

3.1 Study area

The model was applied to a study location, the embanked floodplain ‘Afferdensch en Deestsche Waarden (ADW)’, for assessing the ecological risks of cadmium contamination. This floodplain measures about 285 hectares and is located along the river Waal, which is the main distributary of the river Rhine in the Netherlands (Figure 4). The floodplain area between the summer and the winter dike (about two-thirds of the entire floodplain) is periodically flooded during times of high river discharge, usually once or twice a year between November and May (Wijnhoven et al. 2005).

During the past decades, large amounts of sediment and particulate-bound heavy metal pollution were deposited on the floodplain (Middelkoop & Asselman 1998). Because the concentrations of these heavy metals show large spatial variability in floodplain soils (Middelkoop & Asselman 1998; Middelkoop 2000; Thonon 2006), floodplains seem ideal locations for modelling in a spatially explicit manner. The case study focuses on cadmium, for parameterization and evaluation of the model, since the results of several studies indicate that especially this heavy metal might potentially cause ecological risks in river floodplains (Kooistra et al. 2001; Van den Brink et al. 2003).

Currently, the floodplain is the subject of an ecological rehabilitation program in which safety precautions against high river discharges are combined with the conversion of agricultural land into natural floodplain ecosystems. Nature development is foreseen for almost the whole area (Ministry of V&W 2001) and hence a realistic assessment of ecological risks is highly relevant for this floodplain.

Figure 4. Map of the study area, the Afferdensche and Deestsche Waarden (ANONYMOUS, 2003)

3.2 Model input data

3.2.1 Environmental variables

Spatially explicit model input concerning environmental variables consists of cadmium concentrations in soil or sediment, the distribution of ecotopes, and inundation characteristics of the floodplain.

Cadmium concentration

A point database consisting of 192 cadmium concentration values measured in the study area was compiled based on data derived from Kooistra et al. (2005) – in turn derived from five datasets (CSO 1995; Grontmij 1995; Kooistra et al., 2001; Schröder, n.d.; Kooistra et al., 2004) –, Van Vliet et al. (2005) and Wijnhoven (in prep.). The point data were interpolated to obtain continuous data for the whole study area. This was done with inverse distance weighted interpolation (IDW) using the Gstat software (Pebesma & Wesseling 1998). As for the other environmental variables, a spatial resolution of 5x5m was applied, resulting in a total grid of 245 rows and 912 columns (Figure 5).
Ecotope Distribution
A map displaying the spatial distribution of ecotopes in the ADW was derived from the Ministry of V&W (1997). In order to make this map compatible with the model, the vector data were converted into a grid (with ArcGIS\textsuperscript{TM} 9.1; ESRI\textsuperscript{®} 2005). Each model cell was labelled with the ecotope type covering the largest part of the cell area (Figure 6).

Inundation characteristics
From daily river discharge data (1901 – 2004) obtained in Lobith, the Netherlands, the median value was determined for those discharges leading to inundation of the study area (i.e. discharges greater than 6300 m\textsuperscript{3} s\textsuperscript{-1} measured in Lobith; Thonon 2006). The stand-alone hydraulic model WAQUA (MX. Systems 2003) was used to determine the water level in the study area corresponding with the selected median discharge value. To delineate flood-free areas corresponding with this discharge, the calculated water level was compared with a digital elevation model (DEM) of the area. The DEM was created by means of inverse distance interpolation of elevation data obtained with laser altimetry (AHN; Van Heerd \textit{et al.} 2000). Subsequently, for each grid cell the shortest distance to the thus obtained flood-free terrain was calculated, shown in Figure 7.
3.2.2 Ecological variables

Relevant ecological information includes information on food web relations, species-specific values for habitat quality, and information on relevant species characteristics such as body weights, life expectancies, consumption rates etc.

Food web

For the construction of a floodplain-specific food web (Figure 8), a top-down approach was followed: top predators were selected first, subsequently inferring the lower levels of the food web according to diet preferences. Data was obtained from literature, whereby selection was based on the following criteria: the geographical area of the studies, the method applied to analyse diet composition (preferably based on guts or stomach content rather than pellet analysis) and the number of samples. Prey items were included in the food web according to the percentage of the total mass of food consumed by the predator, the prey’s ability to accumulate high metal concentrations and the availability of the prey in the study area. Diet preferences were expressed as fresh weight fractions of the total amount of food consumed by a specific organism and, thus, recorded fractions expressed as volume percentage or relative frequency were converted to weight percentage. See Appendix III for a overview of the food web with the diet fractions specified.

Four top predator species (3rd level food web species) were selected, namely the least weasel (Mustela nivalis), the Eurasian badger (Meles meles), the common kestrel (Falco tinnunculus), and the little owl (Athene noctua). The least weasel and the common kestrel are currently present in the study area, whereas the Eurasian badger, the little owl and the common kestrel are so-called target species for river floodplains according to Dutch national policy (Postma et al. 1996; Bal et al. 2001).

The outlined procedure led to the selection of six small mammalian species making up the 2nd level of the food web, namely the common vole (Microtus arvalis), the bank vole (Clethrionomys glareolus), the wood mouse (Apodemus sylvaticus), the common shrew (Sorex araneus), the European mole (Talpa europaea) and the rabbit (Oryctolagus cuniculus). The 1st level of the food web was designed according to the diet preferences of both level 2 and level 3 species and consists of plant material and terrestrial invertebrates, whereby the invertebrate species were aggregated into classes based on accumulation characteristics. The invertebrate species classes are earthworms, hexapods & myriapods, isopods, and spiders. Plant material was subdivided into vegetation (herbs and grasses), corn and fruit.
Species-ecotope matrix

The species-ecotope matrix that was used for linking species-specific habitat quality values to the different ecotopes present in the study area was based on expert knowledge and literature review. For each species, one of three values was assigned to each ecotope: 0 for unsuitable habitat, 0.5 for marginal habitat, and 1 for suitable habitat. Habitat quality values assigned to the ecotopes for the mice, vole and shrew species were mainly based on live trapping field study in the ADW by Wijnhoven et al. (2005). For other small mammals and top-predators habitat descriptions in literature were translated to ecotopes in the ADW.

The species-ecotope matrix is presented in Appendix IV.

Species traits

The principal species traits included in our model are: home range size, minimum suitable fraction of home range, colonizing distance, life expectancy, body weight, feeding rate, and diet composition. An overview of the values used for the species traits is available in Appendix V (except for the diet compositions, which are described in Appendix III).

The home range values result from literature review and calculated based on minimum and maximum values. For modelling purposes, the values were converted to a home range radius, which is the number of cells that represents the extent of the home range measured from the starting position in four directions (North, South, West and East).

The minimum fraction of suitable cells within the home range ($f_{suitable\_habitat}$) is calculated by dividing the minimum home range value recorded by the median of the home range values:

$$f_{suitable\_habitat} = \left( \frac{HR_{min}}{HR_{median}} \right)$$  \hspace{1cm} (15)

$HR_{min} = \text{minimum home range area reported in literature (m}^2\text{)}$  
$HR_{median} = \text{median home range area (m}^2\text{)}$  
$f_{suitable\_habitat} = \text{minimum required suitable habitat fraction (dimensionless)}$

The colonisation distance (CD) was obtained by expert judgment, considering data on species life expectancies, moving capabilities and reproduction rates. The CDs that are specific for the vole, mice and shrew species range between 120 and 500 m (Appendix V). For all other species, whose life expectancies exceed one year, the CD is given in correspondence with moving capability. Flying organisms are assumed capable of colonising the whole floodplain, as they nest in trees: they are not limited by a certain CD within the floodplain. Some of the terrestrial organisms (least weasel, Eurasian

---

Figure 8. Food web of the study area for four selected top predators. H&M = Hexapods and Myriapods
badger, European mole) have a preference for nesting in areas that do not flood every year: their Cd was assumed to be zero. Rabbits are assumed to nest in the whole floodplain, because the high competition for nesting sites in flood-free terrain forces them to nest in uncolonised areas that are periodically flooded. Rabbits live in warrens and tend to stay close to their home warren. The rate at which new warrens are created depends on the extent of competition for nest sites within existing warrens and the availability of suitable uncolonised areas (Cowan, 1987). Due to their breeding capability (gestation period 28 days, nests contain up to 7 young, young can reproduce themselves at the age of 3 – 4 months (Armstrong, 1982) and females can become pregnant within 12 hours after producing a litter (Southern, 1965) in combination with the availability of suitable uncolonised areas (after the floodings the floodplain represents a suitable uncolonised area), rabbits are assumed to nest everywhere in the floodplain.

Four species (wood mouse, bank vole, common vole, and common shrew) were given life expectancies of 9 months due to the fact that, in the study area, periodical floodings limit their life span. For all the other species, life expectancies were directly obtained by literature review (Appendix V). Likewise values for body weight were also directly obtained by literature review.

Feeding rate (FR) values used in the model are the geometric mean of the FR values that were either directly obtained from literature or – when no appropriate FR values were available – calculated with an allometric relation based on feeding rates and body weights recorded for the other species. Values for all the species were available in literature, except for the wood mouse and the bank vole. For the latter two species, FR values were hence calculated according to the allometric relation derived (equation 16).

\[
\log (FR) = 0.6185 \cdot \log (BW) + 0.4836 \quad (R^2 = 0.9136)
\]

FR = Feeding rate (g·day\(^{-1}\))
BW = Body Weight (g)

### 3.2.3 Ecotoxicological variables

Ecotoxicological information consists of regression coefficients and bioaccumulation factors (BAFs), to determine internal cadmium concentrations in basic-level organisms, and several species-specific ecotoxicological characteristics for 2\(^{nd}\) and 3\(^{rd}\) level organisms, such as predicted no effect concentrations (PNECs), contaminant assimilation efficiencies (CAE), and gut content correction factors (GCF).

**BAF or Regression equations**

Either regression equations or bioaccumulation factors (BAFs) were used to derive internal metal concentrations in 1\(^{st}\) level, soil-dwelling and plant organisms from soil concentrations, depending on the availability of data collected from literature. Regression equations were selected based on parameters used in the equation, coefficients of determination \(R^2\) and significance of the relations \(p\). Significance levels were derived from Rohlf & Sokal (1995). The equations selected are listed in Table 2. For corn, vegetation, fruits and gastropods insufficient data were available to establish regression equations and hence BAFs were selected to determine the cadmium concentrations in these diet items (Table 3). Laboratory studies on cadmium accumulation in gastropods revealed that soil and vegetation contribute 40% and 60% to the total Cd bioaccumulation respectively (Viard et al., 2004) and hence for these organisms, soil and vegetation specific BAFs were selected. The internal concentration in gastropods is calculated according to equation 17.

\[
\begin{align*}
C_{DW, gastropods}^{i} &= 0.4 \cdot C_{i, soil} \cdot BAF_{soil} + 0.6 \cdot C_{i, vegetation} \cdot BAF_{vegetation} \\
C_{DW, gastropods}^{i} &= \text{contaminant concentration in gastropods in model cell } i \text{ (mg·kg}^{-1} \text{·dw)} \\
C_{i, vegetation} &= \text{contaminant concentration in vegetation in model cell } i \text{ (mg·kg}^{-1} \text{·dw)} \\
C_{i, soil} &= \text{contaminant concentration in soil in model cell } i \text{ (mg·kg}^{-1} \text{·dw)}
\end{align*}
\]
The diet type showed to have a significant influence on cadmium absorption, i.e., more fibrillar and less absorption), and age (older, less absorption). The contaminant assimilation efficiency (CAE) was used to determine the net whole-body assimilation of cadmium. Regression equations to calculate internal cadmium concentrations (mg∙kg\(^{-1}\) dw) in basic-level diet items are given in Table 2.

\[
PNEC_{sp} = NOEC_{food} \cdot \frac{EMR}{FMR} \cdot \frac{FCC_{field}}{FCC_{lab}} \cdot \frac{FAE_{field}}{FAE_{lab}}
\]

\(PNEC_{sp}\) = species-specific predicted no effect concentration in food (mg∙kg\(^{-1}\) food)  
\(NOEC_{food}\) = no-effect concentration in food (mg∙kg\(^{-1}\) food)  
\(EMR\) = existence metabolic rate (kJ∙day\(^{-1}\))  
\(FMR\) = field metabolic rate (kJ∙day\(^{-1}\))  
\(FCC\) = food caloric content (kJ∙g\(^{-1}\))  
\(FAE\) = food assimilation efficiency (dimensionless)

**DMC**

Metal concentrations in soil and sediment, bioaccumulation factors and regression equations are often expressed on a dry weight basis, whereas food web diet fractions, contaminant assimilation efficiencies, feeding rates and parameters used in PNEC calculations are mainly available on a fresh weight basis. Therefore, we used a conversion parameter, dry matter content as fraction of fresh weight (DMC), to convert internal concentrations in basic-level species from a dry to a fresh weight basis. The values for the DMC result from literature review on moisture content (Appendix VII).

