11.0 Terrestrial Food Web Module

11.1 Purpose and Scope

The Terrestrial Food Web Module calculates the annual average contaminant concentrations in terrestrial plants and prey (such as earthworms or small mammals) eaten by wildlife. In addition, the module calculates spatially-averaged soil concentrations in two soil horizons— surficial soil and root zone soil—for the receptor home ranges placed within each of the habitats delineated within the area of interest (AOI). These concentrations are used as input to the Ecological Exposure Module to calculate the applied dose to receptors of interest, and the root zone soil concentration is also used by the Ecological Risk Module to predict risks to terrestrial plants and soil communities. Figure 11-1 shows the relationship and information flow between the Terrestrial Food Web Module and the 3MRA modeling system.

For each home range delineated within the AOI, the Terrestrial Food Web Module predicts a time series of annual average concentrations of contaminants in soil, along with concentrations in the specific plant and prey categories shown in Table 11-1. The Terrestrial Food Web Module uses the same algorithms and contaminant-specific data as the Farm Food Chain Module to calculate concentrations in plants.

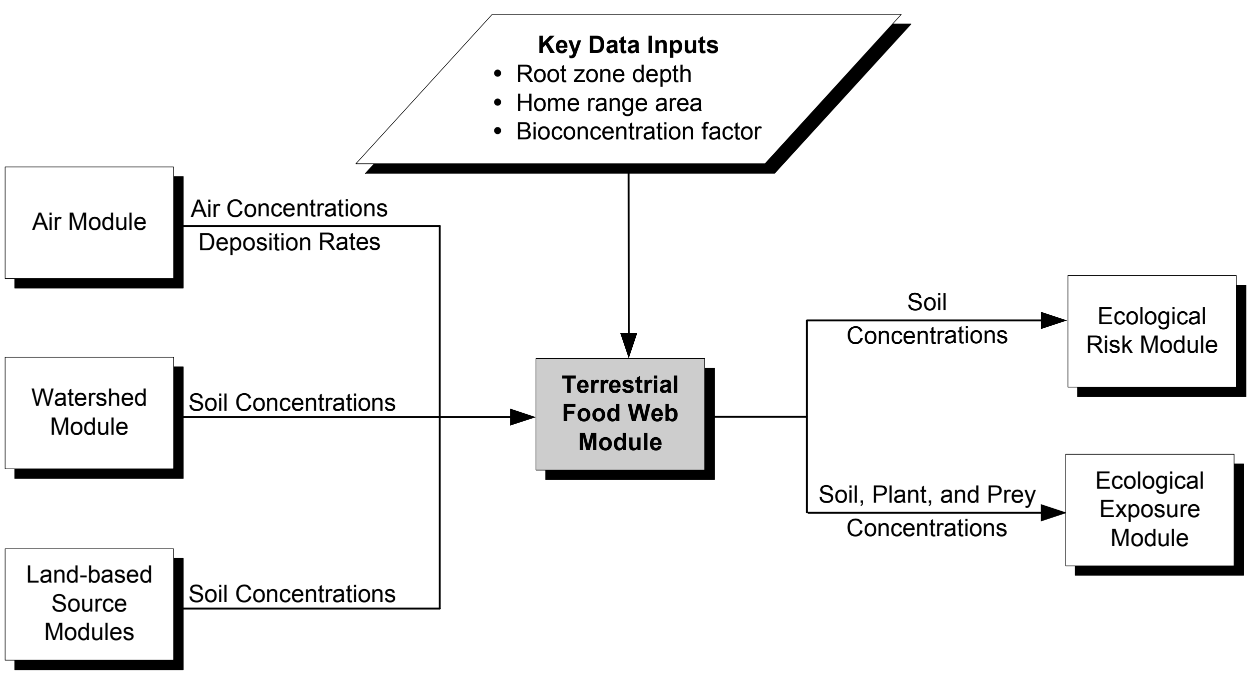

Figure 11-1. Information flow for the Terrestrial Food Web Module in the 3MRA modeling system.

