GUIDANCE DOCUMENT

Improvement, Verification, and Refinement of Spatially Explicit Exposure Models in Risk Assessment

Spatially Explicit Exposure Model (SEEM)

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Distribution Statement A

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Spatially Explicit Exposure Model (SEEM)

USER'S MANUAL
VERSION 4.2

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LIST OF ACRONYMS

ACAC	Average Concentration with Area Curve Model
BAF	Bioaccumulation Factor
EHQ	Ecological Hazard Quotient
EPA	US Environmental Protection Agency
GIS	Geographical information system
HSI	Habitat Suitability Index
LOAEL	Lowest observed adverse effect level
NOAEL	No observed adverse effect level
PEF	Population Effects Foraging Model
SEEM	Spatially Explicit Exposure Model
TRV	Toxicity reference value

PREFACE

This manual, *Spatially Explicit Exposure Model (SEEM) User's Manual (Version 4.2)*, outlines the theoretical foundation for the modeling work, presents the conceptual mechanics of model operation and provides stepwise user instructions.

Drawing from user-defined input parameters, SEEM is a tool by which to complete a wildlife exposure assessment guided by wildlife habitat preferences and foraging behaviors. SEEM incorporates habitat suitability indices and two foraging strategies to capture exposures that are more realistic than assuming uniform exposure across a heterogeneous site (i.e. site-wide averages). Building off of earlier work (Freshman and Menzie 1996; Hope 2000, 2001), SEEM offers an accessible and flexible tool by which to capture the foraging activities of all individuals in a local population. The modeling approach and level of complexity are user-defined. As a result, SEEM can be employed to assess a variety of wildlife exposure problems. Ultimately, SEEM can assist risk managers and remedial engineers to better understand the costs and benefits of remediating certain parcels based on the HSI, potential exposures and acreages.

1 INTRODUCTION

1.1 Background

The tools for wildlife exposure analysis available to the risk assessment community vary from simple statistical calculations applied broadly across an entire site (average, maximum, 95% UCL, and percentiles) to complex GIS modeling. Simple spreadsheet models provide site assessors with a balance between ease of application and strength/power of the analysis. Combining the most basic models, the 'Average Concentration with Area Curve Exposure Model' (ACAC) and the 'Population Effects Foraging Model' (PEF), with more sophisticated habitat suitability models (E[HQ]), the Spatially Explicit Exposure Model (SEEM) offers risk assessors and risk managers an accessible and flexible wildlife exposure assessment tool that captures the influence of habitat preferences and foraging behaviors on overall wildlife exposure (Freshman and Menzie, 1996; Hope, 2000, 2001).

The ACAC examines the change in exposure concentration as the area of a site increases. It has utility in hotspot analyses and in assisting in remedial decision-making; however it does not directly incorporate habitat suitability indices. The resulting average concentration with area curve can be used to review conditions at the site in reference to effects concentrations and the foraging areas of common wildlife species (Freshman and Menzie, 1996).

The PEF Model generates a pattern analysis incorporating foraging area, spatial distribution of contamination and soil effect levels. The resulting figure provides the assessor with the percent of the population affected based on a foraging habitat ratio that varies from 0 to 1 (Freshman and Menzie, 1996).

The ACAC and PEF Models include a habitat area component, but it is also important to include a habitat suitability component that is a direct reflection of the ecology of each receptor species. Regardless of the chemical concentrations, a poor habitat suitability should result in reduced exposure. In some cases, chemical concentrations might improve habitat. The Habitat Area and Quality Conditioned Exposure Estimator (E[HQ]) is a modification of the PEF model and incorporates both exposure components (Hope 2000, 2001; Hope 2005). This model adjusts the concentration of chemical using both the habitat area and habitat suitability and completes multiple exposure iterations across a grid overlying the site. The model also offers the opportunity to incorporate and evaluate the percentage of individual E[HQ]'s that exceed screening levels, remedial goals etc.

SEEM (Spatially Explicit Exposure Model) combines various features from the three models through an easy to use interface.

1.2 Purpose and Scope

The purpose of SEEM is to provide assessors and managers with a powerful, flexible exposure assessment tool that more closely approximates reality. Historically, simplifying assumptions led to the assessment of an entire site independent from the larger landscape and with limited recognition of the influence of habitat heterogeneity and the uniqueness of wildlife foraging

behaviors on wildlife exposure. Often a single statistic or series of statistics is used to generate a site-wide exposure value. SEEM incorporates habitat suitability and foraging habits to improve the value of wildlife exposure assessment. Also, rather than assess risk for a single representative individual, SEEM tracks the foraging behavior of all individuals in a local population.

SEEM is a terrestrial wildlife exposure model designed to evaluate exposures to mammals and birds. By design, the model is focused on terrestrial habitat. While the model does not support the evaluation of fish exposure per se beyond the application of bioaccumulation factors to sediment concentrations, SEEM could support the assessment of semi-aquatic mammals and birds that feed on fish. Assessing these pathways using SEEM will be discussed in the Sections that follow. User's should consider the unique characteristics of target receptor species, e.g. home range size, and the heterogeneity of the surrounding habitat when considering the application of SEEM. Determining how those characteristics will be integrated into SEEM will provide insights into the value of SEEM for answering specific questions. Where a home range is very small and/or habitat is homogeneous, SEEM will be a less valuable assessment tool.

The User's Manual provides the user with a conceptual introduction to the design and mechanics of SEEM. In addition, a detailed stepwise description of model operation is provided and will help users populate and run SEEM. We do not, however, provide guidance regarding the collection of the data inputs.

1.3 Application

SEEM has been developed for a number of applications. Within the Ecological Risk Assessment Framework (EPA 1998), SEEM could be applied to examine issues within the exposure and effects components, in the risk characterization, and SEEM can be an invaluable communication and decision-making tool during risk communication and risk management (Figure 1). Examples of applications for SEEM within each of these steps include:

Exposure Assessment: Visualize exposure pathways and identify where chemicals and habitats intersect; assess the impact of receptor habits on exposure; increase realism because species are more likely to forage in areas with available habitat;

Effects Assessment: Visualize the intersection of potential effects for different receptors;

Iteration and Sensitivity: SEEM run multiple times with variable inputs can be used to evaluate risk driving assumptions;

Risk Characterization: Identify areas of concern; identify local populations and associated habitat types that are most susceptible;

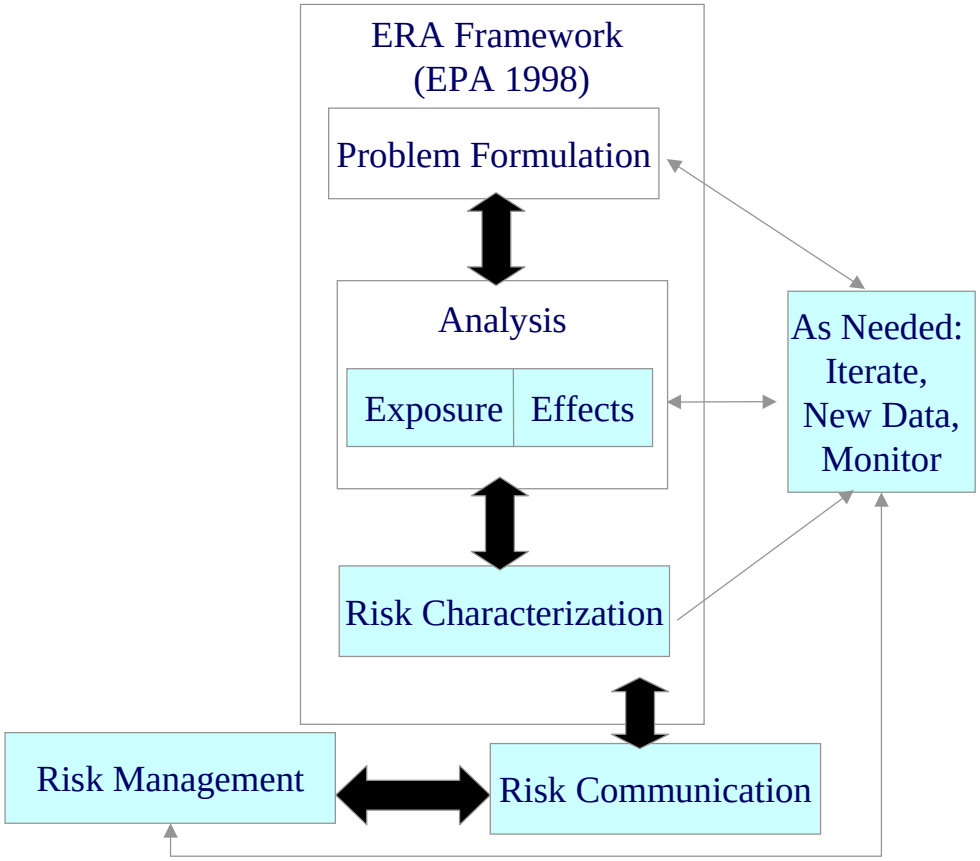

Figure 1. SEEM Applications within the ERA Framework (arrows indicate that SEEM outputs can inform multiple steps and the results of different steps can inform SEEM)

Risk Communication: Illustrate problematic portions of the site from the perspective of each receptor; because habitat is a consideration, avoid highlighting areas with no or poor quality habitat because exposure unlikely; communicate the cost and benefits of different remedial strategies in terms of acreage requiring remediation, habitat loss and risk reduction; and,

Risk Management: Increase efficiency and effectiveness of remedial strategies by focusing attention on areas where habitat and chemicals intersect and conversely avoid costly cleanup in areas where there is no habitat and therefore complete exposure pathways are not present.

Because SEEM includes visualization tools such as criteria screening summary maps and foraging pathway animation, users are able to observe problem areas in terms of habitat, chemistry, receptor behavior and acreage. SEEM can be run and re-run under varying scenarios to assess potential remedial strategies and arrive at a final strategy that best balances risk reduction, habitat loss due to remediation, cost, and acreage remediated.

1.4 Installation and Requirements

SEEM[1] will run on Microsoft Windows© supported systems (Operating System: Windows© 98, NT 4.0, 2000, XP, 7). The report viewer for SEEM requires Microsoft Excel© (Version: 1997 or higher). SEEM requires 25 mb of free hard drive space. SEEM is distributed as a single zip file. Download the zip file to any folder on your system (for example, Desktop). Right click the zip file, select 'Extract All,' and select a folder of your choice in which you want to install SEEM. Within this folder, click on the SEEM42 shortcut to open the program. There is also a user manual in this folder. If in the future you need to move the program folder, move it as an entire folder.

The model is designed to open files created during the previous model run automatically each time a user opens the model. The first time you open the model you will receive a message that states – 'Model is not found, default model is loaded'. Click OK and begin work on your SEEM project. In the future, SEEM will open with the active model from the last run.

[1] The current version of SEEM is a BETA Test Version. As a result, by using, copying, or installing this software, the user understands that the software is provided 'AS IS' and with no warranties of any kind, whether expressed or implied. The user acknowledges that the software is still in development and continues to undergo review. The developer does not warrant, guarantee or make any representations regarding the use or the results of the use of SEEM. The developer does not warrant that the operation will be uninterrupted or error-free.

2 MODEL STRUCTURE

2.1 Conceptual Description

SEEM has been developed to increase the realism of wildlife exposure assessment and improve the analysis of population risk. In general, "population-level" assessments consider the individuals that comprise the "population" within the area of interest[2]. SEEM tracks exposure of all of these individuals in a local population (rather than calculating exposure for a single representative individual one-time). In addition, SEEM increases the realism of the exposure assessment process by incorporating habitat suitability at a finer resolution than the entire site and by considering foraging behaviors.