**CAE**

The contaminant assimilation efficiency (CAE) of cadmium was estimated based on reports in literature on cadmium retention in laboratory mammals and birds (Appendix VII). The values reported vary between 0.3 and 7.8%. The study of Andersen et al. (1992) was taken as a starting point to determine the net whole-body absorption rate of cadmium. There are several factors that influence this absorption: i.e. diet type (more fibrous, less absorption), co-contamination with zinc (more zinc, less absorption) and age (older, less absorption). The diet type showed to have a relevant influence on cadmium absorption and it was decided to make a distinction in the cadmium absorption rate between...
diet items rich in fibers (vegetation, corn, and fruit) and protein rich diet items (non-vegetable organisms). When comparing the data of Andersen et al. (1992) with the data of Engstrom & Nordberg (1979) and Andersen et al. (1988), cadmium absorption seems slightly underestimated in the first study. The cadmium absorption from vegetation and other plant products is put at 1.0% and from non-vegetable organisms at 2.5%.

**GCF**

For four species (wood mouse, bank vole, common vole, and common shrew) a GCF of 2 (Walker et al. 2002) was applied, while for the European mole and the rabbit a GCF of 1.5 was applied, as for a lower relevance of the cadmium burden in the gut, due to the longer life expectancies of these species compared with the mice species (Appendix VII).
4. Model simulations

After parameterising the model to the specific case study settings, simulations were carried out for the 10 species selected. In order to represent 1000 individuals, an equal number of runs were simulated for each species, except for the common kestrel and the European badger. For these species, 50 and 150 simulations were performed respectively, because the large home range sizes of these species (Annex III) considerably enhanced the amount of time required per simulation.

4.1 Model analysis

The model contains several components that embody variability in spatial information, namely habitat availability, habitat quality, contaminant concentration in soil, prey age, and food availability. To investigate the influence of the spatial variation on exposure predictions in more detail, simulations were carried out for seven different scenarios, each embodying different levels of detail concerning spatial variation, by switching on and off the various components. These simulations were carried out for fixed starting positions for two of the top-predators representing a flying and a walking species, i.e. the little owl and the least weasel respectively. For each of the species, two different starting positions were selected, based on spatial heterogeneity of both soil cadmium concentrations and ecotope distribution within the accompanying home ranges. The results of 1000 simulations with scenario 7 (complete version of the model) for each of these four test cases were compared with the results of the six other scenarios applied to the same species with the same starting positions and home ranges, representing increasing variability in spatial information (Table 4).

Table 4. Spatial variability taken into account for each scenario applied in model analysis.

<table>
<thead>
<tr>
<th>Scenario</th>
<th>Habitat quality determining foraging area (HQ_{i,e})</th>
<th>Soil cadmium concentrations (C_{i,soil})</th>
<th>Prey age (A_{i,j})</th>
<th>Food availability</th>
<th>Habitat quality determining foraging behaviour (HQ_{i,f})</th>
<th>Exposure duration per visit (HQ_{i}/\Sigma(HQ_{i}))</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
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<tr>
<td>2</td>
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<tr>
<td>3</td>
<td>X</td>
<td>X</td>
<td></td>
<td>X</td>
<td>X</td>
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<tr>
<td>4</td>
<td>X</td>
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<td>X</td>
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<tr>
<td>5</td>
<td>X</td>
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<td>X</td>
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<tr>
<td>6</td>
<td>X</td>
<td>X</td>
<td></td>
<td>X</td>
<td>X</td>
<td></td>
</tr>
<tr>
<td>7</td>
<td>X</td>
<td></td>
<td></td>
<td>X</td>
<td>X</td>
<td>X</td>
</tr>
</tbody>
</table>

In the first scenario, all components mentioned above were switched off, resulting in the most simplified model scenario, with the least spatial variability included. This means that all spatial variability within the home ranges was neglected by calculating exposure concentrations based on soil cadmium concentrations averaged per home range.

In the second scenario the ‘habitat availability component’ was switched on. Spatial variation in habitat quality (HQ_{i,e}) was taken into account, resulting in reduced availability of habitat, confined to those areas within the home ranges with ecotopes suitable for the species. Thus exposure estimates were generated based on average soil concentrations for those areas where HQ_{i,e} = 1.

Then, in scenario 3 the ‘soil contaminant concentration component’ was switched on. For each test case 1000 model simulations were carried out within those areas where HQ_{i,e} = 1 and exposure concentrations were calculated on a cell-by-cell basis. As spatial variation in both HQ_{i,e} and HQ_{i,f} was absent within the area to forage in, habitat quality HQ was uniform and spatially explicit behaviour was directed exclusively by the random element of the foraging behaviour module. Thus, scenario 3 tests the influence of spatial variation in soil cadmium concentrations within suitable ecotopes. For the scenarios 1 - 3, spatial variability in food availability was neglected and all diet items were assumed to be available in each cell, i.e. each cell was characterised by HQ_{i,f} = 1 and whereby the age A_{i,j} of each
second level prey item was set to an average value. It was assumes that an equal amount of time was spent in each cell visited.

Scenario 4 is similar to scenario 3, except that the ‘prey age component’ was switched on. The age \( A_{ij} \) of each second level prey item was generated randomly, thus testing the influence of variation in prey age on the variation in the predicted concentrations.

In the fifth scenario, the ‘food availability component’ was switched on, but only in the exposure module. Thus spatial variability was added concerning the availability of diet items \( HQ_{i,f} \) and the effect of spatial variability in foraging behaviour guided by food availability was tested. Hence foraging behaviour was simulated analogue to scenario 4, but the subsequent calculation of exposure concentrations on a cell-by-cell basis was influenced by spatial variation in the presence and absence of diet items \( f_{i,j} \).

Subsequently, the effect of spatial variability in exposure duration, which is habitat quality weighted (equation 13), was tested with scenario 6, by switching on the ‘food availability component’ in the foraging path module. Thus foraging behaviour was influenced by cell-specific differences in habitat quality in terms of ecotope \( HQ_{i,e} \) and food availability \( HQ_{i,f} \).

Finally, in the complete version of the model, scenario 7, the ‘exposure duration component’ was switched on. This scenario no longer assumes an equal amount of time is spent in each cell visited, rather the amount of time depends on the habitat quality in a cell \( HQ_i \) in relation to the cumulative \( HQ \) of the path foraged in, and hence the duration of exposure depends on \( HQ_i \) (Equations 1, 2 and 13). The calculation of exposure concentrations on a cell-by-cell basis was therefore influenced by exposure duration.

### 4.2 Model validation

In order to test the predictive performance of the model, internal cadmium concentrations predicted were compared with concentrations measured in five mammalian species originating from the study area, i.e. least weasel, wood mouse, bank vole, common vole and common shrew (Wijnhoven et al. 2006). To obtain location-specific comparisons between predicted and measured concentrations, the model was applied using the capture locations of the animals as starting positions. For each starting position of each species 100 simulations were executed, to get insight in the species-, location-specific variation (mean PEC and SD stabilised at 100 simulations). For the weasel only 60 simulations were executed, because its large home range size implied an increased simulation time. Concentrations were determined per species and per capture location by calculating an average value of the internal cadmium concentrations acquired during the successive steps of the life span for all simulations (Equation 11) thus representing individuals of various ages.
5. Results

5.1 Case study

For each of the 10 mobile species selected 1000 individuals were simulated to estimate their predicted exposure concentrations (PECs) for the ADW floodplain. These PECs were then compared with the predicted no effect concentrations (PNECs) to estimate the corresponding risk. Figure 9 shows the results of the simulations. Figure 10a and 10b show the risk indicator estimations of the simulations for a single species set out in a frequency histogram.

![Figure 9. Predicted exposure concentrations (PECs) and predicted no-effect concentrations (PNECs) of cadmium for higher-level model species in mg • kg⁻¹ food. Error bars represent standard deviations. SD = standard deviation; CV = coefficient of variation; calculated as SD • mean⁻¹; N = number of model simulations.](image)

The differences in PECs between the species – the model predicts considerably higher mean exposure concentrations for the species common shrew, European mole, Eurasian badger, least weasel and little owl, than for the other five species (wood mouse, bank vole, common vole, European rabbit and common kestrel) – can predominantly be explained by interspecific differences in diet composition. The latter five species are predominantly herbivorous, or feeding on herbivorous prey (common kestrel), whereas the former five species have substantial proportions of invertebrates in their diets, either directly (common shrew, European mole and Eurasian badger, and little owl; Appendix III) or indirectly (least weasel and little owl). Internal concentrations in food web items of plant origin (vegetation, fruits, corn) are considerably lower than corresponding soil concentrations, whereas 1st trophic level organisms such as spiders, isopods and especially earthworms are characterised by bioconcentration, i.e. processes leading to internal concentrations higher than the concentrations in the environment (Janssen et al. 1993). Hence invertebrate-eating species and their respective main predators are exposed to higher cadmium concentrations than the mainly herbivorous species and their respective predators. These results, i.e. exposure concentrations of cadmium being higher via food chains based on terrestrial invertebrates than on diet items of plant origin, are consistent with the findings of numerous previous studies (Ma et al. 1991, Shore and Douben 1994, Traas et al. 1996, Van den Brink et al. 2003, Hamers et al. 2006).

The standard deviations (SD) of the PECs potential between the individuals of one species, expressed as coefficients of variation (CV) to facilitate inter-specific comparison, reflect: (1) spatial variation in cadmium concentrations in the soil (C_{i, soil}) within habitat units of variable quality (HQ_i), (2) spatial variation in diet item availability (f_{i,j}) determining the diet composition, and (3) variation in prey age (for top-predators only). The standard deviations are influenced by the ratio between the
spatial scope of the simulation (home range size) and the spatial resolution and heterogeneity of the stressor (cadmium contaminant concentration) and by diet preferences. Figure 10a and 10b show a more detailed view of the intraspecific variation in risk.

The influence of home range size (relative to the resolution of cadmium concentrations) is illustrated by, for example, the difference in variation coefficients between the common kestrel and the small mammal species. The large home range of the common kestrel encompasses an area characterised by great heterogeneity in cadmium concentrations in soil. This heterogeneity is levelled out during the foraging, when the kestrel visits both high and moderately contaminated areas in one simulation. This leads to relatively small differences between different simulations and hence a small coefficient of variation. Contrastingly, the small mammal species are characterised by small home ranges. Therefore locally occurring spots with high or low contamination levels will have large influence on exposure estimates for encompassing home ranges. Differences between areas visited in subsequent runs will hence be larger, leading to considerably larger coefficients of variation (Figure 9).

The influence of the diet item availability is illustrated by the results for the little owl, for which the large standard deviation and coefficient of variation cannot be explained by a small home range size. Its influence depends in the first place on life expectancies of prey items ($\text{LE}_i$) in relation to their bioaccumulation potential. Strongly accumulating items with a high $\text{LE}_i$, such as the European mole, are characterised by a large range of possible internal concentrations and hence exert large influence on the CVs of the exposure concentrations for their predators. In addition, the fractions of strongly and moderately accumulating diet items in the diet of a specific receptor play a role. Because the absence of diet items in a certain cell is compensated for by enlarging the diet fractions $f_{i,j}$ of items that are actually present in that cell, the share of each item in the diet of a receptor species is spatially variable. Consequently, the absence of an item with relatively low bioaccumulation potential might lead to an increased share of an item with higher bioaccumulation potential and the other way around. The little owl’s diet (Appendix III) contains both large fractions of strongly accumulating diet items, such as earthworms and European moles, and large fractions of items that accumulate less strongly, such as the common vole. Therefore spatial variation in availability of the different diet items has large influence on the variation in exposure concentrations predicted for this species. The relatively high frequency of little owls with an estimated risk between 1.5 and 2.0 can be explained by the fact that they are modelled in an area were the European mole is absent. The difference between the two other frequency peaks (10.0-11.0 and 12.0-13.5; figure 10a) can generally be explained by differences in soil contaminant concentrations at corresponding locations. Around these peaks risk estimate distribution appears to be resemble a normal distribution.
The estimated risks for the least weasel (Figure 10b) are primarily related to the soil contaminant concentration. Like the little owls (Figure 10a) the frequency distribution is approaching a normal distribution with some local peaks due to location-specific conditions. Cadmium contamination poses the greatest risk for invertebrate-eating species. All predominantly herbivorous species appear not to be at risk in the study area. The little owl, the European mole, and the Eurasian badger suffer the greatest risk, with risk indicators of 11.6, 9.3 and 5.8 respectively. Their diets are all characterised by the fact that earthworms constitute the highest proportion.
5.2 Model analysis

To illustrate the performance of the foraging behaviour module, cell-visit frequencies are depicted for two top-predators, i.e. the least weasel and the little owl, for 250 model simulations with a fixed starting position (Figure 11). Generally, a minimum of 100 simulations were required to get stable results. The influence of habitat quality $HQ_i$ on the foraging behaviour is visible for both species, as cells with higher habitat quality are visited more frequently. This effect, however, is more pronounced for the little owl than for the weasel, because the former is assumed, as a flying organism, capable of moving from one habitat-containing cell to any other habitat-containing cell within its home range. Consequently, the spatial distribution of habitat units of different quality does not influence the order in which cells are visited. In contrast, the least weasel, a walking animal, is assumed to be forced to investigate neighbouring cells in the cell selection process and hence cells of high habitat quality might not be reached if they are located in a remote corner of the home range. This explains why the little owl visits habitat units proportionally to their habitat quality, whereas the least weasel might deviate from this partition, depending on whether habitat units can be reached. As a consequence, the highest cell visit frequencies for the weasel are generally located around the centre of its home range. Exposure concentrations predicted with the six different model scenarios as described in section 4.1 were compared with the results of scenario 7 (complete version of model) for two different starting positions for both the little owl and the least weasel (Figure 11).