Table 11-1. Terrestrial Plant and Prey Categories in the Terrestrial Food Web

Terrestrial Plant Categories	Terrestrial Prey Categories
Fruits, fruit/seeds (*exposed fruit*)	Worms
Fern(s), fungi, shoots (*exposed vegetation*)	Other soil invertebrates
Forbs, grasses, shrubs (*forage*)	Small mammals
Roots (*root vegetables*)	Small birds
Crops, corn (*silage*)	Small herpetofauna
Seeds/nuts (*grains*)	Herbivorous vertebrates
	Omnivorous vertebrates

The parentheticals shown under the terrestrial plant categories provide the crosswalk between categories of fruits, vegetables, and forage discussed under the Farm Food Chain Module, and the analogous vegetation categories that are eaten by wildlife.

The Terrestrial Food Web Module uses both predictive models and empirical data to calculate contaminant concentrations in terrestrial food items. Specifically, the Terrestrial Food Web Module performs the following four functions:

1. **Calculates contaminant concentrations in soil.** The module calculates spatially averaged soil concentrations for each home range in each habitat. The soil concentrations reported for each site by the Land-based Source Modules and the Watershed Module are catalogued by waste management unit (WMU) and watershed subbasin, respectively. The Terrestrial Food Web Module determines the overall spatial average contaminant concentration based on the proportion of subbasins and/or WMU that overlaps the home range of wildlife species assigned to a given habitat.

2. **Calculates total contaminant concentrations in plants.** The Terrestrial Food Web Module sums plant concentrations across relevant mechanisms, including direct deposition of particle-bound contaminants, vapor-phase uptake, and translocation from soil into the edible parts of plants. The module uses the same approach as described for the Farm Food Chain Module to calculate total contaminant concentrations in plants. The only significant difference in the respective modules is that the Terrestrial Food Web Modules defines plant categories for consumption by wildlife rather than humans.

3. **Calculates contaminant concentrations in soil invertebrates.** Earthworms and other soil invertebrates constitute a significant dietary component for many wildlife species. Contaminant-specific soil-to-biota bioconcentration factors are used to calculate the contaminant concentrations in soil invertebrates based on the spatially averaged, root zone soil concentration for each wildlife species' home range.

4. **Calculates contaminant concentrations in vertebrate prey categories.** Small to medium sized terrestrial vertebrates are eaten by larger predators (e.g., fox, black bear, and red tailed hawk). Contaminant-specific soil-to-vertebrate bioconcentration factors are used to estimate the tissue concentrations of contaminants in vertebrate prey categories based on the spatially averaged, root zone soil concentration for each wildlife species' home range.[1] The module reports the minimum and maximum tissue concentrations in each vertebrate prey category; these outputs allow the Ecological Exposure Module to sample from the spatial variability of possible prey species.

The Terrestrial Food Web Module is applied to the margin habitats in freshwater systems and wetlands and to terrestrial habitats, such as the representative forest or grassland. Simple terrestrial food webs were constructed for each terrestrial habitat to depict the major functional and structural components of healthy terrestrial ecosystems. The components represent major dietary categories for terrestrial wildlife, and represent a broad range of sizes, feeding guilds, and taxa typical of terrestrial food webs. In addition, the terrestrial prey categories reflect available methods and data required to estimate prey concentrations. For example, the category of "small mammals" was developed specifically to take advantage of recent research (Sample et al., 1998) on estimating tissue concentrations of contaminants in small mammals as a function of the soil concentration. This research provides a significant improvement over previous approaches that aggregated a variety of prey items into a single category of "terrestrial invertebrates."

11.2 Conceptual Approach

The Terrestrial Food Web Module was developed to allow for flexibility in calculating contaminant concentrations in soil, plants, and prey eaten by wildlife. Despite the advantages in such a flexible design, it was critical that the Terrestrial Food Web Module perform spatial averaging in a manner that was both ecologically relevant and simple to implement. Therefore, the module was designed to calculate contaminant concentrations in food items and soil in a way that reflects the spatial scale of interest and conserves the role of various species as both predator and prey. Most importantly, the approach takes full advantage of the information available in the site layout file that defines the spatial character of the habitats and species' home ranges assigned to the AOI. Indeed, the habitats and home ranges are a key feature of the 3MRA modeling system ecological risk assessment framework, describing the spatial extent of exposure as well as providing an important metric for reporting ecological risks.