The model will track an individual over an ecologically relevant period of time as it travels across a landscape. The individual will move according to a set of pre-determined rules. The model operates based on a foraging radius/distance. The radius describes the maximum distance over which an animal may forage in one day and in any direction. Each day an animal forages over an area defined by a foraging radius. Although the radius is fixed per day, the actual number of polygons to which a receptor is exposed may vary based on the geometry of the polygons and the current position of the receptor[3]. Exposure occurs during a foraging event. A foraging event is a point at which an individual consumes a prey item and associated media (soil, sediment, water)[4]. It is located by an X,Y coordinate. A user selects the number of foraging events that occur per day within the foraging radius based upon knowledge of the species' habits as well as the habitat and food availability.

Receptors in SEEM are mobile and each individual may follow a unique exposure pathway across the landscape. The movement algorithm employs Markov Chain Monte Carlo, a rejection method that uses habitat suitability to determine the probability that an individual will remain in an area and forage, rather than move to another area. Conceptually, the wildlife species do not necessarily follow a pathway through the most suitable habitat across a landscape and may cross areas with a low HSI; the species will not forage in areas with an HSI equal to 0. However, in SEEM, the species are more likely to spend more time and actually forage in areas that have a higher habitat suitability. Each day, for each individual and foraging event, the Markov Chain Monte Carlo is employed to generate exposure events. Users may select between two foraging

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[2] Population as used in this document refers to 'modeled population'. This is a user-defined number of individuals which may or may not reflect the ecological population in an area. As discussed in the Sections that follow, we highly recommend modelers run the model for multiple iterations to capture the inherent variability in exposure. Therefore, any population number may be interpreted as the number of individuals or the number of iterations for a single individual.

[3] NOTE: the SEEM calculator uses an underlying grid (user-defined number of cells) to efficiently estimate exposures As users draw polygons or select grid cells, SEEM internally estimates an area-weighted exposure concentration for each fixed internal grid cell. This concentration is used in the calculations. The same concept applies to the HSI values.

[4] A medium in SEEM refers to the non-biological source of chemical exposure – soil, sediment or water. SEEM uses bioaccumulation factors to estimate tissue concentrations based on exposure to the media. It should be noted that to date SEEM has only been used to estimate exposures to soils. The opportunity to model exposures from sediment or water is available but has not been tested in depth.

submodels. They include: a movement-based free-ranging submodel, and the static home range foraging model in which the boundary demarcated by the foraging radius does not change, although the position of the individual foraging events may change. These submodels are discussed in detail below.

For each day and each individual, SEEM calculates an ecological hazard quotient (EHQ). The average daily EHQ captures all of the daily exposure events for each individual. For each individual, a lifetime average and maximal EHQ may be calculated. From the individual EHQ statistics, population statistics and graphical summaries are calculated including the population EHQ curves which display the percent of the population potentially impacted.

2.2 Foraging Submodels

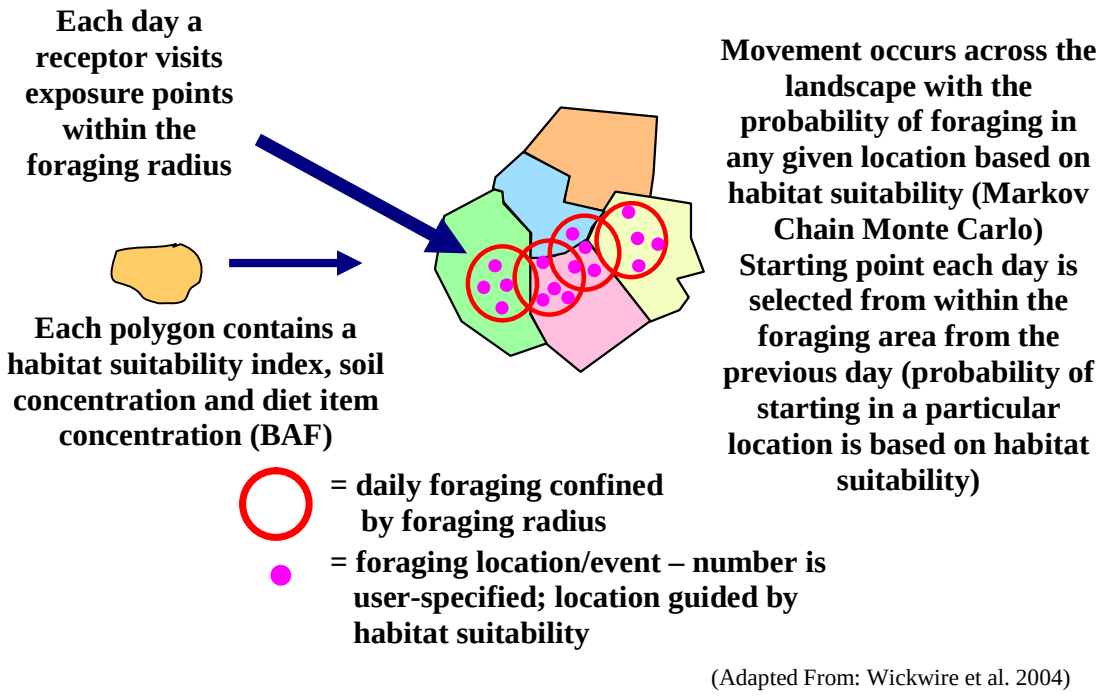
SEEM employs two different foraging submodels. The submodels determine how a wildlife species may be exposed to chemicals in the environment. Each submodel contains a set of rules that determine the position, movement habits and exposure calculations. The submodels do not include the universe of potential behaviors or unique methods that some species might utilize. The submodels do, however, provide a broad approximation of foraging habits and SEEM is flexible and may be used to explore subtlety in foraging behaviors through sensitivity testing, modification of exposure events, time periods and foraging ranges.

The three primary foraging parameters for free-ranging and static home range submodels are the *foraging radius*, the *foraging event*, and *habitat suitability indices*. EPA (1993) defines a *foraging radius* as "the distances the animals are willing to travel to potential food sources". Although it is a simplification for heterogeneous habitats, SEEM operates within a foraging area defined by the foraging radius, i.e. a circular area (EPA 1993). In SEEM the foraging radius defines the area over which an individual will search for food each day. A *foraging event* is a point at which an individual consumes a diet item and may ingest soil or sediment incidentally or water. The location of a foraging event is an x,y coordinate, therefore foraging is not directly associated with polygon locations. A user specifies the number of foraging events that occur each day and the location of each event (x,y) is determined through a Monte Carlo rejection method which uses habitat suitability to guide the selection of a location (SEE INSERT A). A *habitat suitability index* (*HSI*) compiles the suite of measurable parameters that reflect the preference a wildlife species might have for one area over another. In the case of SEEM, the measurable parameters are combined and expressed as a single index value (0-1) for each habitat polygon within the landscape. SEEM provides an HSI calculator for assistance with habitat suitability estimation (Kapustka et al. 2005; Kapustka et al. 2004a, 2004b; Kapustka 2003; Kapustka et al. 2001; Terrell and Carpenter 1997). Each model requires species-specific habitat parameters and will generate an HSI. The calculator is integrated directly into SEEM. The HSIs are used to determine the probability that a receptor will visit and/or forage at a given location. An HSI equal to zero indicates that there is no suitable habitat for the specific species, e.g. a paved parking lot. However, depending on the contiguous extent of the non-habitat area and the foraging radius for the receptor, an individual may cross non-habitat areas.

In the sections that follow, the two submodels are explored in detail.

2.2.1 Free-Ranging Foraging Submodel

In the ***free-ranging foraging*** submodel, wildlife move across a landscape guided by habitat suitability and species-specific foraging areas. Initially, each individual in the population is placed into a starting position (x,y) on the landscape. The position is influenced by habitat suitability, but also utilizes a random component (See Insert A). Each day, wildlife forage at a specified number of locations (Figure 2). An average of the exposures for all foraging events for each individual is calculated and tallied. Each day the starting point is the last location visited by each individual receptor the previous day. The foraging area shifts so that the new starting point is the center of the circle. Over time and for each individual, the circles defined by the foraging radii move across the landscape. For each individual, movement is independent from the movement of other individuals, i.e. paths may cross. Although each individual will not necessarily visit the areas with the highest habitat suitability, the probability to forage in areas with better habitat is higher than the probability to forage in an area with lower HSIs or poor habitat.

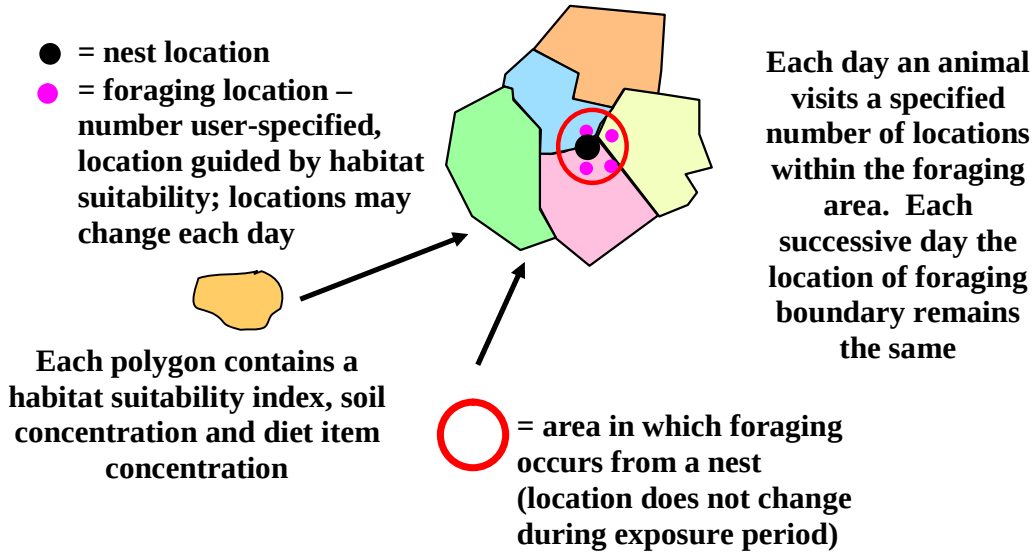


(Adapted From: Wickwire et al. 2004)

Figure 2. SEEM – Free Ranging Foraging Submodel – Conceptual Overview

2.2.2 Static Home Range Submodel

In contrast to the free ranging foraging submodel, the foraging area for each individual in the ***static home range*** submodel does not change each day, but remains fixed. This may approximate the function of a nest from which an individual leaves each day to gather food, only to return at night and begin the routine the next day (Figure 3). It also may characterize a species that forages more locally. As a result, the circular area defined by the foraging radius remains fixed on the landscape for each individual throughout the modeling period. However, the location of the foraging events may change each day.



(Adapted From: Wickwire et al. 2004)

Figure 3. SEEM – Static Home Range Foraging Submodel – Conceptual Overview

2.2.3 Biota or Plant Tissue Concentrations

Food item[5] tissue concentrations in SEEM are calculated using a bioaccumulation factor (BAF). Higher order species may consume plants, small mammals, invertebrates or other lower order species that may have independent exposures as well. The food item bioaccumulation calculation is made for every polygon in which there is suitable habitat for the consumer; the

[5] *Food items* and *diet items* are used in SEEM to refer to different model components. A *food item* is not assessed directly in the model. Instead, a BAF is used to estimate the body burden. A *diet item* is either a food item or another receptor that is consumed by an assessed wildlife species. Receptor concentrations when serving as diet items are based on the receptors diet composition and the concentration of the diet (excluding excretory and digestive loss).

assumption follows that if the habitat is suitable for the receptor, food items will occur in the polygon as well. For example, a fox may consume a meadow vole. The meadow vole is assumed to obtain a tissue concentration of site chemicals via the soil through the diet. Therefore, every polygon with any suitable habitat (an HSI > 0) will contain a non-diminishing food item; though not every receptor will consume every food item type. The tissue estimation is made for all food items that comprise the diet of a higher order species.