<table>
<thead>
<tr>
<th>Habitat quality ($HQ_i$)</th>
<th>Cell visiting frequency (250 runs)</th>
</tr>
</thead>
<tbody>
<tr>
<td><img src="image1" alt="Little owl" /></td>
<td><img src="image2" alt="Little owl cell visits" /></td>
</tr>
<tr>
<td><img src="image3" alt="Least weasel" /></td>
<td><img src="image4" alt="Least weasel cell visits" /></td>
</tr>
</tbody>
</table>

$\times =$ starting position

Figure 11. Spatial distribution of habitat quality ($HQ_i$; calculated according to equation 11) and cell visit frequencies for 250 model simulations with a fixed starting position for little owl (top) and least weasel (bottom).

The scenario study reveals that the soil contaminant concentration influences the exposure. Higher cadmium concentrations in soil lead to higher PECs, as illustrated by the PECs for the little owl being generally higher in case 1 than in case 2 (Figure 12), corresponding with higher soil concentrations within the home range (Appendix VIII). Differences between the scenarios 1 and 2 are also governed by differences in average soil cadmium concentration. The standard deviations generated by scenario 3
indicate that the influence of spatial variation in soil cadmium concentrations within suitable habitat is rather small in three of the cases. In case 1 for the weasel the standard deviation is somewhat larger, because the remote parts of this home range are characterised by a large variation in soil concentrations. Cells in these remote parts are not likely to be visited in all simulations, resulting in larger differences between subsequent runs.

Differences in standard deviations between the scenarios 3 and 4 indicate that the influence of spatial variation in prey age is larger for the little owl than for the weasel. This can be explained by differences in diet composition, as the little owl’s diet contains a large fraction of European moles (27.0% of the little owl’s diet compared to 1.5% of the diet of the least weasel), which combine strong cadmium accumulation with a high life expectancy. The variation in prey age is so large for the little owl that, compared with the variation in soil contamination, it predominantly contributes to the variation in PECs.

Incorporating spatial variation in diet composition $f_{ij}$ (scenario 5) leads to considerably lower PECs for the little owl. For the little owl at location 2 average soil contaminant concentrations are practically the same for scenarios 1, 2 and 5 (2.20 mg kg$^{-1}$, 2.21 mg kg$^{-1}$ and 2.204 mg kg$^{-1}$ respectively), but the PECs are not because the absence of European moles is compensated for by larger fractions of less strongly accumulating diet items in a considerable part of the habitat area (Appendix VIII). For the weasel, spatial variation in diet item availability leads to more variation, but on average the PECs are comparable to scenario 4. Apparently, foraging in areas with a larger share of strongly accumulating prey items is balanced by foraging in areas with a larger share of less accumulating diet items.

Concerning the influence of HQ$_i$ on exposure estimates via foraging behaviour (scenario 6), two factors are of importance, i.e. the quality value and the surface area of the units of different quality (habitat quantity), as both factors influence visiting frequencies. Large areas with high quality coinciding with high contaminant concentrations in soil, will generate high PECs for the weasel, as illustrated by case 2 where 60% of the cell visits is paid to an area with soil concentrations higher than average, resulting in higher than average PECs. For the little owl, however, for which spatial variation in diet composition is more important than for the weasel, scenario 6 will generate high PECs when large areas with high quality coincide with the absence of moderately accumulating diet items. For example, in case 1 the little owl pays over 60% of the cell visits to areas where the wood mouse is absent and the shares of moles and earthworms are enhanced, yielding higher than average PECs despite lower than average soil concentrations.
Figure 12. Effect of different model scenarios (Table 1) on predicted exposure concentrations (PECs) for the little owl (top) and the least weasel (bottom). Error bars represent standard deviations based on 1000 model simulations. CV = coefficient of variation; calculated as SD • mean - 1; Diff. indicates the relative difference with scenario 1, i.e. PECs based on soil concentrations averaged for the entire home range.

The effect of high habitat quality coinciding with either high soil concentrations or strongly accumulating diets increases when HQ influences exposure duration as well as foraging behaviour (scenario 7 vs. scenario 6), resulting in even higher PECs. For example, the little owl at location 2 will be exposed not only more frequently, but also longer in the area with highest visiting probability (i.e. habitat unit with HQ = 0.80 and HQ*SA = 62%; Appendix VIII), where the average PEC is 27.85 mg kg⁻¹. This PEC value happens to be higher than the average PEC value in the whole home range, calculated with scenario 1 (24.19 mg kg⁻¹), caused by a combination of contaminant concentration in soil and availability of diet items. Resultantly, the average PEC calculated with scenario 7 is higher than the average PEC calculated with scenario 6, and also is even higher than the average PEC calculated with scenario 1. Generally, differences between scenario 5 and 6 are larger than differences between scenario 6 and 7, indicating that the influence of HQ on the model results is less profound through exposure duration per cell visit than through visit frequency.

Summarising, the simulation of spatially explicit behaviour, governed by spatial variation in habitat characteristics, yields intraspecific variation in PECs whereby four environmental characteristics are of influence:
- Contaminant concentrations in soil;
- Habitat quality (through influence on visit frequency and exposure duration per visit);
- Habitat quantity (through influence on visit frequency);
- Food availability (through generating spatial differences in the shares of different diet items with specific characteristics concerning bioaccumulation).

### 5.3 Model validation

For the small mammals, differences between measured and predicted internal cadmium concentrations are an average factor of 7.0, within the range 1.1 – 32.1. The maximum factor of 32.1 for the common vole on location F, however, corresponds with a rather small actual difference (<1 mg·kg⁻¹ dw; Figure 13) and excluding this specific case yields an average factor of 3.9. Especially for the common shrew the predictions agree very well with the measurements (factor of 1.1 – 1.3). The large overestimation
for the top-predator weasel can most likely be ascribed to the effect of age. The animal captured was a juvenile individual, whereas the prediction is an average of internal cadmium concentrations acquired in all cells visited in the course of the animal’s life, i.e. concentrations corresponding with the range of ages up to its maximum life expectancy. Further, the differences between the mean model predictions and measurements might partly be explained by the fact that the capture locations of the animals are modelled as the centre of their home range. However these animals might well be caught at the edge of their home range. Consequently, such a misallocated home range used for the simulation leads to a different internal concentration predicted.

Figure 13. Location-specific measured and predicted internal cadmium concentrations for five species. N indicates the number of individuals captured per location. Error bars represent maximum values. *= juvenile individual. Note that a logarithmic scale is used.

The model tries to comprehend the variation of the exposures that can be seen in real world situations and, resultantly, limit the probability of underestimation or overestimation. Field variation is governed by spatial variation in environmental conditions and intra-specific variation in ecological and ecotoxicological species traits. Most of the species traits incorporated in our model (e.g. feeding rate, body weight, etc.) are standardised, i.e. one representative value is applied for each parameter. Except for variation in environmental factors (soil contamination, habitat quality and quantity, and food availability), variation is only included in receptor and prey age. This explains why ranges of internal concentrations are generally smaller for the predictions than for internal concentrations obtained from the field (Figure 13).
6. Discussion

Model validation
The model was validated with several small mammals and one weasel. The model validation showed that it predicts reasonably well for small mammals. However, the model has not yet been sufficiently validated for top-predators, as the validation was based on only one juvenile weasel of unknown age.

Model Assumptions
With regard to the simulation of foraging behaviour and in the calculation of exposure several assumptions have been made in the present model either for keeping it as simple as possible or due to limited modelling possibilities in the current programming environment or due to limited availability of information. These assumptions may affect the predicted exposure and risk or affect the spatial behaviour of the organisms modelled, which may therefore also have an effect on their predicted exposure and risk. In the section ‘foraging behaviour’ and ‘exposure calculation’ some important model assumptions are discussed.

Foraging behaviour
The model uses simplified movement algorithms, which do not generate fully realistic movement patterns. In the model only a distinction is made between mammalian and avian species; species within these groups exhibit the same type of spatially explicit foraging behaviour driven by habitat preference and stochasticity. However, animal movement may be more complex, potentially leading to different foraging paths. Some animals, for example, are not willing to cross barriers (e.g. small mammals such as voles); other species forage according to specific foraging paths from a specific nest-site to which they return each day (e.g. badgers; Rosalino et al. 2005). Furthermore, seasonal differences cause changes in habitat use and diet preferences for several species (Rödel 2005; Lodé 1994). All of these types of behaviour are not incorporated.

As foraging pathway is governed by the assumption that an organism has a preference for cells with higher HQ, the habitat quality is crucial for the movement of organisms, and thus for their exposure and risks. This foraging behaviour may seem a primitive approach and conceivably too reliant on a correct classification of the habitat quality. Nevertheless, we consider this approach sufficiently realistic to obtain an impression of the influence of spatially explicit behaviour on exposure estimates. Introducing species interaction and more detailed principles of the optimal foraging behaviour, such as bioenergetics, might improve simulation of the behaviour and reduce its dependency on the HQ parameter.

Organisms modelled are confined to the borders of the study area; they cannot forage outside the floodplain. In reality these borders do not exist for the organisms and part of them will probably partly forage outside the study area. Since this area is generally less polluted, the present model probably leads to conservative PEC estimates.

As mentioned before, the current model is based on the conceptual model approach from Hope (2000, 2001, 2005) and we have adopted the same stopping criterion. However, we are aware of the fact that it is a rather arbitrary criterion with little ecological meaning. It seems more meaningful to simulate organisms until they reach a certain age (e.g. average life expectancy). This requires time to be modelled explicitly.

Preys do not exhibit spatial foraging behaviour. When preyed upon, they are assumed to have lived their entire life in one model cell. The representation of preys as being immobile is obviously not very realistic for those prey species that have a larger home range than the area of a model cell (25 m²) and may lead to erroneous exposure predictions of top-predators consuming such prey species. However, results showed that variation in prey age, which is included in the model, contributes for a large extent to the variation in PECs. The contribution of spatially explicit behaviour to variation in internal concentrations of mobile preys to the variation in PECs might not be as great. It is therefore expected that inclusion of spatial behaviour of prey would lead to slightly decreased standard deviations of exposure predictions, but that it will not lead to drastically different average exposure concentration predictions. Until now spatial foraging behaviour of preys has not been included due to the limited flexibility of the current programming environment.
Predators in this model are not capable of learning; they do not have spatial memory that can influence their foraging behaviour by visiting profitable cells more often. Several studies (O’Keefe & Nadel 1978; Rudy & Sutherland 1995; Day & Schallert 1996; Eichenbaum 1996; Whishaw & Jarrad 1996) have demonstrated enhanced spatial memory in species that must search intensively for resources. Including spatial memory in the model should be considered when refining the foraging behaviour.

A combination of bottom-up and top-down approach is used to simulate foraging behaviour. The last three cells visited are assumed depleted and can therefore not be visited for foraging (top-down); foraging behaviour is largely dependent on the HQ, which is assumed to reflect the prey abundance (bottom-up). There is quite some debate on the top-down or bottom-up regulation in food webs (Smith and Lancelot 2004; White 1978; Power 1992; Hairston et al., 1960; Paine, 1966, 1974). A more realistic (and dynamic) bottom-up approach in food web regulation is only possible to model when landscape (prey availability) is modelled dynamically. Modelling interspecific interaction will give rise to possibilities for refining food web regulation approaches. In the current modelling environment this is not easily implementable.

In general, further refinement of simulation of more realistic foraging behaviour is meaningful. Modelling of interspecific and intraspecific interaction, simulating time explicitly, including bioenergetics, etc. can be thought of as major improvements.

**Exposure calculation**

Bioaccumulation factors (BAFs) and regression equations are used to calculate internal concentrations in 1st trophic level organisms. The application of these factors and equations is based on the assumption of a stable ratio between a certain concentration in soil and a corresponding internal concentration in the 1st level organisms. However, for non-essential metals such as cadmium and lead, regulation is either limited or absent (Van Straalen et al. 1987, Van Gestel et al. 1993) and strong bioaccumulation is observed in a wide range of species (Hunter et al. 1987b, Shore and Douben 1994, Van den Brink and Ma 1998, De Jonge et al. 1999, Komarnicki 2000, Heikens et al. 2001, Hendrickx et al. 2003). Nevertheless, several species are usually being sampled for the determination of the BAFs. They make up a more or less random sample of different age classes and may be assumed representative of the diet compositions of 2nd and 3rd level organisms. Hence the application of these BAFs and regression equations to determine the internal concentrations can be justified also for the non-essential metal cadmium.

For simplicity reasons, a regression equation was used linking spiders directly to soil properties although these organisms have their own food web and are not directly exposed to soil. This may possibly explain the relatively low fitting performance ($R^2 = 0.37$).

Availability of metals from soil to organisms varies considerably among soil types and among species of organisms (Peakall & Burger 2003). For example, Lock et al. (2000) found that the toxicity of Zn and Cd to the earthworm (Enchyraeus albidus) varied by two orders of magnitude for a range of different soils. The principal influences affecting bioavailability are pH and cation-exchange capacity. The processes affecting bioavailability of substances are not explicitly modelled. However, the bioaccumulation factors that were used in the model were selected from areas closely matching the study area, concerning physical and chemical characteristics. As these BAFs thus relate soil contaminant concentrations to internal concentrations in organisms in situations comparable to the study area, bioavailability is accounted for indirectly.