As described in Section 3, the ecological setting for each site layout file includes one or more habitats. Within each habitat, four home range sizes are delineated, and the receptor-specific home ranges are assigned to the smallest one of these four home ranges. For example, the home range of the short-tailed weasel (135,000 m2) fits into home range 3, but not home ranges 2 or 1. Therefore, the short-tailed weasel is always assigned to home range 3. The receptor-specific home ranges were simplified to consist of four size ranges because the current

[1] Root zone, rather than surficial, soil concentrations were used to be more representative of the types of exposures likely to be reflected in soil-to-organism bioaccumulation factors (e.g., direct ingestion of soil invertebrates from deeper soil horizons; ingestion of prey that feed primarily on plant matter).

version of the 3MRA modeling system requires all spatial information to be specified in the site layout file *a priori* (i.e., home ranges cannot be created on the fly).[2] The four home range areas overlap within each habitat so that the predatory-prey relationships are maintained. Thus, physical access by predator species to prey species is built into the site layout file by ensuring that each home range overlaps the other home ranges. From an exposure perspective, a receptor species eats plants, earthworms, and soil invertebrates within its home range, as well as any mobile prey species that cross into its home range. From the perspective of the Terrestrial Food Web Module, the contaminant concentrations in plants, earthworms, and soil invertebrates are spatially consistent within the *receptor species'* home range; the concentrations in other prey categories are spatially consistent within the *prey species'* home range. Consider the following simple example.

In a hypothetical forest habitat shown in Figure 11-2, the short-tailed weasel is assigned to home range 3. Its diet consists of soil invertebrates as well as small vertebrates, including mammals, herpetofauna, and birds. Table 11-2 provides example concentrations of contaminant *y* for soil and prey categories relevant to the weasel's diet calculated by the Terrestrial Food Web Module during a simulation. The calculated concentrations in soil, soil invertebrates, and other prey categories within home range 3 are internally consistent to that home range. That is, the concentration of contaminant *y* in small mammals assigned to home range 3 is 6.7E-07 mg/kg; this concentration includes prey species that are eaten by the short-tailed weasel (e.g., mice, shrews), but does not reflect the concentration for the prey category to which the short-tailed weasel belongs (omnivorous vertebrates). As described in Section 15 (Ecological Exposure Module), the weasel will eat any combination of small mammals, herpetofauna, and small birds in its diet if prey species that belong to these categories are assigned to home ranges that overlap the weasel's home range. However, the weasel may only eat soil invertebrates from within its home range (because these organisms are relatively sessile), and the incidental ingestion of soil is presumed to come exclusively from within the weasels's home range. The concentration of omnivorous vertebrates assigned to home range 3 in this example is not shown in Table 11-2.