2.3 Calculations

SEEM completes exposure calculations each day for each individual. The calculations are summarized in Insert B. For each individual, daily exposure estimates are tallied for the entire lifetime. Individual lifetime statistics (average and maximum, currently) are compiled to create the population effects curves.

Additional calculations on a cell-by-cell basis[6] (e.g. intake, ecological hazard quotient) are generated automatically when the input parameters are entered.

[6] SEEM calculations uses an underlying grid (user-defined number of cells) to efficiently estimate exposures . As users draw polygons or select grid cells, SEEM internally estimates an area-weighted exposure concentration for each internal grid cell. This concentration is used in the calculations. The same concept applies to the HSI values.

INSERT A
Movement Detail

In contrast to other exposure models, foraging within SEEM does not occur at the level of a grid cell or entire polygon. Foraging within SEEM occurs at specific points (x,y coordinates) called *foraging events*. The number of foraging events that occur per day is a user-specified parameter. The polygons (or grid cells) are used to define the landscape in terms of chemical concentration distribution and habitat suitability. In the case of both the free-ranging and static home range submodels, foraging event locations change from event to event and each day. In the case of the free-ranging submodel only, the boundary defined by the foraging radius also changes position each day, i.e. the center point of the circle defined by the foraging radius shifts each day.

Positioning a foraging event or nest in the landscape and determining the movement of a foraging area in the free-ranging scenario are both accomplished using elements of a Markov Chain Monte Carlo approach. This methodology combines randomized direction and distance within foraging area constraints with habitat suitability indices in a rejection method to select the position for a foraging event. Foraging is not entirely random, nor does a receptor necessarily follow the pathway of perfect habitat suitability. Conceptually, this approach also does not mean that a receptor cannot cross poor habitat; a receptor may forage in an area with poor habitat, but it is less likely.

Polygon data are translated into a fixed grid for calculations using area-weighted averaging to arrive at a value for each cell; in some cases multiple polygons may intersect a single cell.

A random number sequence is employed to locate the starting cell taking into account the HSIs assigned to the cell (using the Rejection Method). An additional series of random numbers are generated to locate a receptor's position within the cell. In this case those random numbers, a1 and a2, are used to calculate x and y coordinates in: x=x_lower_left_corner_of_the_cell+cell_width*a1; the y coordinate is calculated in the similar way.

Movement is simulated using another algorithm, but it uses the same basic pseudo-random sequence used to select an initial position. For the purposes of explanation, assume that an animal is located at x0,y0 on the map with a foraging radius of R and the free-ranging foraging strategy. Movement to a new position begins when two random numbers are generated from the pseudo-random sequence. The first number is used to simulate the direction angle for movement. This angle falls uniformly from 0 to 2*pi: angle=2*pi*a1, where "a1" is the first random number for this series. Movement distance is simulated as follows: distance=R*sqrt(a2), where "a2" is the second random number. Given a direction and distance, SEEM calculates a new position as follows: x1=x0+distance*cos(angle),y1=y0+distance*sin(angle). However, this will not necessarily be a final position or become a foraging event. Up to this point the position has not taken habitat suitability into consideration. To account for the habitat suitability and determine if this temporary location will become a foraging event, SEEM employs a rejection method. In this method, a maximal HSI is calculated (HSImax). The HSImax is defined as the maximal habitat suitability within the circle of foraging radius R centered in x0, y0. A temporary position is located by the method discussed previously. The HSI at this location, x1,y1, is recorded. Next the ratio HSI(x1,y1)/HSImax is calculated. This ratio can be interpreted as the "probability to remain and forage at x1,y1". Then, SEEM generates the next random number from our basic sequence. If this number is less than HSI (x1,y1)/HSImax, then x1,y1 becomes the receptor's position. If the number is greater than HSI (x1,y1)/HSImax, the algorithm begins by generating a new temporary position x2,y2 (using random numbers and the direction and distance algorithms). The HSI ratio is generated for the new position and the comparison is made until a foraging event position is identified.

INSERT B
Exposure Averaging

As discussed in Insert A, SEEM employs components of a Markov Chain Monte Carlo to simulate the locations of foraging events within a foraging radius and to position foraging starting points and nest locations assuming that the probability distribution of spatial positions of the foraging events is proportional to the HSI. The actual exposures are averaged across the positions of the foraging events, and since the foraging events happen more frequently in the higher HSI areas, the result is effectively HSI exposure weighting.

The calculations are discussed below:

Exposure is calculated for each (i-th) foraging event using the following equation (additional media may also be included):

Ei=Exposure Dose (mg/kg/day) = $\{[\text{chemical}]_{soil} \times IR_{soil}\} + \{[\text{chemical}]_{prey\text{-}1} \times IR_{prey\text{-}1}\} + \ldots + \{[\text{chemical}]_{prey\text{-}k} \times IR_{prey\text{-}k}\}$ (1)

[chemical] = chemical concentration
IR = ingestion rate
prey-i is the number of diet items
k is total number of potential diet items

This exposure is recorded for each event and averaged at the end of each day. Because habitat suitability is employed in locating foraging events, the foraging event locations are effectively weighted by habitat suitability. Therefore, an average of the events is calculated each day:

$$E_{day} = 1/n\ (E1 + E2 + E3 + \ldots + En) \quad (2)$$

E_{day} = average daily exposure dose for an individual
Ei = individual exposure dose in the i-th foraging event
n = number of foraging events

For each day in the modeling period an ecological hazard quotient (EHQ) is calculated for each individual:

$$\text{Daily EHQ} = E_{day}/TRV \quad (3)$$

TRV = toxicity reference/benchmark value

After the model has been run for the full modeling period, an average EHQ and a maximum EHQ is calculated for each individual in the population. Statistical distributions of individual EHQs are used to develop the population effects curves.

3 STEPWISE INSTRUCTIONS (GUIDED INPUT)

3.1 Input Introduction

Data entry in SEEM occurs through guided input. For new users the guided input provides an introduction to the required data through input screens that are split with data entry occurring on the left-hand side and guidance text provided on the right-hand side. Also, it is an efficient way to organize data entry for experienced users of the model. The entry point (home screen) for SEEM is the main form displayed below (Figure 4). From this page a user may initiate the development of a new model, modify an existing model, open a saved model, save data entry, run a completed model, view output reports, access/view/edit the habitat suitability database and shutdown/close the model.

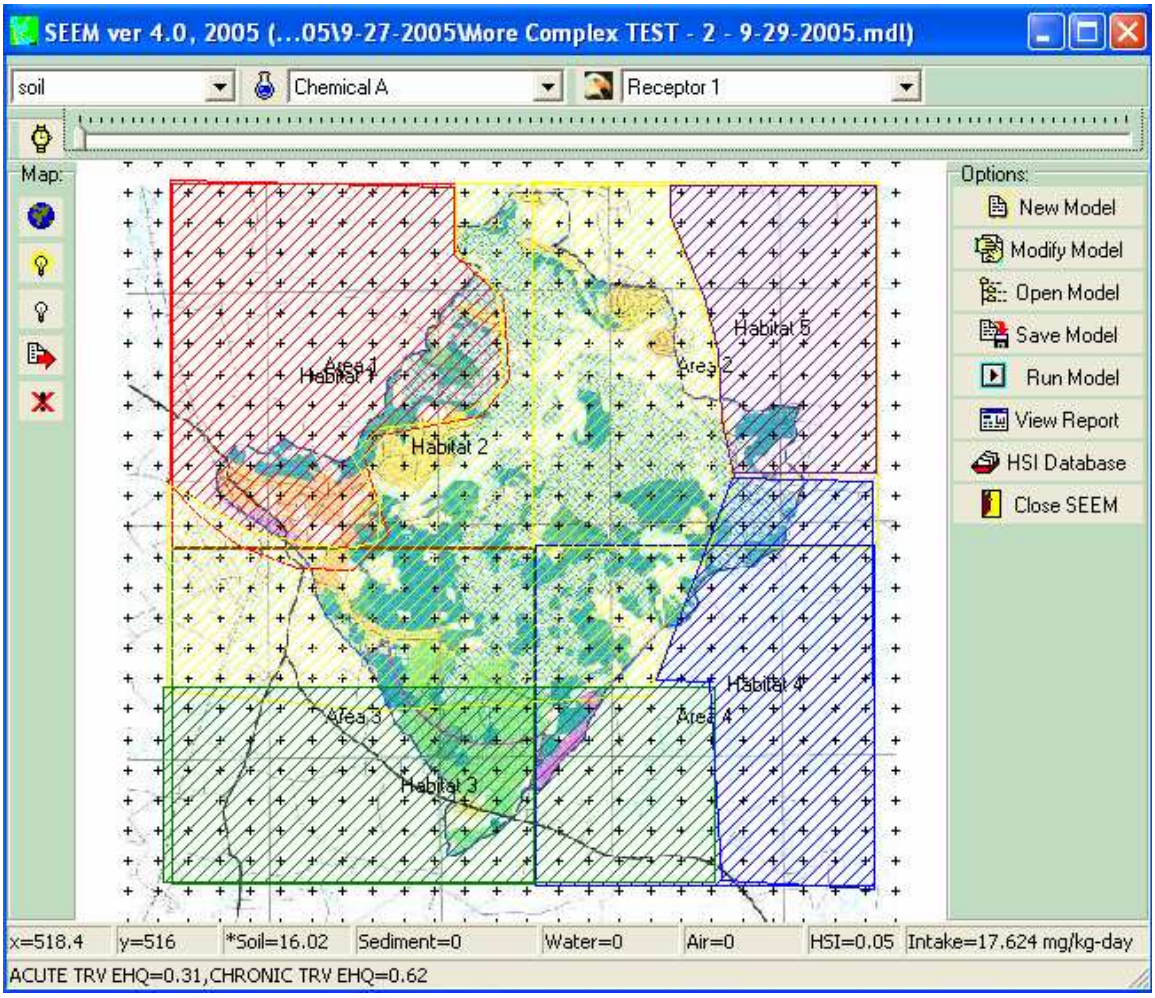


Figure 4. Home screen in SEEM[7]

[7] SEEM will open with a project already loaded from the previous session or from the default library. New projects may be created directly or past projects may be opened from the home screen.

The focal point of the model interface is the site base map. The map orients the user, organizes spatial chemical and habitat suitability data and also provides a clear way to identify different portions of the site in terms of potential for harm. In addition to the different file options, users may also run a screening tool, modify inputs directly by jumping to a specific step and use the real-time summary information at the bottom of the entry window.

The primary model functionality available from the main form of the model is summarized below (Figure 5). A user may create, modify, open, save, run, view and open the HSI database (**1**). In addition, users may jump to specific guided input series focusing on chemical information or receptor information and view different polygon/grid sets (if already entered) (**2**). Along the top of the window, next to the SEEM version number, is the active file name. A screening tool is available to allow a user to screen the cell defined grid[8] based on ecological hazard quotients, intake, and concentration (**3**). Finally, a status bar presents location, concentration, habitat suitability, intake and EHQ summaries by area (**4**).