Results showed that variation in prey age has an important influence on the variation of the predicted exposure concentrations (PECs). In the model, variation in prey age is randomly generated following a uniform distribution. However, age class distribution is generally deviating from uniform and some species have a preference for preys of a typical age. For example, Derting (1989) conducted an experiment showing that although the least weasel exhibits opportunistic foraging behaviour, it captures adults less frequently than juveniles of the Microtus pennsylvaticus species. In the model, preys have an average age of half their maximum life expectancy (following the uniform age distribution). This for example results in possible overestimation of exposure for weasels, as they generally prey upon younger animals, with lower internal contaminant concentrations. It is more realistic to incorporate prey-specific age class distribution and predator-specific prey age preferences. However, the ecological data needed to parameterise the model for age-specific predation is scarce.
Time is not explicitly simulated in the exposure and risk calculations. The PNECs that are used in the model are expressed in milligrams of contaminant per kilograms of food (ppm in food) and exposure is calculated in the same units. However, internal concentrations need to be calculated for preys of level 3 species and these concentrations are dependent on the duration of exposure and thus on the age of the preys. This implicitly introduces a time basis in the internal concentration calculations, namely the basis would be the life expectancy of organisms. It would be more transparent and clear to model time explicitly.

A distinction has been made between the life expectancies of the 2nd and 3rd level species. For the 2nd level species actual life expectancies were used. These species also act as prey species and modelling 2nd level species using maximum life expectancies would result in overestimation of exposure to their predators (3rd level species). For the top-predators (3rd level species) maximum life expectancies were used and this leaves us the option to calculate internal concentration for every possible age of the predator up to its maximum life expectancy, thus including its actual life expectancy.

A relatively high accumulation is predicted for the European mole. For example, if we only consider the earthworm route to the European mole, and assume a 16.8 ppm dry weight (dw) concentration in earthworm (approximately 1ppm dw in soil according to equations in Table 2) this equation results in an internal concentration of approximately 30 ppm (assuming $A_{i,j}$: 0.5; LE: 1095; FR: 111.8; BW: 95.4; $C_{i,j}$: 2.63; f: 0.7; GCF: 1; CAE: 0.025). So, 1 ppm (dry weight) in soil results in 30 ppm in the European mole (fresh weight). Explanations for this rather high prediction may include: (1) excretion is not taken into account in the model, (2) life expectancy may be too high for the mole, and/or (3) feeding rate of the mole might be lower. To verify whether the predicted accumulation is too high field data from internal concentrations in moles are needed. To predict internal concentrations more accurately, more data must be known about life expectancy, feeding rate, excretion, etc.
7. Conclusion

The aim of this study was to develop a spatially explicit generic model for exposure and risk assessment for both ecological and human receptors, and to tailor and apply such a model to a case study.

7.1 Case study

This study investigated the influence of spatially explicit behaviour of 10 terrestrial species on their exposure to cadmium contamination in a river floodplain. The results showed that the simulation of spatially explicit behaviour, governed by spatial variation in environmental characteristics, yields intraspecific variation in exposure whereby four environmental characteristics were of influence on the predicted exposure concentrations (PECs), namely (1) soil concentrations, (2) habitat quality, (3) habitat quantity, and (4) food availability.

Interspecific differences in exposure, however, were governed by variations in diet preferences rather than spatial variation in environmental factors. Food chains based on terrestrial invertebrates resulted in considerably higher predicted exposure concentrations for higher trophic (2nd and 3rd) level organisms than food chains based on diet items of plant origin.

Comparison of location-specific predicted and measured internal cadmium concentrations for several mammalian species revealed that standard deviations of the latter generally exceeded those of the former. This indicates that not all factors governing intraspecific variation in exposure concentrations are incorporated in our model. Nevertheless, model predictions were generally in the right order of magnitude and hence it is concluded that the model provides a valuable tool to generate spatially explicit exposure estimates that include intraspecific variation specifically resulting from spatially explicit behaviour. It predicts exposure fairly well, especially considering all uncertainties generally involved in ecological exposure and risk assessment.

7.2 Generic model

Model applications

The modelling approach used in this study serves as a useful tool for spatially explicit exposure assessment for higher trophic level species. The model has been parameterised for the heavy metal cadmium and proved to generate reasonably accurate predictions of exposure of receptors to this stressor. This improves our understanding of complex exposure situations and can prove a useful tool for ecological managers in decision-making and management.

The same approach can easily be employed to predict spatially variable exposure to other stressors. Even more, the model might not only predict exposure to single substances, but also to multiple stressors (Hope, 2005). The spatial component is regarded as an important contributor to variation in exposure (Kooistra et al., 2001; Hope, 2000; Clifford et al., 1995; Kareiva & Wennergren, 1995) and therefore relevant to include when predicting exposure to co-occurring stressors. At different locations, receptors are exposed to varying combinations and concentrations of multiple stressors. By means of combining input of multiple stressors, the model can predict location-specific integrated exposure to these stressors in a spatially explicit and receptor-oriented manner. The model approach developed therefore seems especially suitable for exposure assessment to cumulative stressors.

The model can also be used to predict exposure at other study areas. However, the model requires information on landscape (contamination input, habitat info) and on species to be modelled. So in order to apply the model to other areas sufficient information should be available about these areas.

Recommendations and future plans

Modelling in a spatially explicit manner provides us with insight in the amount of variation of exposure and risk between individual organisms. As such the model is a first step towards modelling cumulative exposure, where spatial information may be expected relevant for predictions at both species and population levels.

The model has been successfully validated for several small mammal species, yet for the top-predator species validation has been minimal. It is therefore advisable to validate the model with more field data from species of the highest trophic level. As the capture and sacrifice of top-predators is not encouraged, more refined solutions should be found to validate the model predictions for top-
predators. Examples are the sampling of recoverable tissues (e.g. blood, feathers, hair and uropygial gland oil; Van den Brink et al., 2003) and of traffic victims (Van den Brink & Ma, 1998).

For future development of the model several recommendations for improvement can be done. It is recommended to include interspecific and intraspecific interaction. The current model can estimate whether a species might potentially be at risk. It, however, can not predict if a certain population of a species can survive such a risk. Individuals might be at risk, but the population as a whole might still survive. If we want to obtain insight in the survival of a population, we need to simulate cumulative exposure to multiple stressors and incorporate ecological processes, such as reproduction, mortality, competition, etc., that influence individual and population survival. The ecological processes mentioned arise from interspecific and intraspecific interaction between the organisms. The inclusion of interspecific and intraspecific interaction would result in a conceptually more realistic simulation. Including a predator - prey model component, simulating various organisms of different trophic levels simultaneously would also enable preys to exhibit spatial foraging behaviour and approach food web regulation more realistically. The modelling environment of the current model does not readily allow for the inclusion of these kinds of interactions. However, with object-orientation it is possible to let individual organisms of either the same or different species interact. The architecture of object orientation overall closely resembles the real world and is therefore very suitable for spatially explicit exposure modelling. It is planned to model interspecific and intraspecific interaction with the use of object-oriented programming.

Further, when there are clear indications that specific foraging behaviour is unrealistic in that sense that it leads to incorrect estimation of exposures, it is advisable to incorporate more (ecologically) realistic behaviour and/or species traits in the model. For example, the stopping criterion should ideally be based on the age of receptors modelled and age class distribution of preys should be more realistic. Where necessary, improvement of behaviour algorithms will be considered, given the fact that there is information available on more realistic behaviour.

**Cumulative approach**

It is intended to extend the model enabling it to assess the exposure to more stressors. As yet, the model has been applied to the ADW floodplain and for the heavy metal cadmium. The model can easily be parameterised for other metals, by adjusting the input data with the contaminant-specific ecotoxicological parameters and adapting contaminant uptake formulas in case of altered contaminant-specific accumulation processes. This is currently being done for other heavy metals (nickel, zinc, cupper and lead) and the model will be applied to the same study area to assess the cumulative exposure of the same floodplain organisms to these contaminants.

In the exposure modelling possible interactions between the stressors themselves will not be considered. In the risk estimation, in principle, either concentration addition or independent action (response multiplication) approaches will be used. However, if sufficient information is known about the interactions between their effects on organisms, incorporating these effects may be an option, when predicting risk.

**Suitable programming platform**

The current version of the model is developed and implemented in MS Excel® with the MS Visual Basic Application® (VBA). Experiences show that this platform has some serious limitations in terms of flexibility, efficiency, data storage capacity and processing speed. To overcome these problems, future versions of the model will be implemented in a more suitable platform during the second phase of the project. The software platform Microsoft Visual C++® has been chosen as the new modelling environment. This selection was based on literature review of similar models and criteria such as (programming) flexibility, efficiency, re-usability of software components, user community and data storage capacity. The C++ environment supports object-oriented programming, which is required for species interaction modelling and which has an additional advantage of facilitating easy re-use of software components. Besides, C++ is currently one of the most widely used programming languages. Using this language therefore more frequently facilitates easy code exchange with other models using the same language. Additionally, it would have greater potential for getting a large user community.
References


NoMiracle. 2006. Pages NoMiracle / European Communities, URL: http://nomiracle.jrc.it/default.aspx


Schröder, T. unpublished results. Soil Science Centre, Wageningen University, The Netherlands.


Appendices

Appendix I  Objectives of NoMiracle

The main NoMiracle Objectives:

1. To develop new methods for assessing the cumulative risks from combined exposures to several stressors including mixtures of chemical and physical/biological agents
2. To achieve more effective integration of the risk analysis of environmental and human health effects
3. To improve our understanding of complex exposure situations and develop adequate tools for sound exposure assessment
4. To develop a research framework for the description and interpretation of cumulative exposure and effect
5. To quantify, characterise and reduce uncertainty in current risk assessment methodologies, e.g. by improvement of the scientific basis for setting safety factors
6. To develop assessment methods which take into account geographical, ecological, social and cultural differences in risk concepts and risk perceptions across Europe
7. To improve the provisions for the application of the precautionary principle and to promote its operational integration with evidence-based assessment methodologies
Appendix II  Source Code

Within the VBA program the different modules are controlled from the main module, and the main model parameters are declared here. Before each module is called, input data required by the module to run properly is read from input data spreadsheets and stored in arrays. These data include species-specific data such as weight, age, etc., and food web relationships. The Visual Basic code for the principle modules are shown in the subordinate appendices. The entire model including its Visual Basic code will be made available via the NoMiracle website (http://nomiracle.jrc.it/default.aspx).

Appendix IIa  Main module

Option Explicit 'every variable must be declared. Otherwise, this condition will retrieve error.

'.......................................................................................................................................................................
'Variables are defined here
'......................................................................................................................................................................

Public Max_number_Individuals As Integer 'Number of modelled individuals/number of runs
Public modelledSpecies As Integer 'type of species to model in these simulation runs
Public Use_Soil_C As Boolean 'Choosing between Cd values for soil or sediment
Public HQ_TV As Single 'This will be the minimum Hq_Total value a cell must have in order to individuals to move on/live in
Public Organism(1 To 18) As organism_type 'organism 1 to 18 = earthworms to badger in "Basic_Data"
Public Organism_number As Integer 'organism code number
Public Floodplain() As floodplain_Type 'reflects the characteristics of the floodplain.
Public X_range As Integer, Y_range As Integer 'Number of cells in the x_axis and y_axis
Public X As Integer, Y As Integer 'These variables will be used for searching the floodplain as coordinates
Public Cell_area As Integer 'The area of the cell
Public Foodchain_sheet(1 To 18, 1 To 8) As Foodchain_type 'reflects foodweb relationships. 1 - 20 are the predators and 1 to 8 are the preys.
Public Species_ecotope_key(3 To 32, 0 To 18) As Single 'Is used to read the species_ecotope_key
Public position() As position_type 'This will store information concerning position choosing
Public Foraging_Path() As Foraging_Position_type 'this array will store information concerning the foraging positions
Public Run As Integer 'Run number
Public Preys_of_third_level() As Preys_third_level_type
Public Print_positions As Boolean 'Print foraging positions coordinates
Public Print_position_concentration As Boolean 'Print Average Concentration in food and internal concentration acquired in each cell?
Public Print_home_range_Hq_visits As Boolean
Public Print_final_results As Boolean 'Print Averages of all runs and risks
Public Moving_organism() As moving_organism_type 'Used to store Sum HQs of the foraged cells to each run and Maximum number of cell visited from all runs
Public Position_number As Long 'Used as foraged position identification/counter
Public Run_results() As run_results_type 'used to save the results of the runs
Public counter As Integer 'Variable used to printing functions
Public All_Runs_Average_internal_concentration_acquired(9 To 18) As Single
Public All_Runs_Average_concentration_food(9 To 18) As Single
Public All_Runs_Average_Risk_Indicator(9 To 18) As Single
Public Preys_Age_and_concentration_for_printing() As Preys_age_and_concentration_type
Public Age() As Double
Public max_number_positions As Long
Public home_range_cells() As position_type 'Will store the positions of the home range cells. It'll be used in FA calculations
Public Sample_Type As String
Public Home_range_cells_for_printing() As position_type

Public Type Preys_age_and_concentration_type
  Age As Single
  concentration As Single
End Type