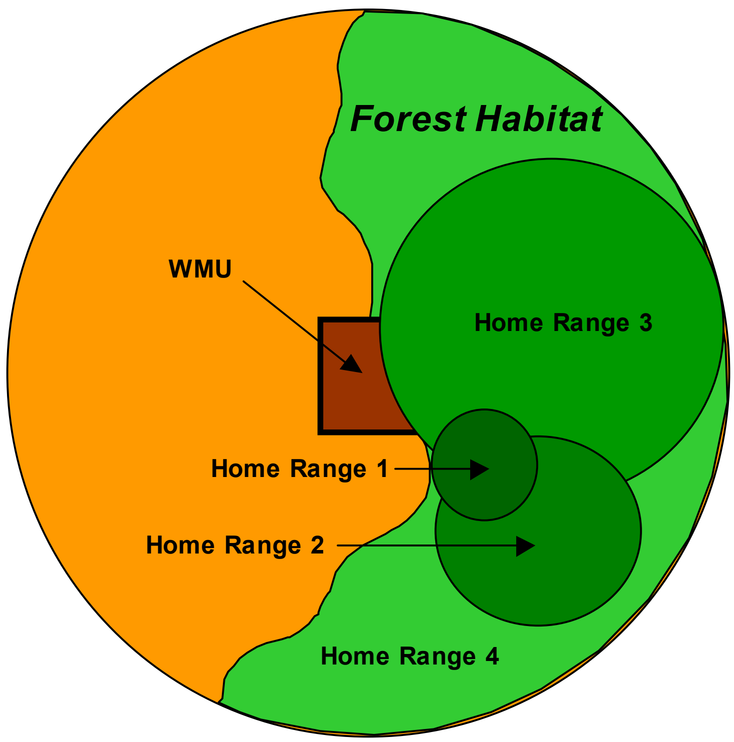

Figure 11-2. Hypothetical forest habitat with four home ranges shown.

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[2] The Terrestrial Food Web Module was designed to accept a unique home range for each wildlife species assigned to a habitat. Although this scheme has been simplified by using only four sizes, the module is blind to the fact that home ranges of the same size and geographical location are found in the site layout file.

Table 11-2. Example Exposure Concentrations for Contaminant *y* Calculated by the Terrestrial Food Web Module

Food Item	Home Range 1 (mg/kg)	Home Range 2 (mg/kg)	Home Range 3 (mg/kg)	Home Range 4 (mg/kg)
Soil	2.6E-07	4.9E-07	3.8E-08	3.1E-09
Small mammals	1.3E-06	1.6E-06	6.7E-07	NA
Small herpetofauna	9.4E-07	3.2E-06	NA	NA
Soil invertebrates	2.3E-06	9.1E-06	4.3E-07	1.1E-08
Small birds	2.3E-06	5.9E-06	NA	NA

NA = no receptor species in this prey category were assigned to this home range.

The methods used by the Terrestrial Food Web Module to calculate contaminant concentrations in soil, plants, soil invertebrates (and earthworms), and vertebrate prey species are described in the following sections. Additional detail on the data can be found in Volume II of this report.

11.2.1 Calculate Contaminant Concentrations in Soil

The Terrestrial Food Web Module calculates contaminant concentrations in both surficial soils and root zone soils for each home range. Because the difference between calculated surficial and depth-averaged soil concentrations depends only on the depth of the soil horizon, the same equations are used to calculate the spatially averaged contaminant concentration in each home range. The surficial soil, or top layer (top 1 cm), is relevant to incidental soil ingestion by foraging animals; thus, the surficial soil concentration is used only by the Ecological Exposure Module to calculate the applied dose to terrestrial receptors. The root zone soils (concentrations averaged over 5 cm) represent deeper soils that are relevant to plant uptake through root-to-plant translocation and to direct exposures of soil fauna such as earthworms. Consequently, the root zone soil concentrations are used by the Terrestrial Food Web Module to predict plant and prey concentrations, and are passed to the Ecological Risk Module for use in evaluating risks to the soil community and terrestrial plants (as receptors).

The spatially averaged soil contaminant concentrations may include a contribution from regional watershed subbasins as well as from drainage subbasins associated with the WMU. However, erosion and runoff within the local watershed is only relevant to certain types of WMUs. For aerated tanks and surface impoundments, it is assumed that controls are sufficient to prevent erosion and runoff releases within the drainage subbasin that contains the unit (i.e., there is no erosion or runoff directly from the aerated tank or surface impoundment). For the land application unit, the average soil concentration in each home range may include contributions from both the drainage subbasin and the regional watershed subbasin, depending on the placement of the home range with respect to the WMU. In the hypothetical example in Figure 11-2, the contaminant concentrations in soil for home range 3 and home range 4 could include a contribution from the drainage subbasin associated with the WMU. It was assumed that wildlife could use parts of the land application unit as habitat; however, because the landfill and waste pile are assumed not to serve as suitable habitat for plants or prey species, these units are assumed to not contribute to direct, soil-based exposures to terrestrial receptors. The calculation of spatially averaged contaminant concentrations in soil for each home range is a three-step process (equations apply to both surficial soils and root zone soils). First, the contaminant concentration in soil for the home range due to contributions from watershed subbasins that overlap the home range is calculated as follows:

$$C_{soil}{}^{WS}{}_{HomeRange^j} = \sum (C_{soil}{}^{WS^i} \times Frac^{WS^i}_{HomeRange^j}) \tag{11-1}$$

where

$C_{soil}{}^{WS}{}_{HomeRange}{}^{j}$	=	annual average contaminant concentration in soil for home range *j* due to contributions from watershed subbasins (mg/kg soil)
$C_{soil}{}^{WSi}$	=	annual average contaminant concentration in watershed subbasin *i* (mg/kg soil)
$Frac^{WSi}{}_{HomeRange}{}^{j}$	=	fraction of home range *j* impacted by watershed subbasin *i* (unitless).

Second, if the home range overlaps the WMU local drainage subbasins, the contaminant concentration in soil for the home range due to contributions from drainage subbasins associated with the WMU is calculated as follows:

$$C_{soil}{}^{dsb}{}_{HomeRange^j} = \sum (C_{soil}{}^{dsb^i} \times Frac^{dsb^i}_{HomeRange^j}) \tag{11-2}$$

where

$C_{soil}{}^{dsb}{}_{HomeRange}{}^{j}$	=	annual average contaminant concentration in soil for home range *j* due to contributions from watershed subbasins (mg/kg soil)
$C_{soil}{}^{dsbi}$	=	annual average contaminant concentration in watershed subbasin *i* (mg/kg soil)
$Frac^{dsbi}{}_{HomeRange}{}^{j}$	=	fraction of home range *j* impacted by watershed subbasin *i* (unitless).

Finally, the total spatially averaged contaminant concentration for soil in the home range is calculated by summing the contributions from the watershed subbasins and the drainage subbasins associated with the WMU as follows:

$$C_{soil}{}^{AVE}{}_{HomeRange^{j}} = C_{soil}{}^{WS}{}_{HomeRange^{j}} + C_{soil}{}^{dsb}{}_{HomeRange^{j}} \tag{11-3}$$

where

$C_{soil}{}^{AVE}{}_{HomeRange}{}^{j}$ = annual spatially averaged contaminant concentration in soil for home range *j* (mg/kg soil)

$C_{soil}{}^{WS}{}_{HomeRange}{}^{j}$ = annual average contaminant concentration in soil for home range *j* due to contributions from watershed subbasins (mg/kg soil)

$C_{soil}{}^{dsb}{}_{HomeRange}{}^{j}$ = annual average contaminant concentration in soil for home range *j* due to contributions from WMU local drainage subbasins (mg/kg soil).

11.2.2 Calculate Total Contaminant Concentrations in Plants

The Terrestrial Food Web Module calculates the total contaminant concentration in the plant categories shown in Table 11-1 by summing the concentrations for all potential exposure pathways for plants. Unlike the Farm Food Chain Module, the Terrestrial Food Web Module does not distinguish between protected and exposed fruits and vegetables, because wildlife are assumed to consume the outer surfaces of fruits and vegetables. Therefore, the exposed fruit and vegetable algorithms from the Farm Food Chain Module are used for all plants in the Terrestrial Food Web Module. For all aboveground plants, the total contaminant concentrations are converted from dry weight (DW) to wet weight (WW) by adjusting for the plant moisture content. These WW concentrations (also referred to as whole weight or fresh weight) are required by the Ecological Exposure Module. This conversion is not needed for root vegetables, because the concentration is calculated in WW directly. The methodology used to calculate contaminant concentrations in plants is described fully in Section 10 (Farm Food Chain Module).

11.2.3 Calculate Contaminant Concentrations Soil Invertebrates

Contaminant concentrations in soil invertebrates are estimated as a function of the root zone soil concentrations in each home range using contaminant-specific soil-to-tissue bioconcentration factors[3] for earthworms and other soil invertebrates. For each home range, the tissue concentrations in earthworms and other terrestrial invertebrates are calculated as follows:

$$C_{invert}{}^{AVE}{}_{HomeRange^{j}} = C_{soil}{}^{AVE}{}_{HomeRange^{j}} \times BCF_{invert} \tag{11-4}$$