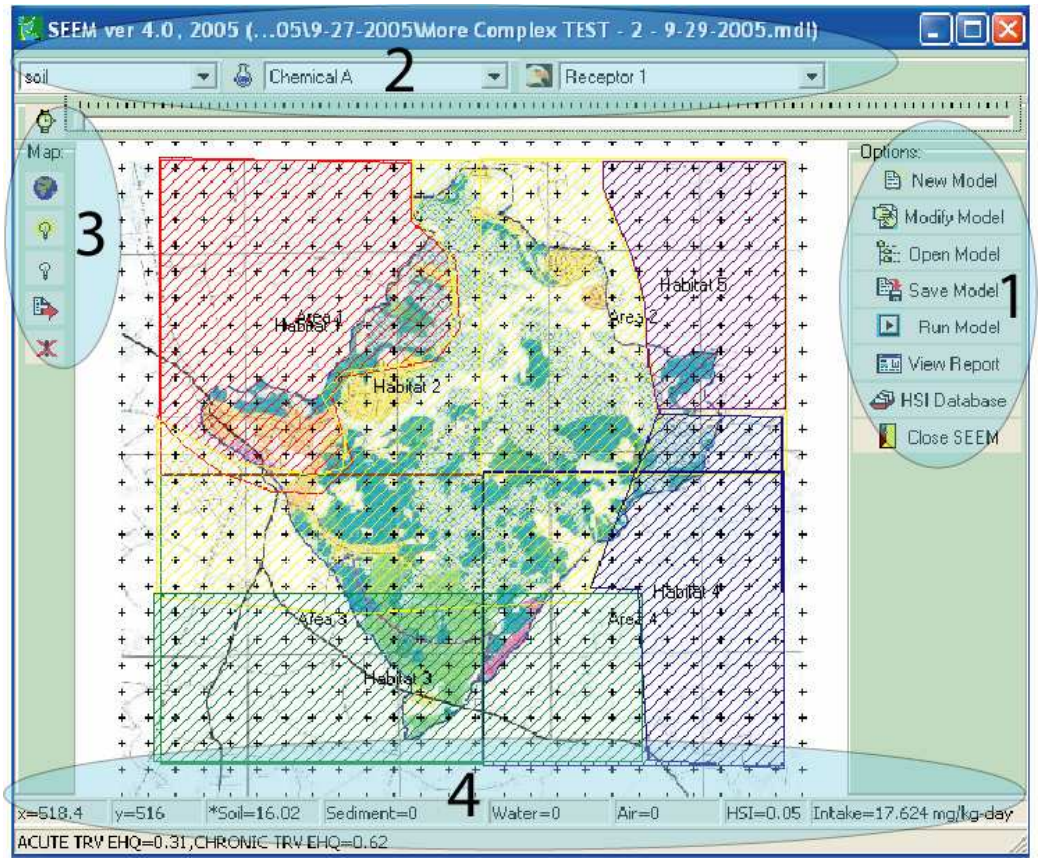


Figure 5. Overview of home screening functionality

[8] NOTE: the SEEM calculator uses a fixed grid (25 x 25 cells). As users draw polygons or select grid cells, SEEM internally estimates an area-weighted exposure concentration for each fixed internal grid cell. This concentration is used in the calculations. The same concept applies to the HSI values.

Data entry and internal model guidance are organized by data entry 'steps'. Whether an advanced or a new user of SEEM, the data entry steps are organized to provide users with the ability to assemble the required data in a logical way. The structure of each step is consistent (Figure 6). On the left-hand side of the split screen users enter the required data. Data entry may entail direct entry of values or text, multiple choice selections or highlighting of previously entered data/text (**1**). Along the right-hand side of the split screen, users will find step-specific guidance[9] (**2**). In addition, where applicable, the right-hand side of the screen is also used to reference data entry to a position/polygon on the map. Starting in Step 8, when users click on data entry cells with a spatial component, the base map will pop-up on the right-hand side with the active polygon or cell highlighted.

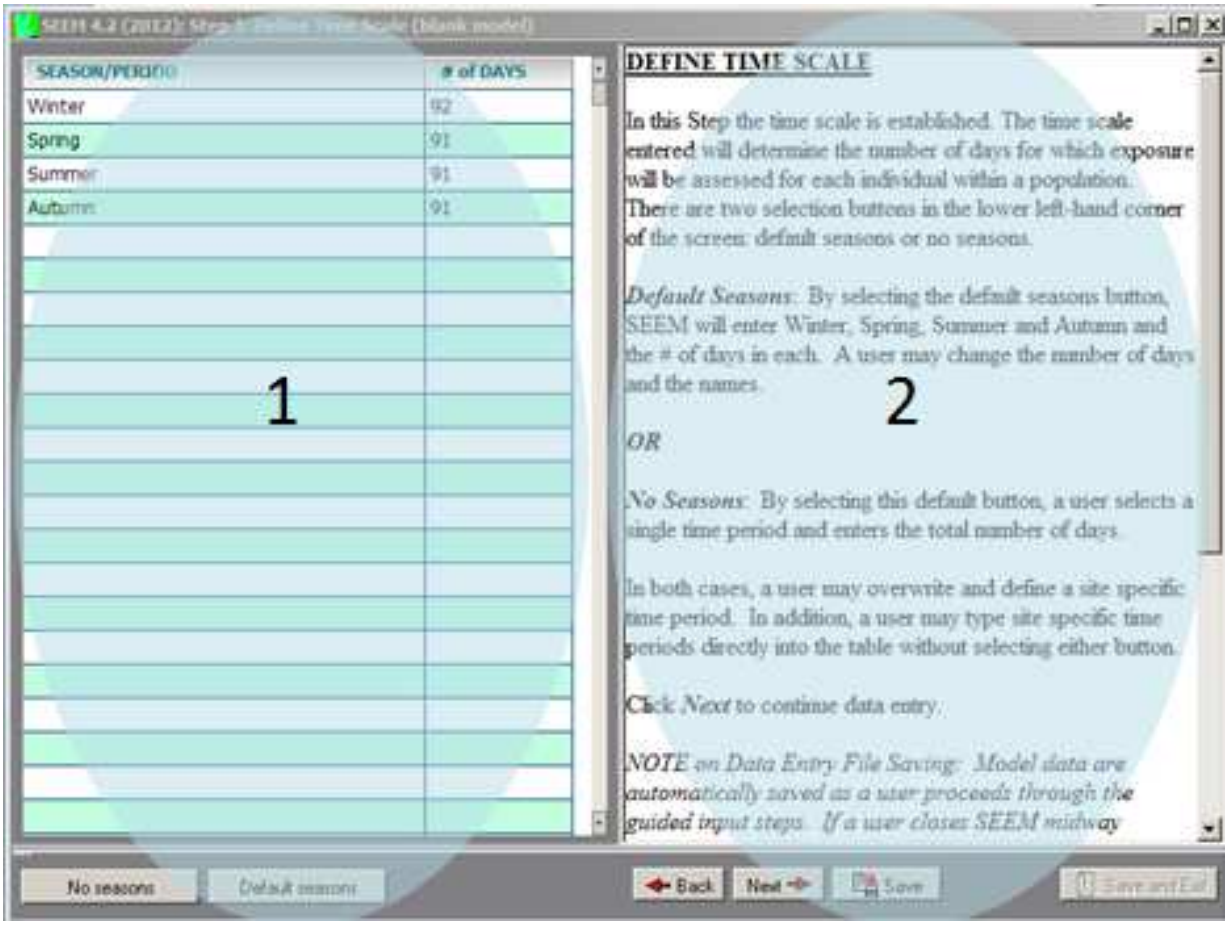


Figure 6. Example of split screen input screen

Reviewing the guidance for each step prior to entering data is recommended for first-time users.

[9] The guidance text may extend beyond the active window. In those cases, a scroll bar is available to view the full-text.

Users navigate through the input steps using three buttons in the lower right-hand corner of the input window. Click ***Next*** to move forward and click ***Back*** to view the previous window. Enter the required data before advancing through the model; SEEM will block forward movement if input data are missing from a Step. ***Save and Exit*** is used to exit the guided input. However, this option is only available on the last data entry step for a new model. When modifying a completed model, users may navigate to the appropriate step, input an edit and then click ***Save and Exit*** to exit the updating process. A fourth button is also available, ***Save***[10]. Because data entry is a time-consuming process, the *Save* button allows a user to save the inputs up to a certain point[11] in an external file. This file may be transferred to another computer or user. In addition to saving data to an external file, data are automatically saved as a user proceeds through the guided input steps. If a user closes SEEM midway through data entry, the data will be available (up to the last completed input step) upon the user's return by clicking on ***Modify Model*** or ***New Model***; these functions in this context will generate a pop-up message asking if the user would like to continue with data entry. If a user selects 'No', previously entered data will be permanently lost.

In the Sections that follow, each of the specific data entry steps is introduced in series.

3.2 Step 1: Define Time Scale

SEEM operates over a user-defined time period. The time period selected provides users with the opportunity to examine exposure for an extended period of time; in some cases, the time period may capture a life time of a species. Coupled with optional seasonal adjustments, extended analytical periods improve the realism of the wildlife exposure assessment.

The time scale entered will determine the number of days for which exposure will be assessed for each individual within a population (**1**) (Figure 7). There are two selection buttons in the lower left-hand corner of the screen (**2**): ***default seasons*** or ***no seasons***. Each is described briefly below:

Default Seasons: By selecting the default seasons button, SEEM will create season-based time categories including: Winter, Spring, Summer and Autumn and the # of days in each. A user may overwrite the number of days and the names; and,

No Seasons: By selecting this default button, a user selects a single time period and enters the total number of days. By default, 365 days are applied if no seasons is selected, but this value may be modified by the user.

[10] In earlier versions of the model this was called Intermediate Save. In the current version there is a button called SAVE. The functions are the same.

[11] Save captures the data entered through one step prior to the step in which the Save button is selected in an external .MDL file.

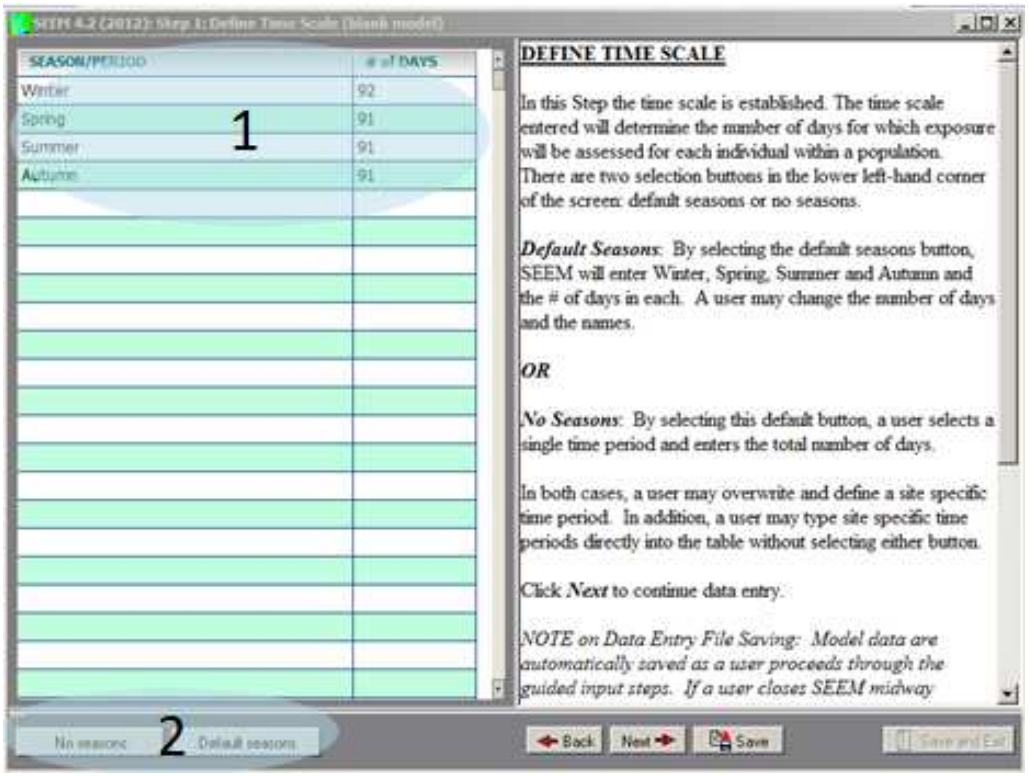


Figure 7. Time-Scale date entry screen

In both cases, a user may overwrite and define a site specific time period. In addition, a user may type site specific time periods directly into the table without selecting either button (**1**).