Public Type run_results_type
X_coord As Integer 'x-coordinate of starting position (nest)
Y_coord As Integer 'y-coordinate of starting position (nest)
Time_weighted_average_concentration_food As Single 'Average concentration
internal_concentration_acquired As Single 'Internal Concentration Acquired
Time_weighted_Average_internal_concentration_acquired As Single
risk_indicator As Single

End Type

Public Type moving_organism_type

Sum_of_HQS As Single 'Sum of habitat Quality values for each run
Number_positions As Long 'Number of foraging positions
number_home_range_cells As Long

End Type

Public Type Preys_third_level_type

internal_concentration As Single 'Potential Internal concentration for a Life Expectancy old animal
Internal_concentration_Acquirable As Single
Q_number As Integer 'Prey identification
relative_fraction As Single

End Type

Public Type floodplain_Type 'These are the variable of the array floodplain(), which reflects the characteristics of the floodplain

Ecotope As Integer 'This is the Ecotope number
Hq_floodplain As Single 'This represents de HQ value that is read in the species ecotope key
Hq_food As Single 'This represents the HQ related with food availability
HQ_Total As Single 'This is the product of both other HQs
First As Boolean 'This will determine if a cell can be a starting position
Colonizable As Boolean 'This will determine if a cell is colonisable for organisms with a maximum dispersion distance (from unflooded areas)
availability As Boolean 'This will retrieve whether or not a cell as any food items available
Prey_sum As Single 'Sum of C.f and CAE's for each cell
average_concentration_food As Single 'Average concentration in food for a second level species that forages there
Available_Prey As Integer 'Number of preys available.
Visited As Boolean 'This will reflect if a cell has been visited three selections before.
Visits As Integer 'This is the number of times a cell has been visited
Available_fractions As Single 'This will retrieve the sum of the available fractions.
In As Boolean 'This will retrieve whether or not a cell is part of the floodplain
Home_range As Boolean 'This will retrieve if a cell is within the home range
Flooding_distances As Single 'Distance from unflooded cell
internal_concentration As Single

End Type

Public Type position_type 'These are the variables of the array position(), which will store the positions retrieved by the random walk algorithm

X_Pos As Integer 'X-coordinate
Y_pos As Integer 'Y-coordinate
number_of_visits As Integer
Cumulative_chance As Single
Distance As Single
Chance_index As Single

End Type

Public Type Foraging_Position_type 'Array containing Foraging positions

X_Pos As Integer 'X-coordinate
Y_pos As Integer 'Y-coordinate
Age As Single
Time_spent As Single 'Number of days spent in cell foraged
internal_concentration_acquired As Single 'Acquired internal concentration by foraging in that cell
average_concentration_food As Single 'Average concentration in food of that cell
Hq As Single 'Habitat Quality

End Type

Public Type Foodchain_type 'These are the variables of the array foodchain_sheet, which reflects the foodchain relationships.
    BAF As Single 'Bioaccumulation Factor values
    Fractions As Single 'Fractions of diet
    Q_number As Integer 'Code number of the diet species
    Regression_a As Single 'regression coefficients
    Regression_b As Single
    Regression_c As Single
End Type

Public Type organism_type 'these are the variables of the array organism(), which will store individuals' characteristics.
    Name As String * 20 'Name
    Q_number As Integer 'Unique Identifying Code number for species
    Level_one As Boolean
    Home_range As Integer 'Home Range
    Home_range_fraction As Single 'Percentage of Home Range in order to a cell to be used as a starting position
    Maximum Dispersion As Integer 'Maximum distance within which have to be in order to be colonized
    Max_hq As Single 'This is the variable that represents the maximum Hq value available on the floodplain for each species.
    number_of_startings As Long
    Number_preys As Integer 'Number of preys
    Life_expectancy As Integer
    DCR As Single 'Daily Consumption Factor (=Feeding Rate / Body Weight)
    BW As Single 'Body Weight
    CAE As Single 'Contaminant Assimilation Efficiency
    PNEC As Single 'Predicted No-Effect Concentration
    GCF As Double 'Gut Content Correction Factor
    Number_of_individuals As Integer
    DMC As Single 'Dry Matter Content: dry weight to wet weight conversion factor (species specific)
End Type

Sub model()
    Dim max_number_preys

    Debug.Print "start", Time
    '-----------------------------------------------------------------------------------------------------------------------------
    'Setting are defined here
    '-----------------------------------------------------------------------------------------------------------------------------
    Max_number_Individuals = Worksheets("basic_data").Cells(22, 14)
    Use_Soil_C = True 'If true soil values are used, (Note that IDW interpolated SoilConcentrations are used)
    Print_positions = True
    Print_home_range_Hq_visits = True
    Print_final_results = True
    Cell_area = 25 'square meters
    Y_range = 912 'cells
    X_range = 245 'cells
    HQ_TV = 0
    Sample_Type = "soil" 'Note that IDW interpolated SoilConcentrations are used
    Debug.Print "Soil Calculations"
ReDim Floodplain(0 To 18, 1 To Y_range, 1 To X_range) As floodplain_Type

Call Organisms

For Organism_number = 9 To 18
    If Organism(Organism_number).Number_of_individuals > 0 Then
        modelledSpecies = Organism_number 'only desired species is modelled
    End If
Next Organism_number

Debug.Print modelledSpecies

ReDim home_range_cells(modelledSpecies To modelledSpecies, 1 To 1) As position_type

ReDim Home_range_cells_for_printing(1 To 5, modelledSpecies To modelledSpecies, 1 To 1) As position_type

ReDim Foraging_Path(1 To Max_number_Individuals, modelledSpecies To modelledSpecies, 1 To 1) As position_type

ReDim Run_results(modelledSpecies To modelledSpecies, 1 To Max_number_Individuals) As run_results_type

If modelledSpecies > 14 Then 'if a third-level species is being modelled
    max_number_preys = Organism(modelledSpecies).Number_preys
    ReDim Preys_of_third_level(15 To 18, 1 To Y_range, 1 To X_range, 1 To max_number_preys) As Preys_third_level_type
End If

Call virtual_floodplain

Call species_floodplain

Call Possible_First_Positions

Debug.Print "first Phase finished", Time

Call Foraging_Path_Procedure

ReDim Preys_Age_and_concentration_for_printing(1 To 5, 1 To 18, 1 To max_number_positions) As Preys_age_and_concentration_type

ReDim Age(1 To 18, 1 To max_number_positions) As Double

Debug.Print "exposure started", Time

Call Calculate_exposure

Debug.Print "Ready for Printing", Time

Call Write_in_Worksheets

Use_Soil_C = False 'run model again for sediment contamination
Sample_Type = "Sediment"

Debug.Print "Sediment Calculations"

Print_home_range_Hq_visits = False

Call species_floodplain

Call Calculate_exposure
Appendix IIb  Landscape module

Sub species_floodplain() 'Species-specific virtual floodplains are created.

For Organism_number = 1 To modelledSpecies 'species-specific Habitat Quality data is generated
    For Y = 1 To Y_range 'cell coordinates
        For X = 1 To X_range 'cell coordinates
            If Floodplain(0, Y, X).In = True Then 'If the cell is within the study area boundary then
                Floodplain(Organism_number, Y, X).Hq_floodplain = Hq_floodplain() 'Hq_values considering the ecotopes and species key are calculated:
                    If Organism_number > 7 Then 'Excluding soil/sediment feeding individuals, because soil/sediment is always available, in case of HQ calculations, and excluding sessile individuals, in case of moving parameters
                        Floodplain(Organism_number, Y, X).Hq_food = Hq_food() 'Hq values considering food are given to each cell
                    End If
                    If Organism_number > 8 Then 'for mobile species
                        If Floodplain(0, Y, X).Flooding_distances <= Organism(Organism_number).Maximum Dispersion Then
                            Floodplain(Organism_number, Y, X).Colonizable = True
                        Else
                            Floodplain(Organism_number, Y, X).Colonizable = False
                        End If
                    End If
                Else
                    Floodplain(Organism_number, Y, X).Colonizable = True
                End If
                If Floodplain(Organism_number, Y, X).Colonizable = True Then
                    If Floodplain(Organism_number, Y, X).HQ_Total <= HQ_TV Then 'If there's no suitable HQ_total value then
                        Floodplain(Organism_number, Y, X).availability = False 'the species won't be able to live in the cell, thus, they are not available.
                    Else
                        Floodplain(Organism_number, Y, X).availability = True 'If there is enough hq_total then the individual will exist, thus they are available.
                    End If
                Else
                    Floodplain(Organism_number, Y, X).availability = False
                End If
            End If
        End For
    End For
End Sub
Next X
Next Y
Next Organism_number

Private Function Hq_food()

Dim prey_number As Integer
Dim Number_preys As Integer
Dim availability As Integer

Number_preys = Organism(Organism_number).Number_preys

Hq_food = 0 'Set as default
Floodplain(0, Y, X).availability = True 'Soil/sediment is always available

For prey_number = 1 To Number_preys 'hq_food is calculated according to HQ and fractions of the diet
    If Floodplain(Foodchain_sheet(Organism_number, prey_number).Q_number, Y, X).availability = False Then
        availability = 0 'No
    Else
        availability = 1 'Yes
    End If
    Hq_food = Hq_food + availability * Foodchain_sheet(Organism_number, prey_number).Fractions * Floodplain(Foodchain_sheet(Organism_number, prey_number).Q_number, Y, X).HQ_Total

Next prey_number

End Function

Private Function Hq_floodplain()

Dim Ecotopes As Integer

For Ecotopes = 3 To 32
    If Species_ecotope_key(Ecotopes, 0) = Floodplain(0, Y, X).Ecotope Then
        Hq_floodplain = Species_ecotope_key(Ecotopes, Organism_number)
    End If

Next Ecotopes

End Function

Appendix IIc Foraging path module

Starting position

Sub Possible_First_Positions()

Dim number_of_startings As Long 'This will be used to count possible first positions

'Possible first positions and starting positions probabilities are calculated here:

For Organism_number = modelledSpecies To modelledSpecies
    'Species-specific possible first positions are calculated here:
    For Y = 1 To Y_range
For X = 1 To X_range
    If Floodplain(Organism_number, Y, X).Hq_floodplain = Organism(Organism_number).Max_hq Then
        If Organism(Organism_number).Maximum_dispersion >= 0 Then
            If Floodplain(0, Y, X).Flooding_distances <=
                Organism(Organism_number).Maximum_dispersion Then 'If the cell is not flooded
                Floodplain(Organism_number, Y, X).First = starting() 'it'll be tested as possible first position
            Else
                Floodplain(Organism_number, Y, X).First = False
            End If
        Else
            Floodplain(Organism_number, Y, X).First = False
        End If
    Else
        Floodplain(Organism_number, Y, X).First = starting() 'it'll be tested as possible first position
    End If
End If
Next X
Next Y

'Possible First positions are saved here

number_of_startings = 0
For Y = 1 To Y_range
    For X = 1 To X_range
        Floodplain(Organism_number, Y, X).Visits = 0
        If Floodplain(Organism_number, Y, X).First = True Then 'If the cell is a possible first position then
            number_of_startings = number_of_startings + 1
        End If
    Next X
Next Y
Organism(Organism_number).number_of_startings = number_of_startings

ReDim position(9 To 18, 1 To number_of_startings)
number_of_startings = 0
For Y = 1 To Y_range
    For X = 1 To X_range
        If Floodplain(Organism_number, Y, X).First = True Then
            If Organism(Organism_number).Maximum_dispersion < 0 Then 'organisms with no differentiated probability according to distance from unflooded areas
                number_of_startings = number_of_startings + 1
                position(Organism_number, number_of_startings).X_Pos = X 'Coordinates are saved
                position(Organism_number, number_of_startings).Y_pos = Y 'Coordinates are saved
            End If
        End If
    Next X
Next Y
ElseIf Organism(Organism_number).Maximum_dispersion = 0 Then 'animals with probability for first position according to distance from unflooded areas

number_of_startings = number_of_startings + 1 'counter

class_position(Organism_number, number_of_startings).X_Pos = X 'Coordinates are saved
class_position(Organism_number, number_of_startings).Y_pos = Y 'Coordinates are saved
class_position(Organism_number, number_of_startings).Distance = Floodplain(0, Y, X).Flooding_distances 'Flooding distances are saved
class_position(Organism_number, number_of_startings).Chance_index = 1 - (class_position(Organism_number, number_of_startings).Distance / Organism(Organism_number).Maximum_dispersion)
class_position(Organism_number, number_of_startings).Cumulative_chance = 0

Else

number_of_startings = number_of_startings + 1

class_position(Organism_number, number_of_startings).X_Pos = X 'Coordinates are saved
class_position(Organism_number, number_of_startings).Y_pos = Y 'Coordinates are saved
class_position(Organism_number, number_of_startings).Distance = Floodplain(0, Y, X).Flooding_distances 'Flooding distances are saved
class_position(Organism_number, number_of_startings).Chance_index = 1 - (class_position(Organism_number, number_of_startings).Distance / Organism(Organism_number).Maximum_dispersion)
class_position(Organism_number, number_of_startings).Cumulative_chance = 0

End If

End If

Next X

Next Y

'Choosing starting position

Randomize 'generate random numbers

ReDim Moving_organism(1 To Max_number_Individuals, modelledSpecies To modelledSpecies) As moving_organism_type