[3] Bioconcentration factors (BCFs) for terrestrial prey are defined as the ratio of the contaminant concentration in the animal to the contaminant concentration in soil; BCFs are intended to reflect relevant exposure pathways to the study species (e.g., ingestion of contaminated soil and food).

where

$C_{invert}{}^{AVE}{}_{HomeRange}{}^{j}$ = annual average contaminant concentration in soil invertebrate or earthworms for home range *j* (mg/kg tissue)

$C_{soil}{}^{AVE}{}_{HomeRange}{}^{j}$ = annual average contaminant concentration in soil for home range *j* (mg/kg soil)

BCF_{invert} = contaminant-specific bioconcentration factor for soil invertebrates (kg soil / kg tissue).

11.2.4 Calculate Contaminant Concentrations in Vertebrate Prey Categories

The Terrestrial Food Web Module calculates a range of concentrations in vertebrate prey categories (illustrated in Table 11-1) across the four home range sizes. For example, the dietary data for a fox assigned to a terrestrial habitat indicates that part of its diet will consist of small mammals (e.g., rabbits, shrews, mice). The spatial linkages between the fox (predator) and various small mammals (prey) are represented in the site layout by allowing the respective home ranges to overlap. However, the proportion of each species consumed by the fox is unknown; the fox may consume any combination of these animals depending on prey availability, dietary preferences, and numerous other factors that affect prey selection. To address this uncertainty, the Terrestrial Food Web Module estimates the contaminant concentrations for relevant prey categories in each of the home ranges, and reports the minimum and maximum values. These values are used by the Ecological Exposure Module to randomly select (assuming a uniform distribution) an effective concentration for prey categories that represents the full range of concentrations to which a predator may be exposed.

Contaminant concentrations in prey categories are estimated as a function of the root zone soil concentrations in each home range, contaminant-specific soil-to-tissue bioconcentration factors for each prey category, and the fraction of each prey species home range that is contained within the habitat (i.e., the fraction that does not extend beyond the 2 km radius of the AOI). Vertebrate prey categories considered in the module include small mammals, small birds, small herpetofauna, large omniverous vertebrates, and large herbivorous vertebrates. Because these prey types consist of a variety of species (e.g., a Cerulean Warbler, Marsh Wren, and Northern Bobwhite are all considered small birds), the module calculates the concentration of contaminants for species within each prey category and then selects the maximum and minimum values from that range. Because minimum and maximum concentrations are reported for each prey type, the Terrestrial Food Web Module allows the Ecological Exposure Module to represent variability in wildlife diets. Predatory animals may consume prey in different areas of the habitat (changes in foraging patterns) and are highly likely to be opportunistic in their feeding habits (altering diet due to prey availability).

The concentrations in vertebrate prey species (for each home range) are calculated as follows:

$$C_{prey^i\,HomeRange^j} = C_{soil}{}^{AVE}{}_{HomeRange^j} \times BCF_{prey^i} \times FRAC_{prey^i\,HomeRange^j} \qquad (11\text{-}5)$$

where

$C_{prey^i\ HomeRange^j}$ = annual average concentration in vertebrate prey species *i* in home range *j* (mg/kg tissue)

$C_{soil}{}^{AVE}{}_{HomeRange^j}$ = annual average root-zone soil concentration for home range *j* (mg/kg soil)

BCF_{prey^i} = contaminant-specific bioconcentration factor for vertebrate prey species *i* (kg soil / kg tissue)

$Frac_{prey^i\ HomeRange^j}$ = fraction of home range *j* that falls within the habitat for vertebrate prey species *i* (unitless).

The last term in the equation, fraction of home range that falls within the habitat, is used to prorate the contaminant concentrations calculated in vertebrate prey species. The framework underlying the ecological exposure assessment does not assume that 100 percent of the diet originates from the home range, since the home ranges are sometimes larger than the entire habitat area. Consequently, the Terrestrial Food Web Module prorates the vertebrate species-specific tissue concentrations to reflect the fact that a species may not derive all of its food from within the AOI. Although the contaminant concentrations estimated for various vertebrate prey species are spatially consistent within each home range, there is no requirement that concentrations are based exclusively on food and soil from within the species' home range. Nevertheless, the module assumes that some exposure will always occur, and sets the fraction of home range that falls within the habitat to a minimum of 20 percent.