After entering the time period, the user may navigate to the next step by clicking Next. At any point in the data entry process a user may save the data entered to that point using Save.

3.3 Step 2: List Chemicals

SEEM will operate on any chemical for which users have a bioaccumulation factor or co-located soil and tissue concentrations for diet items for the assessed receptors. If BAFs are not available in the literature, then site-specific studies may be necessary to collect the data required to run SEEM.

In this step, enter the name of all ***chemicals*** that will be assessed in the current model file (**1**) (Figure 8). In addition, enter the ***chemical abstracts service registry number (CASRN or CAS No.)***; a user may elect to enter the CAS No. with hyphens or without. After all inputs have been entered, users may run the model for each receptor and all chemicals in sequence without returning to the input screens.

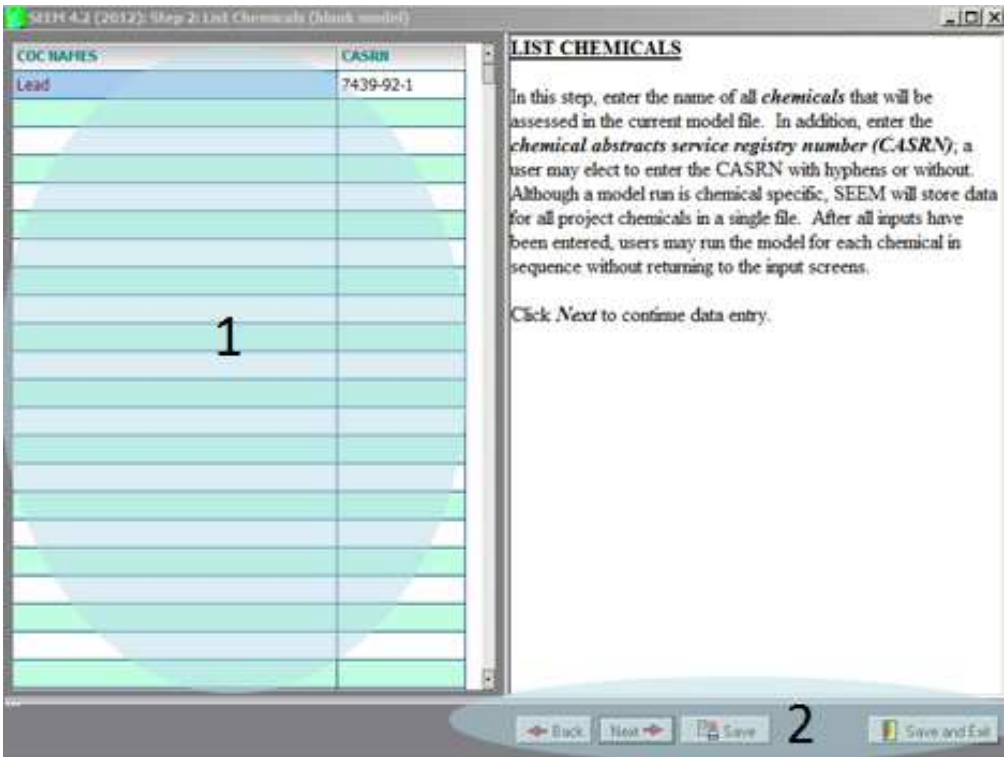


Figure 8. Chemical data entry screen

Navigate to the next step when the chemical names and CASRN have been entered.

3.4 Step 3: Define Food Items and Bioaccumulation Factors

A subset of species are considered food items[12]. As such, they are not evaluated directly in SEEM; however they are consumed by higher order species. SEEM is not a bioaccumulation model, but includes the capability to incorporate BAFs to estimate food item concentrations (Figure 9). SEEM assesses exposure to higher order receptors based on dietary dose and compares the estimated intakes to dose-based toxicity reference values.

To begin data entry to characterize the food/diet items, enter the ***name of each food item (1)***. Next, select the ***medium*** in which each food item occurs, e.g. soil, water (**1**), by double-clicking the medium input box and selecting from the pull-down menu. If the same food item occurs in multiple media, inputs must be entered for each receptor-medium combination.
Chemical names entered in Step 2 appear in the chemical list. If a chemical is not in the list, then return to Step 2, enter the chemical name and return to this Step to complete data entry. Select/highlight the chemical of interest (**2**).

[12] Definition: *food items* are consumed by other species and risk is not assessed directly by SEEM, as compared to *diet items* which may include food items in addition to receptors for which risk is estimated.

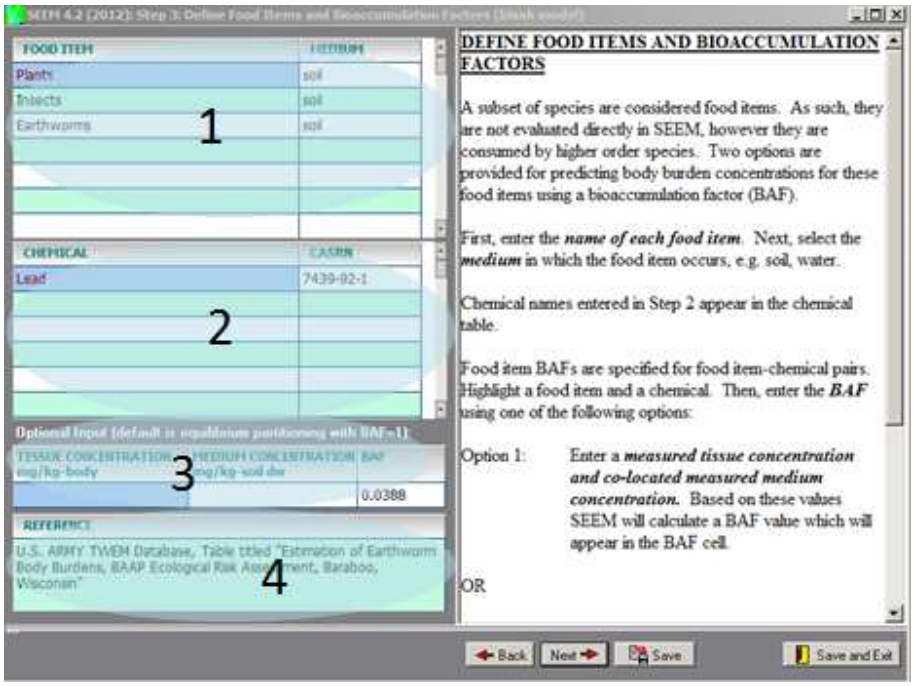


Figure 9. Food item and bioaccumulation data entry

Two options are provided for predicting body burden concentrations for these food items using a bioaccumulation factor (BAF) (**3**)[13]. Food item BAFs are specified for food item-chemical pairs. Highlight a food item and a chemical. Then, enter the ***BAF*** using one of the following options:

Option 1: Enter a ***measured tissue concentration and co-located measured medium concentration.*** Based on these values SEEM will calculate a BAF value which will appear in the BAF cell.

OR

Option 2: Enter a ***BAF*** value directly in the BAF cell.

A user may enter *reference* information for a BAF or measured data in the allotted space at the bottom of the entry screen (**4**). References and input values are tracked and presented in the model report.

Repeat these steps for each food item and chemical pair.

NOTE: The information for each receptor and chemical is active and may be edited when that receptor's and chemical's name/row are highlighted.

[13] SEEM accepts either a BAF or a co-located soil & tissue concentration. Because it is unlikely that a study site will have tissue data for every soil sampling location, SEEM uses a BAF to estimate food item concentrations for each sampling location. If a site has multiple media-tissue concentration pairs, estimate a BAF statistic outside of SEEM and input the single BAF value.

Click ***Next*** to continue data entry.

3.5 Step 4: Define Receptors

SEEM assesses exposure to receptors. SEEM is a terrestrial wildlife exposure model designed to evaluate exposures to mammals and birds. The model does not support the evaluation of fish per se beyond the application of bioaccumulation factors, but can support the assessment of semi-aquatic mammals and birds that feed on fish. Receptors may only feed on a water-based food item if the user allows for water-based foraging for that receptor during data entry.
Receptor selection considers the site management goals, assessment endpoints, habitat availability and the availability of exposure parameters. Exposure for species entered as food items in previous steps is not assessed directly; however, these items serve as a primary route (as diet items) for bioaccumulation by the receptors.

In this Step, receptor-specific exposure parameters are entered (Figure 10). Begin by entering the ***receptor names (1)***. ***Receptors*** include wildlife that consume food items and forage in the study area habitats. SEEM will assess exposure to receptors that occupy habitats with soil, sediment and/or water, though SEEM was designed primarily for terrestrial or semi-aquatic species.

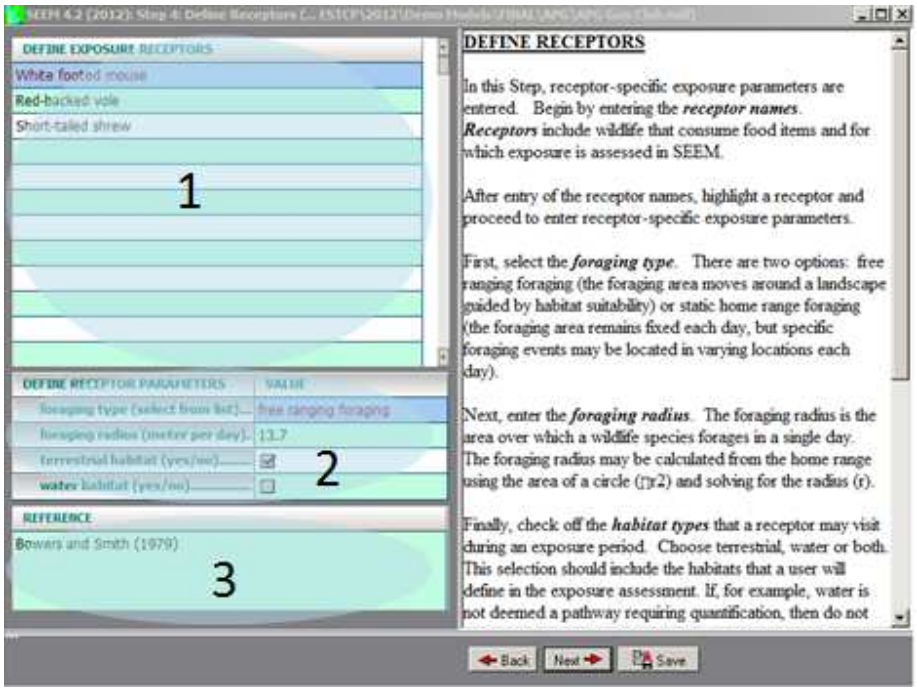


Figure 10. Defining receptors (Species for which exposure is modeled)

After entry of the receptor names, highlight a receptor and proceed to enter receptor-specific exposure parameters (**2**). These parameters characterize the behaviors of the receptors and will impact the extent of exposure.