ReDim home_range_cell_index(1 To Y_range, 1 To X_range) As Long

max_number_positions = 1

max_number_home_range_cells = 0

For Run = 1 To Organism(Organism_number).Number_of_individuals

If Organism(Organism_number).Maximum_dispersion < 0 Then

rnd_index = Int((number_of_startings - 1 + 1) * Rnd() + 1) 'Int((upperbound - lowerbound + 1) * Rnd + lowerbound)

'Select one of the saved positions randomly

X_Pos = position(Organism_number, rnd_index).X_Pos 'coordinate of the position
Y_pos = position(Organism_number, rnd_index).Y_pos 'coordinate of the position
Run_results(Organism_number, Run).X coord = X_Pos 'saving x-coordinate of starting position for organism and run
Run_results(Organism_number, Run).Y coord = Y_pos 'saving y-coordinate

Else

For i = 1 To number_of_startings

sum_of_chance_index = sum_of_chance_index + position(Organism_number, i).Chance_index

Next i

For i = 1 To number_of_startings

Cumulative_chance = Cumulative_chance + position(Organism_number, i).Chance_index / sum_of_chance_index

End If

End If

End For

End For

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position(Organism_number, i).Cumulative_chance = Cumulative_chance
Next i

rnd_index = Rnd() 'one is selected randomly

For i = 1 To number_of_startings
    If rnd_index < position(Organism_number, i).Cumulative_chance Then
        X_Pos = position(Organism_number, i).X_Pos
        Y_pos = position(Organism_number, i).Y_pos
        Run_results(Organism_number, Run).X_coord = X_Pos 'saving x-coordinate of starting position for organism and run
        Run_results(Organism_number, Run).Y_coord = Y_pos 'saving y-coordinate
    Exit For
End If
Next i

End If

Next Run

End Sub

Private Function starting()

Dim North As Integer, South As Integer, West As Integer, East As Integer 'home range coordinates
Dim number_cells As Single 'Number of HQ suitable cells within home range
Dim range_cells As Single 'number of total cells within home range
Dim i As Integer, j As Integer 'coordinates
Dim cell_range As Integer
Dim minimum_fraction As Single

cell_range = Organism(Organism_number).Home_range
minimum_fraction = Organism(Organism_number).Home_range_fraction

' The area to search for other HQ suitable cells is defined

If Y - cell_range > 1 Then
    North = Y - cell_range
Else
    North = 1
End If

If X + cell_range < X_range Then
    East = X + cell_range
Else
    East = X_range
End If

If Y + cell_range < Y_range Then
    South = Y + cell_range
Else
    South = Y_range
End If

If X - cell_range > 1 Then
    West = X - cell_range
Else
    West = 1
End If

number_cells = 0 'Set default
range_cells = 0
For \( j = \text{North} \) To \text{South} 'Look in the area defined (jump range area)
For \( i = \text{West} \) To \text{East}

If Floodplain(0, j, i).In = True Then 'If cells belongs to the floodplain
range_cells = range_cells + 1 'cells within jump range are counted

If Floodplain(Organism_number, j, i).HQ_Total > HQ_TV Then 'If the cell has a suitable HQ_total then

number_cells = number_cells + 1 'it's counted

End If

End If

Next i
Next j

If number_cells > range_cells * minimum_fraction Then 'If there are more cells counted than a minimum fraction of the total cells within home range then

starting = True 'The cell can be a first position

End If

End Function

---

**Foraging path**

Sub Foraging_Path_Procedure()

Dim number_of_runs As Integer
Dim X_Pos As Integer 'X coordinate of the foraging positions
Dim Y_pos As Integer 'Y coordinate of the foraging positions
Dim md_index As Single 'random index to select array members randomly
Dim suitable_destinations As Integer 'number of neighbor cells
Dim Number_positions As Long 'number of foraged cells
Dim suitable_home_cell As Single 'this array will store the HQ suitable neighbor positions
Dim North As Integer, South As Integer, West As Integer, East As Integer 'These will define the coordinates of the home_range area.
Dim FA As Long 'Foraging Area
Dim TAF As Long 'Total area Foraged
Dim visited_cells As Single
Dim i As Single 'Counter for printing
Dim radius As Integer
Dim total_quality As Single, Cumulative_chance As Double
Dim sum_of_chance_index As Single
Dim Sum_of_HQS As Single
Dim Home_range As Long
Dim number_of_startings As Long
Dim home_range_cell_index() As Long
Dim max_number_home_range_cells As Long

Randomize 'generate random numbers

ReDim Moving_organism(1 To Max_number_Individuals, modelledSpecies To modelledSpecies) As moving_organism_type
ReDim home_range_cell_index(1 To Y_range, 1 To X_range) As Long

max_number_positions = 1
max_number_home_range_cells = 0

For Organism_number = modelledSpecies To modelledSpecies
For Run = 1 To Organism(Organism_number).Number_of_individuals

visited_cells = 0
Home_range = Organism(Organism_number).Home_range
sum_of_chance_index = 0 'default
Cumulative_chance = 0
number_of_startings = Organism(Organism_number).number_of_startings
Number_positions = 0
Sum_of_HQS = 0

X_Pos = Run_results(Organism_number, Run).X_coord 'x-coordinate of starting position for organism
Y_pos = Run_results(Organism_number, Run).Y coord 'y-coordinate

'----------------------------------------------------------------------------------------------------------------------------
'Home Range Areas are defined:
'----------------------------------------------------------------------------------------------------------------------------
'REMARK: North is South and South is North in the ADW case study as well as, West is East and Vice versa.

'cell (North, West)---------------------------------------------------------------cell (North, East)

'cell (South, West)---------------------------------------------------------------cell (South, East)

If Y_pos - Home_range > 1 Then
  North = Y_pos - Home_range
Else
  North = 1
End If

If X_Pos + Home_range < X_range Then
  East = X_Pos + Home_range
Else
  East = X_range
End If

If Y_pos + Home_range < Y_range Then
  South = Y_pos + Home_range
Else
  South = Y_range
End If

If X_Pos - Home_range > 1 Then
  West = X_Pos - Home_range
Else
  West = 1
End If

'Cells belonging to home range are defined:

suitable_home_cell = 0
home_range_cells(organism_number, 1).Y_pos = Y_pos
home_range_cells(organism_number, 1).X_Pos = X_Pos

for Y = North to South
    for X = West to East
        if floodplain(0, Y, X).In = True then
            if floodplain(organism_number, Y, X).HQ_Total > HQ_TV then
                suitable_home_cell = suitable_home_cell + 1
            if suitable_home_cell > max_number_home_range_cells then
                max_number_home_range_cells = suitable_home_cell
            redim preserve home_range_cells(modelled_species to modelled_species, 1 to max_number_home_range_cells) as position_type
            if Run < 6 then
                redim preserve home_range_cells_for_printing(1 to 5, modelled_species to modelled_species, 1 to max_number_home_range_cells) as position_type
            end if
        end if
    end if
end if

home_range_cells(organism_number, suitable_home_cell).X_Pos = X
home_range_cells(organism_number, suitable_home_cell).Y_pos = Y
floodplain(organism_number, Y, X).Home_range = True
floodplain(organism_number, Y, X).Visited = False
if Run < 6 then
    home_range_cell_index(Y, X) = suitable_home_cell
    home_range_cells_for_printing(Run, organism_number, suitable_home_cell).Y_pos = Y
    home_range_cells_for_printing(Run, organism_number, suitable_home_cell).X_Pos = X
end if

end if

east

if organism_number = 15 or organism_number = 16 then 'cell visiting probabilities for kestrels and little owls are calculated here

    total_quality = 0
    cumulative_chance = 0
    for i = 1 to suitable_home_cell
        total_quality = total_quality + floodplain(organism_number, home_range_cells(organism_number, i).Y_pos, home_range_cells(organism_number, i).X_Pos).HQ_Total
    next i

    for i = 1 to suitable_home_cell
        total_quality = total_quality + floodplain(organism_number, home_range_cells(organism_number, i).Y_pos, home_range_cells(organism_number, i).X_Pos).HQ_Total
    next i
Cumulative_chance = Cumulative_chance + (Floodplain(Organism_number, home_range_cells(Organism_number, i).Y_pos, home_range_cells(Organism_number, i).X_Pos).HQ_Total / total_quality)
home_range_cells(Organism_number, i).C
Cumulative_chance = Cumulative_chance

Next i

End If

Moving_organism(Run, Organism_number).number_home_range_cells = suitable_home_cell

'Foraging area is calculated here:

FA = 0
FA = CLng(suitable_home_cell) * CLng(Cell_area)

Number_positions = 1
ReDim Preserve Foraging_Path(1 To Max_number_Individuals, modelledSpecies To modelledSpecies, 1 To max_number_positions)

Foraging_Path(Run, Organism_number, 1).Y_pos = Y_pos
Foraging_Path(Run, Organism_number, 1).X_Pos = X_Pos
Foraging_Path(Run, Organism_number, 1).Hq = Floodplain(Organism_number, Y_pos, X_Pos).HQ_Total

Sum_of_HQS = Foraging_Path(Run, Organism_number, 1).Hq
TAF = Cell_area
Floodplain(Organism_number, Y_pos, X_Pos).Visited = True 'Cell is assumed as visited
Floodplain(Organism_number, Y_pos, X_Pos).Visits = Floodplain(Organism_number, Y_pos, X_Pos).Visits + 1 'The visit is added

ReDim Path(suitable_destinations) As position_type 'the array is redimensioned
suitable_destinations = suitable_destinations + 1
ReDim Preserve suitable_pos(1 To suitable_destinations) As position_type 'the array is redimensioned

suitable_destinations = suitable_destinations + 1
ReDim Preserve suitable_pos(1 To suitable_destinations) As position_type 'the array is redimensioned

suitable_pos(suitable_destinations).Y_pos = Y_possible_positions are stored. y coordinate
suitable_pos(suitable_destinations).X_Pos = X_possible_positions are stored. x coordinate

End If
End If

Next X
Next Y

radius = radius + 1 'enlarge search radius

Loop Until suitable_destinations > 0

total_quality = 0
Cumulative_chance = 0
'-------------------------------
"Summing qualities"
'-------------------------------
For i = 1 To suitable_destinations

total_quality = total_quality + Floodplain(Organism_number, suitable_pos(i).Y_pos, suitable_pos(i).X_Pos).HQ_Total

Next i

'cell visiting probabilities for terrestrial organisms are calculated here:

For i = 1 To suitable_destinations

Cumulative_chance = Cumulative_chance + (Floodplain(Organism_number, suitable_pos(i).Y_pos, suitable_pos(i).X_Pos).HQ_Total / total_quality)
suitable_pos(i).Cumulative_chance = Cumulative_chance

Next i

rnd_index = Rnd() 'one is selected randomly

For i = 1 To suitable_destinations

If rnd_index < suitable_pos(i).Cumulative_chance Then

X_Pos = suitable_pos(i).X_Pos
Y_pos = suitable_pos(i).Y_pos
Exit For

End If

Next i

ElseIf Organism_number = 15 Or Organism_number = 16 Then 'for flying organisms

rnd_index = Rnd()

For i = 1 To suitable_home_cell

If rnd_index < home_range_cells(Organism_number, i).Cumulative_chance Then

X_Pos = home_range_cells(Organism_number, i).X_Pos
Y_pos = home_range_cells(Organism_number, i).Y_pos
Exit For

End If

Next i

End If

TAF = TAF + Cell_area 'total area foraged is calculated.