11.3 Module Discussion

11.3.1 Strengths and Advantages

The Terrestrial Food Web Module was developed to predict contaminant concentrations in soil, plants, and terrestrial prey to which receptors may be exposed. The module represents a significant step forward in addressing the spatial and temporal variability of ecological exposures. Specific strengths and advantages of the Terrestrial Food Web Module include the following:

- **Takes full advantage of functionality in the Farm Food Chain Module.** By translating the plant categories described for the Farm Food Chain Module into relevant categories for wildlife, the contaminant concentrations predicted for plants are consistent across both modules. As a result, many of the advantages of the Farm Food Chain Module are also conferred on the Terrestrial Food Web Module. For example, the calculations of contaminant concentrations in plants reflect both the soil and air pathways of exposure, as appropriate, given the properties of a particular chemical constituent. In addition, the Terrestrial Food Web Module also calculates and reports spatially averaged soil concentrations for each habitat and home range delineated at a site; this efficiency reduces the overall run time because average soil concentrations need only be calculated once by the Terrestrial Food Web Module.

- **Maintains spatial attributes of soil, plant, and prey concentrations calculated during the simulation.** A major strength of the Terrestrial Food Web Module is its ability to report concentrations for soil, plants, and terrestrial prey that are spatially consistent with the information in the site layout file. The module calculates these concentrations for each receptor assigned to each habitat, and reports the attributes of that concentration, including space (home range), food category (e.g., small mammals), and time (year of the simulation). The calculated tissue concentrations reflect the spatial boundaries for each ecological receptor assigned to a given habitat. For example, the tissue concentration predicted for a short-tailed weasel (which could be prey for the red-tailed hawk) is prorated by that portion of the weasel's home range that is contained within the habitat. This information is critical to the ecological risk assessment framework in the 3MRA modeling system to ensure that exposures are spatially consistent with the site layout information, and is intended to capture the range of contaminant concentrations in soil, plants, and prey to which any particular receptor may be exposed.

- **Algorithms, methods, and data are consistent with numerous EPA analyses.** The Terrestrial Food Web Module, although highly flexible, was developed to reflect current best practices in use at EPA, such as the Region VI Protocol for Ecological Risk Screening. The module and data inputs were intentionally based on established methods to permit application to a wide variety of chemical contaminants. Alternative approaches, such as fugacity-type models, were considered to be too data intensive (particularly with respect to chemical properties), inconsistent with the performance goals for model run times, and difficult to integrate with other model components. Consequently, the Terrestrial Food Web Module offers significant advantages over other approaches in ease of use for a variety of chemicals, transparency, modeling efficiency, and flexibility in its application and future modifications.

11.3.2 Uncertainty and Limitations

The methodology developed to estimate contaminant concentrations in soil, plants, and prey, as implemented by the Terrestrial Food Web Module, carries certain assumptions and limitations, and acknowledges several important sources of uncertainty. The limitations and uncertainties relevant to calculating forage and produce concentrations discussed under the Farm Food Chain Module are also relevant to the Terrestrial Food Web Module. Thus, the following discussion has been limited to issues exclusively related to the Terrestrial Food Web Module.

- **The Terrestrial Food Web Module is reliant on empirical (or empirically derived) soil-to-tissue bioconcentration factors**. The lack of good quality studies that investigate bioaccumulation in terrestrial systems contributes considerable uncertainty. As explained in detail in Volume II of this report on data collection, values for terrestrial BCFs reflect a broad range of data quality, with some studies reporting only percentiles off of the raw study data (e.g., a 50th percentile from a rank order). Moreover, the bioconcentration factors for a particular prey item vary across species, dietary preferences, seasonal resource requirements, and climatic conditions. For instance, Sample et al. (1998) indicated that vertebrates of varying dietary preferences (i.e., herbivores, omnivores, insectivores) accumulate contaminants to different degrees. A default uptake factor of 1 was used for contaminants for which BCFs could not be identified or calculated. The default value may be unrealistically high for contaminants that are poorly absorbed or are metabolized and excreted by animals. Although biomagnification in the food web has been demonstrated for very few contaminants in terrestrial systems, there is great uncertainty associated with the BCFs derived for prey items in this analysis, particularly in the use of default BCFs.