The first exposure parameter to select is the ***foraging type*** (**2**). There are two options: free ranging foraging (the foraging area moves around a landscape guided by habitat suitability) or static home range foraging (the foraging area remains fixed each day, but specific foraging events may be located in varying locations each day). In SEEM, a foraging event is operationally defined as the simultaneous action of locating and consuming a food item. While a simplification, this characteristic may be modified to reflect specific life stage requirements. When considering the foraging type, consider the life stage and general habits of the receptor. A group of bird and mammal species may spend a period of time in a nest (or mammalian equivalent) foraging in the same area for an extended period of time, while during different times of the year or for some species, the foraging area shifts each day. In some cases food items and other resources may shift forcing receptors to move. The options for this exposure parameter represent two of the primary foraging strategies. While a simplification of the range of foraging type variants, when combined with foraging radius and foraging events, the tool offers users flexibility in creating unique foraging strategies.

After selecting the foraging type, enter the ***foraging radius*** (**2**). The foraging radius defines the circular area over which a wildlife species forages in a single day. The radius defines the area, but does not define the number of actual foraging events occurring in a single day. The foraging radius may be calculated from the home range using the area of a circle (πr^2) and solving for the radius (r).

Finally, check off the ***habitat types*** that a receptor may visit during an exposure period. Choose terrestrial, water or both. This selection should include the habitats that a user will define in the exposure assessment. If, for example, water is not deemed a pathway requiring quantification for one receptor, but it is for another, receptor preferences are defined using these check boxes. Terrestrial and aquatic habitat qualities are defined in a later step. Depending on the available data for water, drinking water sources may or may not be impacted by site-related chemicals. If a user knows that a drinking water source is unavailable, then water can be excluded as a pathway. In such a case, the receptor may consume water, but because chemicals are not discovered in the water, it is excluded from the SEEM analysis. In other cases the water may be impacted by site-related chemicals and the user may want to define the water pathway.

At the bottom of the entry page, users may enter ***references*** for the parameters on this page (**3**). The references will be carried through to the report.

Repeat these steps for each receptor.

Click ***next*** to continue data entry for the active model.

NOTE*: Data entry must be completed for each receptor. The information for each receptor is active and may be edited when that receptor's name/row is highlighted. Also, if a user tries to*

rename a receptor prior to advancing to the next step, the program will generate an error (see Section 5.0).

3.6 Step 5: Define Diets

In this Step, the diet for each receptor and receptor-specific ingestion rates are entered (Figure 11). *Note: The food items and the information required to generate food item concentrations for each receptor were entered in Step 3.*

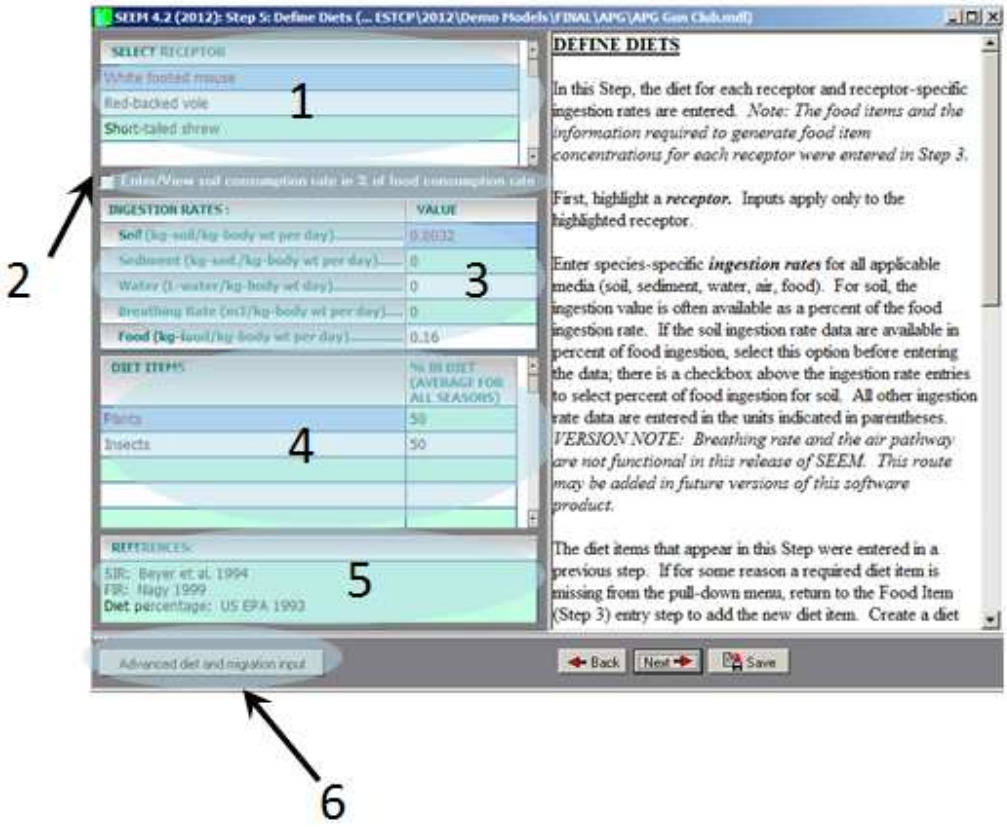


Figure 11. Defining receptor diets

First, highlight a ***receptor*** (**1**)**.** Inputs apply only to the highlighted (active) receptor. If a receptor of interest does not appear in the list, return to Step 4 to enter the receptor.

Because soil ingestion is often presented as a percentage of the food ingestion rate, SEEM provides users with the option to enter the soil ingestion rate as a percentage (**2**) (enter as a whole number, not a decimal, i.e. enter 5% as 5)[14]. Click on the selection box to enter the soil ingestion rate as a percent. Next, enter species-specific ***ingestion rates*** for all applicable media (soil,

[14] A food ingestion rate must be entered in order to use a percentage of that rate as the soil ingestion rate.

sediment, water, food)[15] (**3**). The ingestion rate data are entered in the units indicated in parentheses[16].

The diet items that appear in this Step were entered in a previous step. If a required diet item is missing from the pull-down menu, return to the Food Item (Step 3) entry step to add the new diet item. Create a diet for each receptor. Select the diet composition using the pull-down menu to select each ***diet item*** (**4**). Then enter the ***percent of each diet item*** in the diet. For each receptor, the sum of diet item percentages must equal 100%; SEEM will generate an error message and block further data entry if the percentages do not sum to 1.

Ingestion rate ***references*** may be entered at the bottom of each page and will be carried through to the output report (**5**).

Repeat these steps for each receptor.

SEEM offers users advanced analytical tools to explore the exposures in more detail (Figure 12). If a study area includes species that are highly migratory, then options under the ***Advanced Diet and Migration Input*** tab may enhance the analysis (**6**)**.** The advanced features are available for projects with a time scale that is divided into at least two different units and will have no effect if only a single time period is specified. Seasons are the common unit of time, but users may define any time period of interest. To access the advanced features associated with this data entry step, click on ***Advanced Diet and Migration Input*** to access this screen (**6**). On the advanced screen users begin by selecting a receptor (**7**) and the season (**8**) and may modify onsite versus offsite probabilities (when offsite it is assumed that receptor exposure = 0) by season (**9**). In addition, diet percentages of existing diet items may be modified by season (**10**); however, diet items may not be added. For each season, the sum of diet item percentages must equal 100%. An item may be assigned 0% of the diet, as long as the percentage of the remaining items equals 100%.

The sources for the advanced features data inputs may be added and tracked in the ***reference*** section (**11**). Click ***Ok*** to exit the advanced features area.

Click ***Next*** to continue data entry for the active model.

[15] In this version of SEEM, breathing rate and the air pathway are not functional. This route may be added in future versions of this software product.

[16] Users are responsible for using inputs that are consistent in terms of the dry weight or wet weight basis.

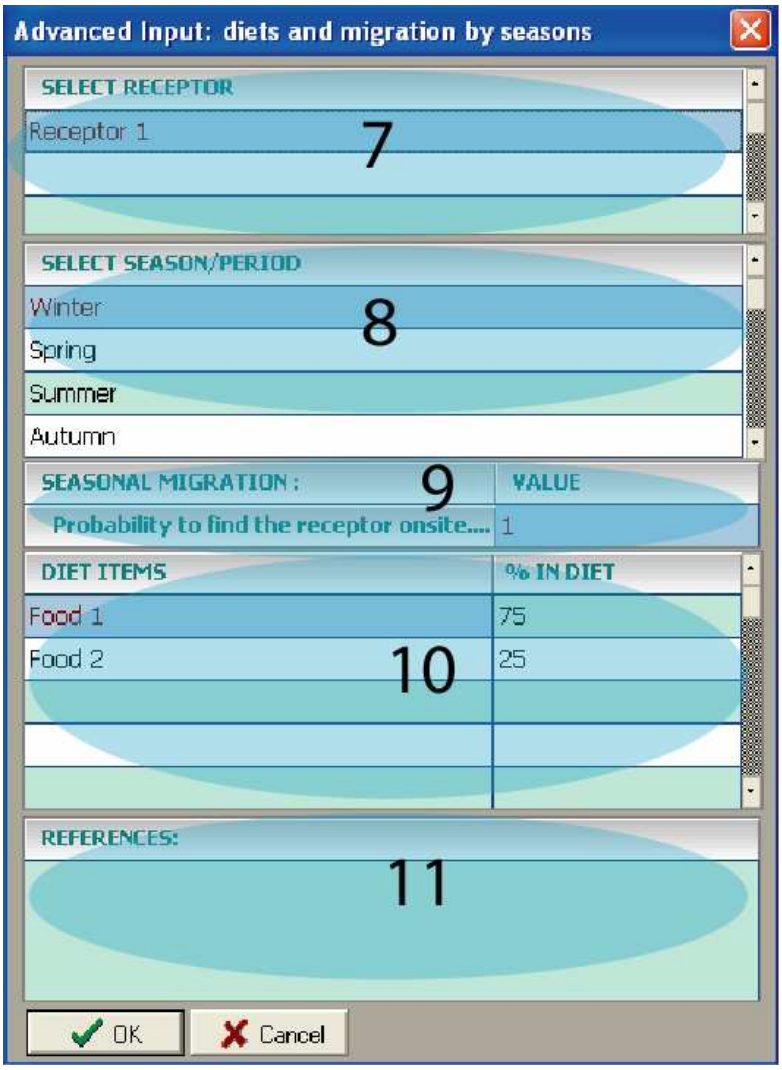


Figure 12. Advanced input for diet and migration activity

3.7 Step 6: Define Benchmarks

Toxicity reference values (TRVs) or benchmarks are used to assess the estimated exposure dose through an ecological hazard quotient (EHQ), i.e. Exposure Dose/Benchmark. In this Step, the toxicity benchmarks are defined and entered for each receptor (Figure 13).

The process is similar to previous steps in that a user first activates a dataset for data entry or editing. The first step is to highlight a ***receptor*** (**1**)**.** Next, highlight a ***chemical*** (**2**). Then enter the *benchmark names* (e.g. Chronic NOAEL – Reproduction). The level of detail expressed in the benchmark name is user-determined. Users may enter unique benchmark name(s) and TRV(s) for every chemical-receptor-endpoint combination (**3**). Finally, enter the TRVs in mg/kg/day (**3**).