Number_positions = Number_positions + 1 'number of cells in the foraging path are counted
'-------------------------------
'Saving Foraging Path

If Number_positions > max_number_positions Then

    ReDim Preserve Foraging_Path(1 To Max_number_Individuals, modelledSpecies To modelledSpecies, 1 To Number_positions) As Foraging_Position_type 'array is redimensioned

    max_number_positions = Number_positions

End If

Foraging_Path(Run, Organism_number, Number_positions).X_Pos = X_Pos 'positions are stored in the array
Foraging_Path(Run, Organism_number, Number_positions).Y_pos = Y_pos 'positions are stored in the array
Foraging_Path(Run, Organism_number, Number_positions).Hq = Floodplain(Organism_number, Y_pos, X_Pos).HQ_Total
Sum_of_HQS = Sum_of_HQS + Foraging_Path(Run, Organism_number, Number_positions).Hq
Floodplain(Organism_number, Y_pos, X_Pos).Visited = True 'Cell is assumed as visited

If Floodplain(Organism_number, Y_pos, X_Pos).Home_range = True And Run < 6 Then 'only paths of 5 runs are printed

    Home_range_cells_for_printing(Run, Organism_number, home_range_cell_index(Y_pos, X_Pos)).number_of_visits = Home_range_cells_for_printing(Run, Organism_number, home_range_cell_index(Y_pos, X_Pos)).number_of_visits + 1

End If

Floodplain(Organism_number, Y_pos, X_Pos).Visits = Floodplain(Organism_number, Y_pos, X_Pos).Visits + 1 'The visit is added

If Number_positions > 3 Then 'Once the 4th cell is selected for foraging

    Floodplain(Organism_number, Foraging_Path(Run, Organism_number, Number_positions - 3).Y_pos, Foraging_Path(Run, Organism_number, Number_positions - 3).X_Pos).Visited = False 'the cell visited 4 selections earlier is assumed as unvisited again

End If

Loop

Moving_organism(Run, Organism_number).Number_positions = Number_positions
Moving_organism(Run, Organism_number).Sum_of_HQS = Sum_of_HQS

Next Run

Next Organism_number

End Sub

Appendix IIId Exposure and Risk module

Internal concentrations

Private Sub concentrations()

Dim availability As Integer 'availability is the variable that retrieves the availability of preys
Dim prey As Integer 'prey number
Dim Internal_concentration_Acquirable As Single
Dim average_concentration_food As Single
Dim internal_concentration_food As Single
Dim Prey_sum As Single 'used as temporal storage of data for calculating internal concentrations for foraging 2nd level individuals

average_concentration_food = 0
Internal_concentration_Acquirable = 0
internal_concentration = 0
Prey_sum = 0

For prey = 1 To Organism(Organism_number).Number_preys 'for each prey

If Floodplain(Foodchain_sheet(Organism_number, prey).Q_number, Y, X).availability = False Then 'if there is no prey available
    availability = 0 'the answer is NO
Else 'if there are preys available
    availability = 1 'the answer is YES
End If

If Floodplain(Organism_number, Y, X).availability = True Then

If Organism_number > 0 And Organism_number < 5 Then 'for organism whose internal concentration is given by regression
    internal_concentration = Organism(Organism_number).DMC * (Foodchain_sheet(Organism_number, prey).Regression_a ^ (Foodchain_sheet(Organism_number, prey).Regression_b)) ^ (cdconcentration() ^ Foodchain_sheet(Organism_number, prey).Regression_c)
ElseIf Organism_number > 4 And Organism_number < 8 Then 'for organisms which [Cd] is given by BAF, except snail
    internal_concentration = Organism(Organism_number).DMC * cdconcentration() * Foodchain_sheet(Organism_number, prey).BAF
ElseIf Organism_number = 8 Then 'for snail which eats both soil and vegetation
    internal_concentration = internal_concentration + (Organism(Organism_number).DMC * cdconcentration() * Foodchain_sheet(Organism_number, prey).BAF) * (Foodchain_sheet(Organism_number, prey).Fractions / Floodplain(Organism_number, Y, X).Available_fractions))
ElseIf Organism_number >= 9 And Organism_number < 15 Then 'for 2nd level food web species
End If

ElseIf Organism_number >= 15 Then 'for 2nd level food web species
    average_concentration_food = average_concentration_food + (Floodplain(Foodchain_sheet(Organism_number, prey).Q_number, Y, X).internal_concentration * availability * (Foodchain_sheet(Organism_number, prey).Fractions / Floodplain(Organism_number, Y, X).Available_fractions))
End If
End If

Next prey

If Organism_number < 9 Then

    Floodplain(Organism_number, Y, X).internal_concentration = internal_concentration

Else

    Floodplain(Organism_number, Y, X).Prey_sum = Prey_sum 'used for foraging 2nd level individuals
    Floodplain(Organism_number, Y, X).average_concentration_food = average_concentration_food 'used for foraging 2nd level individuals

End If

End Sub

Private Sub Prey_Facts()

Dim availability As Integer 'availability is the variable that retrieves the availability of preys
Dim prey As Integer 'prey number
Dim Available_Preys As Integer

For prey = 1 To Organism(Organism_number).Number_preys 'for each prey

    If Floodplain(Foodchain_sheet(Organism_number, prey).Q_number, Y, X).availability = True Then 'if there is prey available

        Available_Preys = Available_Preys + 1
        Preys_of_third_level(Organism_number, Y, X, Available_Preys).Q_number = Foodchain_sheet(Organism_number, prey).Q_number
        If Organism(Foodchain_sheet(Organism_number, prey).Q_number).Level_one Then

            Preys_of_third_level(Organism_number, Y, X, Available_Preys).internal_concentration = Floodplain(Foodchain_sheet(Organism_number, prey).Q_number, Y, X).internal_concentration

        Else


        End If

    End If

End If

Next prey

Floodplain(Organism_number, Y, X).Available_Preys = Available_Preys

End Sub

Exposure and risk calculation

Sub Calculate_exposure()
Dim internal_concentration_acquired As Single
Dim Time_weighted_average_concentration_food As Single
Dim Sum_time_weighted_average_concentration_food As Single
Dim sum_internal_concentration_acquired As Single
Dim age_moving_individual As Single

For Organism_number = modelledSpecies To modelledSpecies
    For Run = 1 To Organism(Organism_number).Number_of_individuals
        age_moving_individual = 0
        For Position_number = 1 To Moving_organism(Run, Organism_number).Number_positions
            Foraging_Path(Run, Organism_number, Position_number).Time_spent = (Foraging_Path(Run, Organism_number, Position_number).Hq / Moving_organism(Run, Organism_number).Sum_of_HQS) * Organism(Organism_number).Life_expectancy
            age_moving_individual = age_moving_individual + Foraging_Path(Run, Organism_number, Position_number).Time_spent
            Foraging_Path(Run, Organism_number, Position_number).Age = age_moving_individual
        Next Position_number
    Next Run
    Sum_time_weighted_average_concentration_food = 0
    sum_internal_concentration_acquired = 0
    For Run = 1 To Organism(Organism_number).Number_of_individuals
        Time_weighted_average_concentration_food = 0
        internal_concentration_acquired = 0
        If Organism_number < 15 Then
            '-----------------------------------------------------------------------------------------------
            'calculate PEC and internal concentration for 2nd level species
            '-----------------------------------------------------------------------------------------------
            For Position_number = 1 To Moving_organism(Run, Organism_number).Number_positions
                '-----------------------------------------------------------------------------------------------
                'Calculate PEC
                '-----------------------------------------------------------------------------------------------
                Time_weighted_average_concentration_food = Time_weighted_average_concentration_food +
                    (Foraging_Path(Run, Organism_number, Position_number).Time_spent / Organism(Organism_number).Life_expectancy) * Floodplain(Organism_number, Foraging_Path(Run, Organism_number, Position_number).Y_pos, Foraging_Path(Run, Organism_number, Position_number).X_Pos).average_concentration_food
                Foraging_Path(Run, Organism_number, Position_number).average_concentration_food =
                    Floodplain(Organism_number, Foraging_Path(Run, Organism_number, Position_number).Y_pos, Foraging_Path(Run, Organism_number, Position_number).X_Pos).average_concentration_food
                '-----------------------------------------------------------------------------------------------
                'Calculate internal concentration
                '-----------------------------------------------------------------------------------------------
                internal_concentration_acquired = internal_concentration_acquired +
                Foraging_Path(Run, Organism_number, Position_number).internal_concentration_acquired =
                    internal_concentration_acquired
            Next Position_number
        Next Run
    Next Organism_number
End For

Run_results(Organism_number, Run).Time_weighted_average_concentration_food = Time_weighted_average_concentration_food

Run_results(Organism_number, Run).internal_concentration_acquired = internal_concentration_acquired

Else

'------------------------------------------------------------------------------------------
-- calculate PEC and internal concentration for 3rd level species
'------------------------------------------------------------------------------------------

Call concentration_food
Call concentration_internal

End If

Sum_time_weighted_average_concentration_food = Sum_time_weighted_average_concentration_food + Run_results(Organism_number, Run).Time_weighted_average_concentration_food

'------------------------------------------------------------------------------------------
-- Calculate Risk Indicator
'------------------------------------------------------------------------------------------

Run_results(Organism_number, Run).risk_indicator = Run_results(Organism_number, Run).Time_weighted_average_concentration_food / Organism(Organism_number).PNEC

sum_internal_concentration_acquired = sum_internal_concentration_acquired + Run_results(Organism_number, Run).internal_concentration_acquired
Run_results(Organism_number, Run).Time_weighted_Average_internal_concentration_acquired = Run_results(Organism_number, Run).internal_concentration_acquired / Organism(Organism_number).Life_expectancy

Next Run

'------------------------------------------------------------------------------------------
-- Calculate average values of results for all runs
'------------------------------------------------------------------------------------------

All_Runs_Average_concentration_food(Organism_number) = Sum_time_weighted_average_concentration_food / Organism(Organism_number).Number_of_individuals
All_Runs_Average_Risk_Indicator(Organism_number) = All_Runs_Average_concentration_food(Organism_number) / Organism(Organism_number).PNEC
All_Runs_Average_internal_concentration_acquired(Organism_number) = sum_internal_concentration_acquired / Organism(Organism_number).Number_of_individuals

Next Organism_number

End Sub

Private Sub concentration_food()

Dim Available_Preys As Integer
Dim prey As Integer
Dim Position_number As Long
Dim Age_prey As Double
Dim prey_number As Integer
Dim sum_average_concentrations_food As Single
Dim average_concentration_food As Single
Dim Time_weighted_average_concentration_food As Single
Dim Sum_time_weighted_average_concentration_food As Single

Time_weighted_average_concentration_food = 0

For Position_number = 1 To Moving_organism(Run, Organism_number).Number_positions

average_concentration_food = 0

Next Position_number

End Sub
For prey = 1 To Available_Preys

prey_number = Preys_of_third_level(Organism_number, Foraging_Path(Run, Organism_number, Position_number).Y_pos, Foraging_Path(Run, Organism_number, Position_number).X_Pos, prey).Q_number

If Organism(prey_number).Level_one = True Then

'calculate PEC from level one preys

average_concentration_food = average_concentration_food +

If Run < 6 Then

Preys_Age_and_concentration_for_printing(Run, prey_number, Position_number).concentration = Preys_of_third_level(Organism_number, Foraging_Path(Run, Organism_number, Position_number).Y_pos, Foraging_Path(Run, Organism_number, Position_number).X_Pos, prey).internal_concentration

End If

Else '
calculate PEC from level two preys

'generate random age for prey:
Age_prey = (Organism(prey_number).Life_expectancy - 1 + 1) * Rnd() + 1 'Int((upperbound - lowerbound + 1) * Rnd + lowerbound)
Age(prey_number, Position_number) = Age_prey

If Run < 6 Then

Preys_Age_and_concentration_for_printing(Run, prey_number, Position_number).Age = Age_prey

End If


If Run < 6 Then


End If

End If

Next prey
Foraging_Path(Run, Organism_number, Position_number).average_concentration_food = average_concentration_food

Time_weighted_average_concentration_food = Time_weighted_average_concentration_food + average_concentration_food * (Foraging_Path(Run, Organism_number, Position_number).Time_spent / Organism(Organism_number).Life_expectancy)

Next Position_number

Run_results(Organism_number, Run).Time_weighted_average_concentration_food = Time_weighted_average_concentration_food

End Sub

Private Sub concentration_internal()

Dim Available_Preys As Integer
Dim prey As Integer
Dim Position_number As Long
Dim Age_prey As Double
Dim prey_number As Integer
Dim internal_concentration_acquired As Single

For Position_number = 1 To Moving_organism(Run, Organism_number).Number_positions


For prey = 1 To Available_Preys

prey_number = Preys_of_third_level(Organism_number, Foraging_Path(Run, Organism_number, Position_number).Y_pos, Foraging_Path(Run, Organism_number, Position_number).X_Pos, prey).Q_number

If Organism(prey_number).Level_one = True Then

'calculate internal concentration from level one preys


Else

'calculate internal concentration from level two preys

Age_prey = Age(prey_number, Position_number)

End If

Next prey
Foraging_Path(Run, Organism_number, Position_number).internal_concentration_acquired = internal_concentration_acquired

Next Position_number

Run_results(Organism_number, Run).internal_concentration_acquired = internal_concentration_acquired

End Sub
### Appendix III  Food web relations

<table>
<thead>
<tr>
<th>Level 3</th>
<th>Species</th>
<th>Diet item</th>
<th>f</th>
</tr>
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<tbody>
<tr>
<td></td>
<td>Common kestrel</td>
<td>Common vole</td>
<td>96.0</td>
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<tr>
<td></td>
<td>Wood mouse</td>
<td>1.9</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Common shrew</td>
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<tr>
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<td>Little owl</td>
<td>European mole</td>
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<td>Earthworms</td>
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<td></td>
<td>H&amp;M</td>
<td>21.0</td>
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<td>Least weasel</td>
<td>Rabbit</td>
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</tr>
<tr>
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<td>European mole</td>
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<td></td>
<td>Vegetation</td>
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H&M = hexapods & myriapods

## Appendix IV  Species-ecotope matrix

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** Source **

0 = unsuitable habitat; 0.5 = marginal habitat; 1 = suitable habitat

A = earthworms; B = spiders; C = isopods; D = hexapods & myriapods; E = corn; F = vegetation; G = fruits; H = gastropods; I = wood mouse; J = bank vole; K = common shrew; L = common vole; M = European mole; N = rabbit; O = little owl; P = common kestrel; Q = least weasel; R = Eurasian badger


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### Appendix V  Species traits

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<th>CD (m) ***</th>
<th>LE (day)</th>
<th>BW (g) *</th>
<th>FR (g \cdot \text{day}^{-1})</th>
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<td>17.8 (13.4-23.7) (^{12})</td>
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<td>Bank vole</td>
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<td>274 (^{23})</td>
<td>18.8 (12.0 – 29.4) (^{12})</td>
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<td>8.0 (4.8 – 13.5) (^{12})</td>
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<td>548 (^8)</td>
<td>1732.1 (1200 – 2500) (^8)</td>
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<td>3650 (^{13})</td>
<td>180.4 (155 – 210) (^{13})</td>
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<tr>
<td>Eurasian badger</td>
<td>109.545 (30 – 400) (^8)</td>
<td>0.27</td>
<td>0</td>
<td>5913 (^{24})</td>
<td>10010 (6000 – 16700) (^{8,15})</td>
<td>702.5 (493.0 – 1001.0) (^{21})</td>
</tr>
</tbody>
</table>