- **The Terrestrial Food Web Module does not capture the movement of contaminants through the food chain.** Because the module relies on soil-to-tissue BCFs to predict contaminant concentrations in food items, contaminant movement from biological compartment to biological compartment is not simulated. For example, although the module predicts concentrations in plant categories such as seeds and nuts, the contaminant concentrations in herbivorous vertebrates are calculated based on soil-to-vertebrate BCFs rather than biotransfer factors from plant matter into the tissues of herbivores. As a result, the module does not represent contaminant movement in the food chain in the sense that the Aquatic Food Web Module simulates movement among various biological compartments of predator and prey species. The BCF approach, although supported by available data, introduces uncertainty in the calculations of exposure concentration in terrestrial food items. Because few contaminants have been shown to accumulate in terrestrial food webs, it is likely that the BCF approach overestimates exposures to wildlife.

- **The derivation methods for some prey categories rely on extrapolation of soil BCFs from sediment studies.** For invertebrates, BCFs based on sediment exposure were adopted in the absence of data quantifying exposure via soil. This approach introduces uncertainty because these two exposure pathways are not equivalent. The primary literature reports bioconcentration data on various terrestrial insects such as beetles, especially for metals; however, these data are difficult (i.e., costly) to locate through traditional search methods because the data are generally found as secondary assessments conducted within larger site-specific risk analyses. The BCFs adopted from Oak Ridge work (Bechtel Jacobs, 1998) represent the best alternative, given current data limitations. Similarly, the BCFs for herpetofauna (i.e., reptiles and amphibians) were also identified from primary literature searches based on sediment rather than soil exposures. Because only sediment data were identified for herpetofauna, these bioaccumulation factors were adopted until soil-derived uptake factors can be identified; however, there is significant uncertainty in applying sediment exposures to estimate soil uptake values. In addition, the bioaccumulation data on herpetofauna were gleaned almost exclusively from studies on amphibians. Application of amphibian-based BAFs and BCFs to reptiles is associated with great uncertainty, given the physiological differences between these classes.

- **The uptake and accumulation of contaminants within categories of plants (e.g., exposed vegetables) is assumed to be similar**. The algorithms used to estimate biotransfer factors do not distinguish physiological differences across various kinds of plants. For example, the category "forage" includes forbs, grasses, fungi, shrubs, trees, and unclassified plants. Therefore, in estimating biotransfer factors for this category, it is implicitly assumed that the physiological differences in different plant species do not significantly affect contaminant loadings in plant tissues. The use of empirical data on selected plant species (typically crops) also assumes similar mechanisms of uptake and accumulation. Adopting the methodology developed for the Farm Food Chain Module to predict contaminant concentrations in plants that are eaten by wildlife introduces additional uncertainty in the application of those model algorithms.

- **A reasonable averaging depth for root zone soil concentrations is 5 cm.** In view of the multiple purposes of this soil concentration (e.g., to evaluate risks to soil fauna and predict tissue concentrations in prey using soil-based BCFs), and given the performance goals for science modules in the 3MRA modeling system, 5 cm was selected as a depth that is ecologically relevant (with regard to many organisms that live in the soil) and still consistent with the design specifications for the science modules (i.e., run time). Although the root zone depth may be specified by the user, the selection of 5 cm represents a balancing of model performance with ecological relevance. However, this assumption built into the Watershed Module limits the value of information on soil concentrations, and constitutes a source of uncertainty in its application within the Ecological Exposure and Risk Modules. In reality, soil fauna can occupy many different soil horizons, and plant roots (and exposures to soil contaminants) can extend well below 5 cm. For example, some important species of soil organisms live primarily in deeper soil horizons, while others live almost exclusively in the top litter layer of soil. This top layer is highly enriched in organic carbon and humics, and may serve as a significant source of exposure to certain soil species.

11.4 References

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