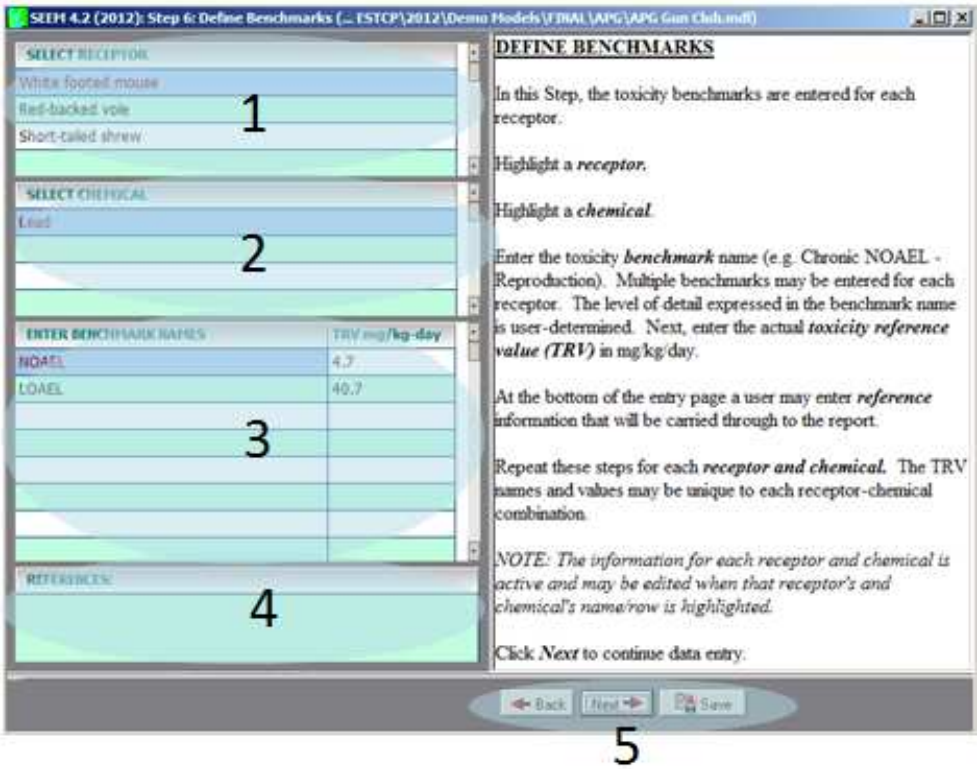


Figure 13. Defining chemical benchmarks

At the bottom of the entry page a user may enter ***reference*** information that will be carried through to the report (4).

Repeat these steps for each ***receptor and chemical.***

Click ***Next*** to continue data entry. A user may also click ***Save*** to save all data entered up to this step in an external file (**5**).

3.8 Step 7: Define Study Area

The component of SEEM that differentiates it from the more traditional wildlife exposure models is the consideration of the spatial context. By parsing the site into concentration polygons and species-specific habitat suitability polygons, exposure is tuned to the characteristics of each receptor. Then, by assessing the exposure to a number of individuals in a population, SEEM assists in the identification of population exposure trends. SEEM tracks the exposure of a population of individuals, each starting the exposure from a different location, proceeding to forage over the landscape.

In order to define the modeling landscape for a specific site and species, a polygon mapping tool is applied. The tool is used to draw chemical exposure areas and to map the habitat suitability of

different portions of the Study Area. In this step, a base map is imported and the polygons are drawn (Figure 14). In the steps that follow chemical concentrations and habitat suitability indices (HSI) are entered for each polygon. To orient the user and the model, use of a base map or site plan is recommended.

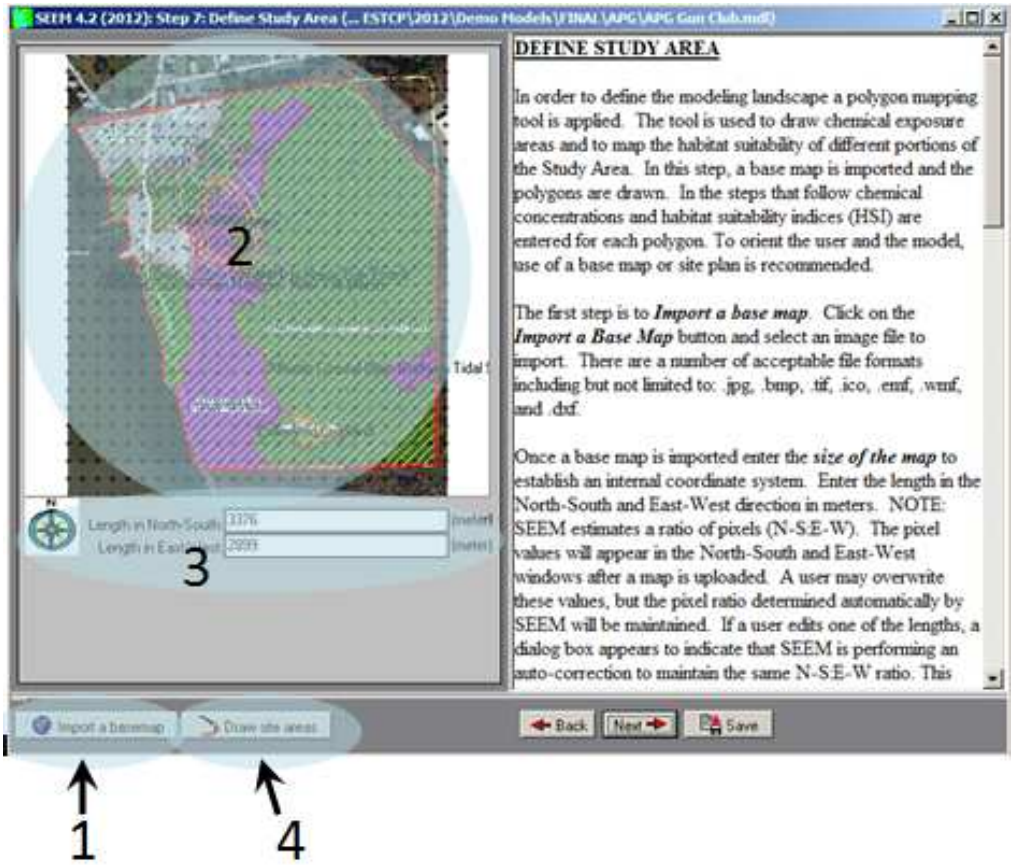


Figure 14. Defining the study area

The first step is to ***Import a base map***. Click on the ***Import a Base Map*** button and select an image file to import (**1**). There are a number of acceptable file formats including but not limited to: .jpg, .bmp, .tif, .ico, .emf, .wmf, and .dxf.

Once a base map is imported (**2**) enter the ***size of the map*** to establish an internal coordinate system (**3**). Enter the length in the North-South and East-West direction in meters. NOTE: SEEM estimates a ratio of pixels (N-S:E-W). The pixel values will appear in the North-South and East-West windows after a map is uploaded (**3**). A user may overwrite these values, but the pixel ratio determined automatically by SEEM will be maintained. If a user edits the N-S ratio, a dialog box appears to indicate that SEEM is performing an auto-correction to maintain the same N-S:E-W pixel ratio. Section 5 discusses in more detail the preferred map format/size. The scale set in this step will be used to set the foraging area for the exposure each day. SEEM does not currently provide users with the functionality to electronically pinpoint geographic locations.

However, important features may be added to the base map external to SEEM and then, when imported, those features may be used to guide polygon drawing.

The next step is to draw polygons to capture site chemistry and habitat suitability. A polygon is defined as an area over which chemical concentrations are the same (or samples have been averaged in some way to obtain a single polygon value) or habitat suitability is the same. The size, position and shape are all user-defined based on the available data.

To activate the polygon tool, click on ***Draw Site Areas (4***) (Figure 15).

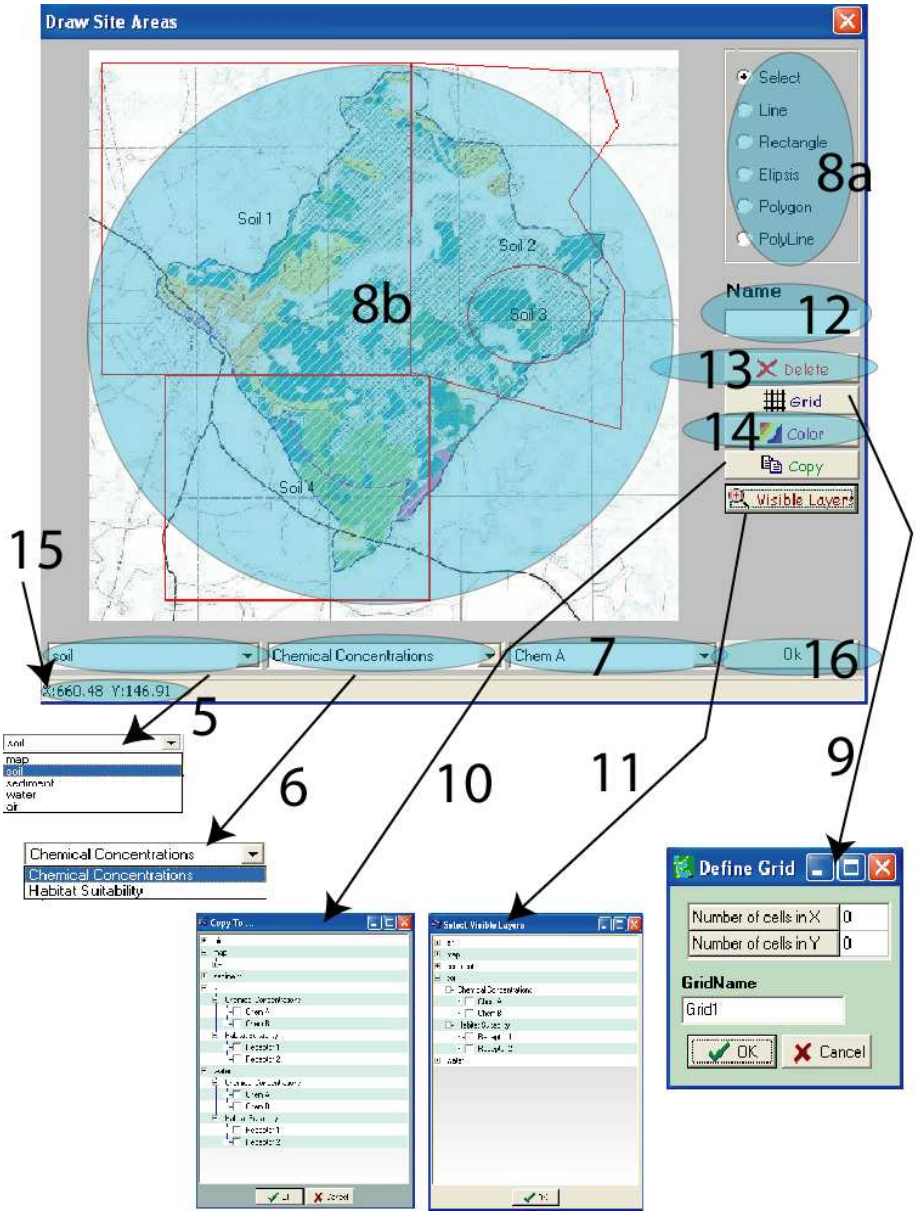


Figure 15. Drawing site polygons/Polygon tool

There are three (3) pull-down menus at the bottom of the Drawing Tool screen (**5-7**). They allow the user to select the medium (map[17], soil, sediment, water) (**5**), the map type (chemical concentration or HSI) (**6**) and the chemical (for chemical concentration) or the receptor (for HSI entry) (**7**). Once the category of polygon is selected, then the user may draw applicable polygons (**8a**). Alternatively, the user may elect to use a grid of fixed cell size (described below) (**9**). To orient users spatially, the x,y coordinates of the cursor are displayed in the lower left-hand corner of the drawing window (**15**).

Polygon Drawing

If the base map covers areas that are outside of the study area, then area user can assign a site value The site polygon is generated automatically and used to assign a user value to any area that is not defined by any user-defined polygons. The areas outside of all polygons can be assigned a non-site related chemical concentration, e.g. background, zero; SEEM.