HR = Home Range; min. HA = minimum Habitat Area; BW = Body Weight; FR = Feeding Rate; LE = maximum Life Expectancy; CD = colonizing distance

* values are given as median (min – max). Median values are calculated as follows: \( \log (\text{median } X) = \log (\text{max } X_{\text{recorded}}) / \log (\text{min } X_{\text{recorded}}) \)

\( f_{\text{suitable habitat}} \) (dimensionless) = (HR\(_{\text{min}}\) / HR\(_{\text{median}}\))

*** no data (-): species are assumed to select nest sites independent of inundation characteristics; 0: species are assumed to restrict nest sites to high-water-free areas

### Appendix VI  Input parameters for the calculation of predicted no effect concentrations in food (PNECs)

<table>
<thead>
<tr>
<th>Species</th>
<th>NOEC&lt;sub&gt;food&lt;/sub&gt; (mg∙kg&lt;sup&gt;-1&lt;/sup&gt;)</th>
<th>EMR/FMR</th>
<th>FCC&lt;sub&gt;lab&lt;/sub&gt; (kJ∙g&lt;sup&gt;-1&lt;/sup&gt;)</th>
<th>FCC&lt;sub&gt;field&lt;/sub&gt; (kJ∙g&lt;sup&gt;-1&lt;/sup&gt;)</th>
<th>FAE&lt;sub&gt;lab&lt;/sub&gt;**</th>
<th>FAE&lt;sub&gt;field&lt;/sub&gt;</th>
<th>PNEC (mg∙kg&lt;sup&gt;-1&lt;/sup&gt; food)**</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wood mouse</td>
<td>4.39&lt;sup&gt;1&lt;/sup&gt;</td>
<td>0.41&lt;sup&gt;4&lt;/sup&gt;</td>
<td>16.8&lt;sup&gt;4&lt;/sup&gt;</td>
<td>4.18</td>
<td>75.68</td>
<td>86.10&lt;sup&gt;4&lt;/sup&gt;</td>
<td>0.39</td>
</tr>
<tr>
<td>Bank vole</td>
<td>3.5&lt;sup&gt;2&lt;/sup&gt;</td>
<td>0.41&lt;sup&gt;4&lt;/sup&gt;</td>
<td>16.8&lt;sup&gt;4&lt;/sup&gt;</td>
<td>3.66</td>
<td>74.56</td>
<td>86.10&lt;sup&gt;4&lt;/sup&gt;</td>
<td>0.27</td>
</tr>
<tr>
<td>Common shrew</td>
<td>4.39&lt;sup&gt;1&lt;/sup&gt;</td>
<td>0.41&lt;sup&gt;4&lt;/sup&gt;</td>
<td>16.8&lt;sup&gt;4&lt;/sup&gt;</td>
<td>6.03</td>
<td>86.64</td>
<td>86.10&lt;sup&gt;4&lt;/sup&gt;</td>
<td>0.64</td>
</tr>
<tr>
<td>Common vole</td>
<td>4.39&lt;sup&gt;1&lt;/sup&gt;</td>
<td>0.41&lt;sup&gt;4&lt;/sup&gt;</td>
<td>16.8&lt;sup&gt;4&lt;/sup&gt;</td>
<td>3.93</td>
<td>74.00</td>
<td>86.10&lt;sup&gt;4&lt;/sup&gt;</td>
<td>0.42</td>
</tr>
<tr>
<td>European mole</td>
<td>4.39&lt;sup&gt;1&lt;/sup&gt;</td>
<td>0.41&lt;sup&gt;4&lt;/sup&gt;</td>
<td>16.8&lt;sup&gt;4&lt;/sup&gt;</td>
<td>3.84</td>
<td>88.00</td>
<td>86.10&lt;sup&gt;4&lt;/sup&gt;</td>
<td>0.36</td>
</tr>
<tr>
<td>Rabbit</td>
<td>4.39&lt;sup&gt;1&lt;/sup&gt;</td>
<td>0.41&lt;sup&gt;4&lt;/sup&gt;</td>
<td>16.8&lt;sup&gt;4&lt;/sup&gt;</td>
<td>3.93</td>
<td>74.00</td>
<td>86.10&lt;sup&gt;4&lt;/sup&gt;</td>
<td>0.36</td>
</tr>
<tr>
<td>Little owl</td>
<td>12.0&lt;sup&gt;3&lt;/sup&gt;</td>
<td>0.41&lt;sup&gt;4&lt;/sup&gt;</td>
<td>13.7&lt;sup&gt;4&lt;/sup&gt;</td>
<td>6.06</td>
<td>77.00</td>
<td>67.00&lt;sup&gt;5&lt;/sup&gt;</td>
<td>2.48</td>
</tr>
<tr>
<td>Common kestrel</td>
<td>12.0&lt;sup&gt;3&lt;/sup&gt;</td>
<td>0.41&lt;sup&gt;4&lt;/sup&gt;</td>
<td>13.7&lt;sup&gt;4&lt;/sup&gt;</td>
<td>7.10</td>
<td>84.00</td>
<td>67.00&lt;sup&gt;5&lt;/sup&gt;</td>
<td>3.17</td>
</tr>
<tr>
<td>Least weasel</td>
<td>4.39&lt;sup&gt;1&lt;/sup&gt;</td>
<td>0.41&lt;sup&gt;4&lt;/sup&gt;</td>
<td>16.8&lt;sup&gt;4&lt;/sup&gt;</td>
<td>7.07</td>
<td>85.01</td>
<td>86.10&lt;sup&gt;4&lt;/sup&gt;</td>
<td>0.74</td>
</tr>
<tr>
<td>Eurasian badger</td>
<td>4.39&lt;sup&gt;1&lt;/sup&gt;</td>
<td>0.41&lt;sup&gt;4&lt;/sup&gt;</td>
<td>16.8&lt;sup&gt;4&lt;/sup&gt;</td>
<td>4.91</td>
<td>84.02</td>
<td>86.10&lt;sup&gt;4&lt;/sup&gt;</td>
<td>0.51</td>
</tr>
</tbody>
</table>

* Calculated according to diet composition (see Appendix III) and mean caloric content of diet items (Apodemus sylvaticus, Talpa europaea, Clethrionomys glareolus, Sorex araneus, Microtus arvalis, Oryctolagus cuniculus 7.1 kJ·g<sup>-1</sup>; earthworms 3 kJ·g<sup>-1</sup>; hexapods & myriapods, isopods, spiders 7.2 kJ·g<sup>-1</sup>; gastropods 5.2 kJ·g<sup>-1</sup> (Traas et al. 1996); vegetation 3.93 kJ·g<sup>-1</sup>; corn 14.48 kJ·g<sup>-1</sup> (CSL 2002); fruits 1.92 kJ·g<sup>-1</sup> (US-EPA 1993)

** Calculated according to diet composition and (see Appendix III) and predator/prey specific food assimilation efficiencies derived from CSL 2002.

*** Calculated according to Traas et al. 1996

1 = Geometric mean of reported NOECs for several mammalian species: Bialonska et al. 2002; Doyle et al. 1974; Loeser 1980; Masaoka et al. 1994; Philips et al. 2003; Powell et al. 1964; 2 = Bialonska et al. 2002; 3 = Geometric mean of reported NOECs for several bird species: Congiu 2000; Leach et al. 1978; Pribilincova et al. 1995; Richardson et al. 1974; Scheuhammer 1987; Supplee 1961; Swiergosz & Kowalska 2000; White & Finley 1978; 4 = Traas et al. 1996; 5 = CSL 2002
**Appendix VII  Species-specific ecotoxicological model parameters**

<table>
<thead>
<tr>
<th>Species</th>
<th>DMC (dimensionless)</th>
<th>CAE (dimensionless)</th>
<th>GCF (dimensionless)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Earthworms</td>
<td>0.16 1,2,3,4</td>
<td>0.025 /8,9</td>
<td>1</td>
</tr>
<tr>
<td>Vegetation</td>
<td>0.19 1,2</td>
<td>0.010 7,8,9</td>
<td>1</td>
</tr>
<tr>
<td>Corn</td>
<td>0.79 1,2</td>
<td>0.010 7,8,9</td>
<td>1</td>
</tr>
<tr>
<td>Hexapods &amp; Myriapods</td>
<td>0.27 1,2,3,4</td>
<td>0.025 7,8,9</td>
<td>1</td>
</tr>
<tr>
<td>Arachnida</td>
<td>0.30 3</td>
<td>0.025 7,8,9</td>
<td>1</td>
</tr>
<tr>
<td>Isopods</td>
<td>0.31 1,2,3,4</td>
<td>0.025 7,8,9</td>
<td>1</td>
</tr>
<tr>
<td>Fruit</td>
<td>0.11 1,2,4,6</td>
<td>0.010 7,8,9</td>
<td>1</td>
</tr>
<tr>
<td>Gastropods</td>
<td>0.17 1</td>
<td>0.025 7,8,9</td>
<td>2 10</td>
</tr>
<tr>
<td>Wood mouse</td>
<td>-</td>
<td>0.025 7,8,9</td>
<td>2 10</td>
</tr>
<tr>
<td>Bank vole</td>
<td>-</td>
<td>0.025 7,8,9</td>
<td>2 10</td>
</tr>
<tr>
<td>Common shrew</td>
<td>-</td>
<td>0.025 7,8,9</td>
<td>2 10</td>
</tr>
<tr>
<td>Common vole</td>
<td>-</td>
<td>0.025 7,8,9</td>
<td>2 10</td>
</tr>
<tr>
<td>European mole</td>
<td>-</td>
<td>0.025 7,8,9</td>
<td>1.5</td>
</tr>
<tr>
<td>Rabbit</td>
<td>-</td>
<td>0.025 7,8,9</td>
<td>1.5</td>
</tr>
</tbody>
</table>

DMC = Dry Matter Content; CAE = Contaminant Assimilation Efficiency of cadmium; GCF = Gut Content Correction factor

### Appendix VIII  Relative habitat quality, relative surface area, visiting probabilities, stay duration probabilities, relative cell visit frequencies, average soil cadmium concentrations, predicted exposure concentrations (PECs) and food availability (FA) for each spatial unit distinguished in four cases investigated in model analysis

<table>
<thead>
<tr>
<th>Case</th>
<th>Spatial unit</th>
<th>HQ %</th>
<th>HQ² %</th>
<th>visits * in 250</th>
<th>Cd Soil</th>
<th>PEC</th>
<th>Food availability (FA)</th>
</tr>
</thead>
<tbody>
<tr>
<td>HQ-weighted</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1 home range</td>
<td></td>
<td>3.01</td>
<td>28.9</td>
<td>0.21</td>
<td>0.21</td>
<td>0.21</td>
<td></td>
</tr>
<tr>
<td>EQ -1</td>
<td></td>
<td>3.01</td>
<td>28.9</td>
<td>0.21</td>
<td>0.21</td>
<td>0.21</td>
<td></td>
</tr>
<tr>
<td>Least weasel</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>HQ-weighted</td>
<td></td>
<td></td>
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<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2 home range</td>
<td></td>
<td>2.24</td>
<td>24.2</td>
<td>0.23</td>
<td>0.23</td>
<td>0.23</td>
<td></td>
</tr>
<tr>
<td>EQ - 1</td>
<td></td>
<td>2.21</td>
<td>24.2</td>
<td>0.23</td>
<td>0.23</td>
<td>0.23</td>
<td></td>
</tr>
<tr>
<td>Least weasel</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>HQ-weighted</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>3 home range</td>
<td></td>
<td>2.16</td>
<td>1.71</td>
<td>0.15</td>
<td>0.15</td>
<td>0.15</td>
<td></td>
</tr>
<tr>
<td>EQ -1</td>
<td></td>
<td>2.16</td>
<td>1.71</td>
<td>0.15</td>
<td>0.15</td>
<td>0.15</td>
<td></td>
</tr>
<tr>
<td>Least weasel</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>HQ-weighted</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>4 home range</td>
<td></td>
<td>3.14</td>
<td>21.8</td>
<td>0.28</td>
<td>0.28</td>
<td>0.28</td>
<td></td>
</tr>
<tr>
<td>EQ - 1</td>
<td></td>
<td>3.14</td>
<td>21.8</td>
<td>0.28</td>
<td>0.28</td>
<td>0.28</td>
<td></td>
</tr>
<tr>
<td>Least weasel</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>HQ-weighted</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

HQ = relative habitat quality; SA = relative surface area; HQ² SA = visiting probability; HQ² SA = stay duration probability; Cd soil = cadmium concentration in soil (mg·kg⁻¹ dw); PEC = predicted exposure concentration (mg·kg⁻¹);
References


Boudewijn, T. J., and N. M. Groen. 1998. Projektplan voor onderzoek naar de mogelijke effecten van contaminanten in uiterwaarden op vogels. 98.017, Bureau Waardenburg, Culemborg.


Wijnhoven, S. 2005. personal communication