Polygon drawing continues from large to small, nesting each smaller polygon within larger polygons as applicable. Polygons may intersect and overlap. The value for any given location is the value of the last polygon (the top polygon when overlapping) drawn over an area. Various drawing methods are available (e.g. ellipse, rectangle, and polygon – free form) (**8a**). Rectangles, ellipses and polygons may all be assigned values and influence the calculations within SEEM as they are closed geometric shapes. Rectangles and ellipses are sized as a completed shaped, but polygon drawing requires the user to draw every side and at the end to double-click where the polygon should close[18]. Polyline and line are used for drawing landmarks and other references that do not directly influence the calculations. Also, a user may click ***select (*8a*),*** then select (click on) a polygon and click the ***copy*** button to place a copy on another polygon layer (**10**). The user may then choose a destination for the copied polygon from the polygon table of contents[19]. The copy feature increases the efficiency of polygon creation. Users may also click on a shape and move it around the map to a new location. Some polygons may be assigned to one portion of the project, but may provide a useful reference in other areas of the model. Users have an option to turn a selected polygon into a visible layer that will be displayed in all windows **(11)**; however, visible layers are only active in calculations on the window in which they were drawn. Items drawn under the map option in the first pull-down menu will appear as a base layer under all polygon layers in the report, but do not impact calculations. Visible layers are only a tool for model development and will not appear in each report map. After drawing each polygon, the program will request a polygon name (**12**). This

[17] The map option refers to any map drawing created by the user that does not impact the calculation but is used for reference purposes only.

[18] Polygon drawing requires a user to use the mouse to draw each side of the polygon by holding down the mouse and dragging it. Each subsequent line begins where the previous line ends and the polygon is closed by double-clicking on the point of closure. For rectangles and ellipses, place mouse pointer at the preferred location, depress the mouse button and drag the shape to the preferred size.

[19] Only a single polygon may be copied at a time. A copied polygon is fully functional. This polygon may be assigned a chemical concentration or an HSI and will be active in the calculations. In contrast, the visible layers button displays polygons on multiple windows/pages, but the visible layers are for reference only and are only active on the window in which the drawing occurred.

should be a unique identifier and will be used to reference the polygon in future data entry steps. SEEM will auto-name polygons and grid cells, but for clarification, users may want to provide site-specific names for polygons; grid cells are named based on the cell location, e.g. cell 1,1. After drawing a polygon, users may decide to delete polygons. Polygons may be deleted by first *selecting* the target polygon and then clicking *delete* (**13**). Also, polygon colors may be selected from the standard color palette (**14**). The user can click on Select then click on a polygon to modify the name or color after the polygon has been drawn and saved. For each medium-chemical combination, draw polygons representing the different concentrations across the landscape. Draw polygons for all receptor-HSI combinations as well. For particularly complex polygons and/or sites, consider importing the base map that includes important landmarks or even the polygons; these reference areas may be traced in SEEM[20].

Using A Grid

In addition to free form polygon creation, SEEM includes an option to use a grid of cells of fixed cell size. Grid sampling offers a comprehensive method for assessing chemical concentrations; although intensive habitat assessments may use a grid, general surveys based on aerial photographs and other readily available resources are likely to be polygon-based. Depending on the grid resolution, sampling may be very intensive. Depending on the sampling intensity, geospatial averaging may not be required to estimate exposures in all portions of a site.

For study areas with grid data, SEEM provides a tool for creating a grid followed by importing grid data directly from a spreadsheet (**9**) (importing occurs using the SEEM XL utility described in Appendix B). To use the fixed grid option, click on the ***define*** button with the grid icon (**9**). Enter the ***grid size***[21]. A ***grid name*** is required before continuing with grid creation. Click ok and a grid outline will appear on the base map (**8b**). The grid is specific only to the specific selections under which it was created (e.g. soil, chemical concentration, chemical A). Other parameters may be defined by free form polygon drawing within the same study site.

When all of the polygons have been drawn and/or grids defined, click OK to return to the main screen for this Step (**16**). Because polygon creation can be a time-consuming activity, performing an Save is recommended.

Infrequently the drawing tool may generate an error. See Section 5.0 for further discussion and workaround.

Then click ***Next*** to proceed to the next data entry step.

[20] Currently, SEEM does not include advanced GIS functionality. Landmarks that are important for polygon definition should be included on the imported base map and can then be traced within SEEM.

[21] Grid cell shape is based on the length entered in the N-S and E-W directions. A user specifies the number of cells.

3.9 Step 8: Define Chemical Concentrations

In previous Steps, a map was imported and medium- and chemical-specific polygons or grids were drawn. In this Step, the ***chemical*** concentrations (**3**) and ***bioavailability adjustments*** (**4**) for each polygon are input (Figure 16). Data entry is completed for each ***medium-chemical*** (**1-2**) combination. The polygon map is displayed for reference, but cannot be modified in this Step.

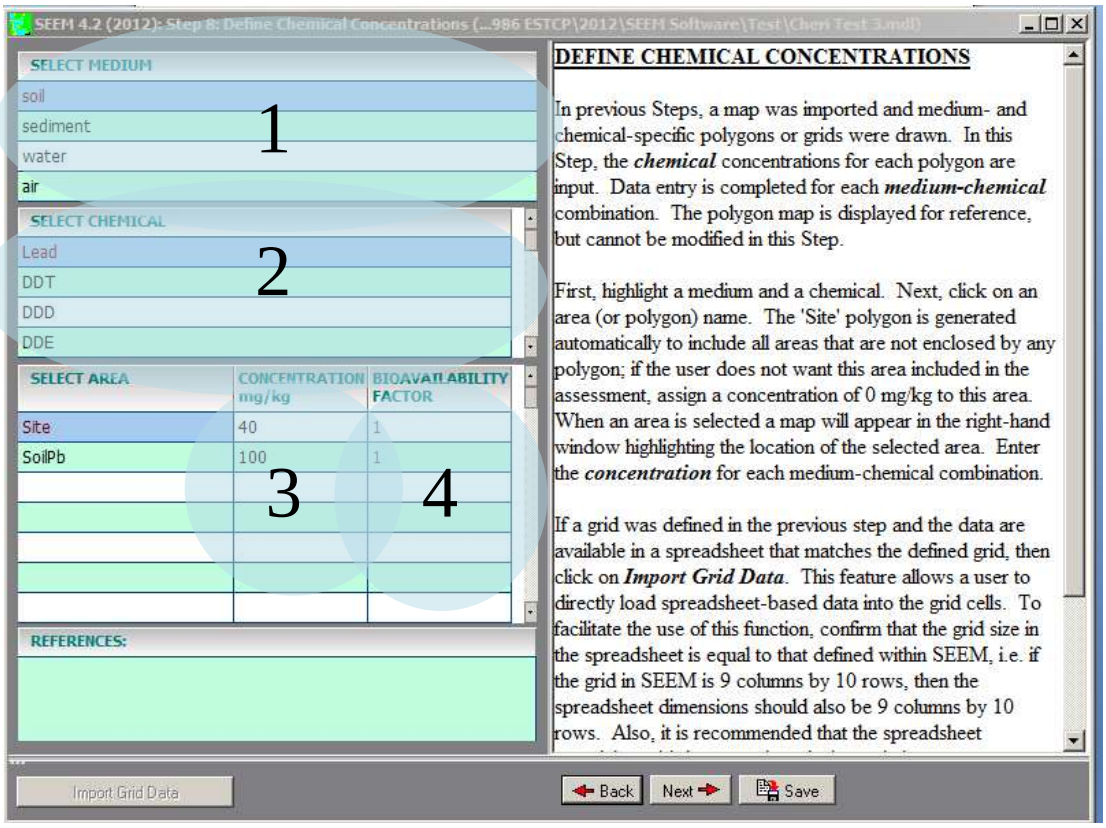


Figure 16. Defining chemical concentrations – guided input view

First, highlight a medium and a chemical. Next, click on an area (or polygon) name. The 'Site' polygon is generated automatically to include all areas that are not enclosed by any polygon; if the user does not want this area included in the assessment, assign a concentration of 0 mg/kg to this area. When an area is selected, a map will appear in the right-hand window highlighting the location of the selected area (Figure 17). Enter the ***concentration*** (**3**) for each medium-chemical combination. In addition, a user may assign a unit less ***bioavailability factor (4)***. This factor is a fraction greater than 0 and less than or equal to 1, where one represents a chemical that is fully available for uptake. A default value of 1 is automatically entered, but may be changed. The factor may be unique to each polygon and is chemical-specific.

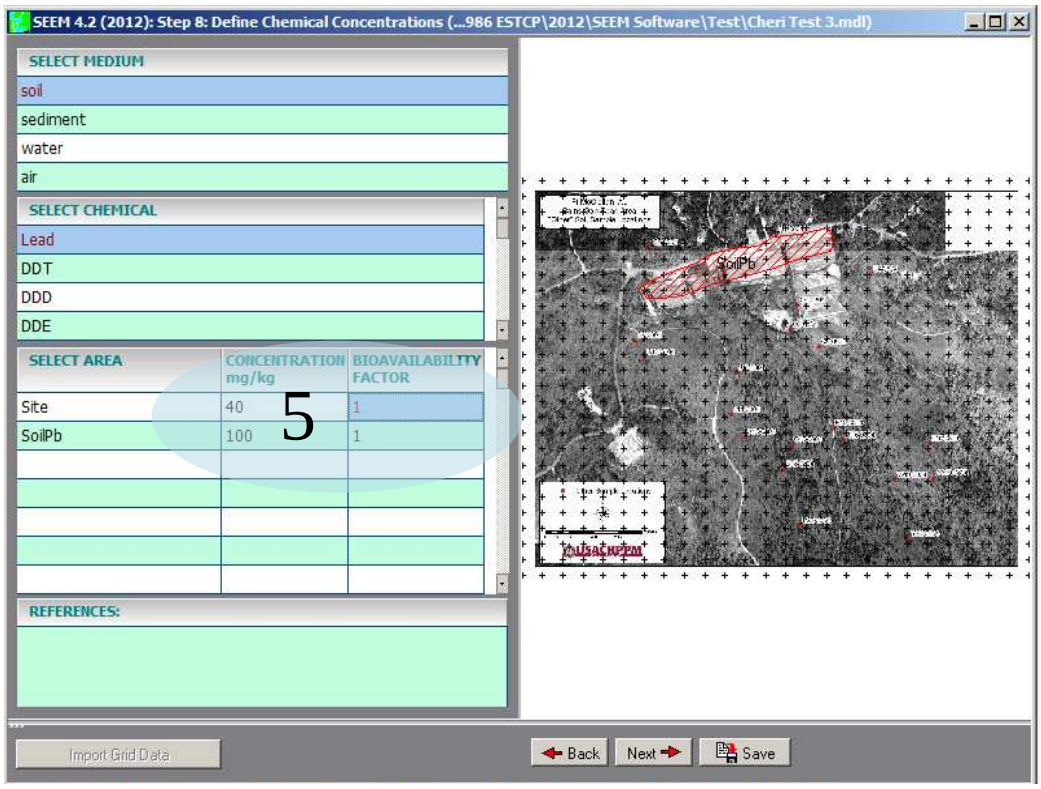


Figure 17. Defining chemical concentrations – map view

The ***import grid*** functionality has been replaced by another file management tool called SEEM XL Utility. Appendix B summarizes the use of this utility to import data directly from Excel.

References may be entered in the space provided at the bottom of the page (**5**).

After concentrations and, if needed, bioavailability adjustments are entered for all medium-chemical combinations, click ***Next*** to continue data entry.

3.10 Step 9: Define Habitat Suitability

In previous Steps, a map was imported and medium- and receptor-specific polygons were drawn reflecting habitat suitabilities. In this Step, the ***habitat suitability indices*** for each receptor are input. Data entry is completed for each ***medium-receptor*** combination independently (Figure 18). The polygon map is displayed for reference, but cannot be modified in this Step.

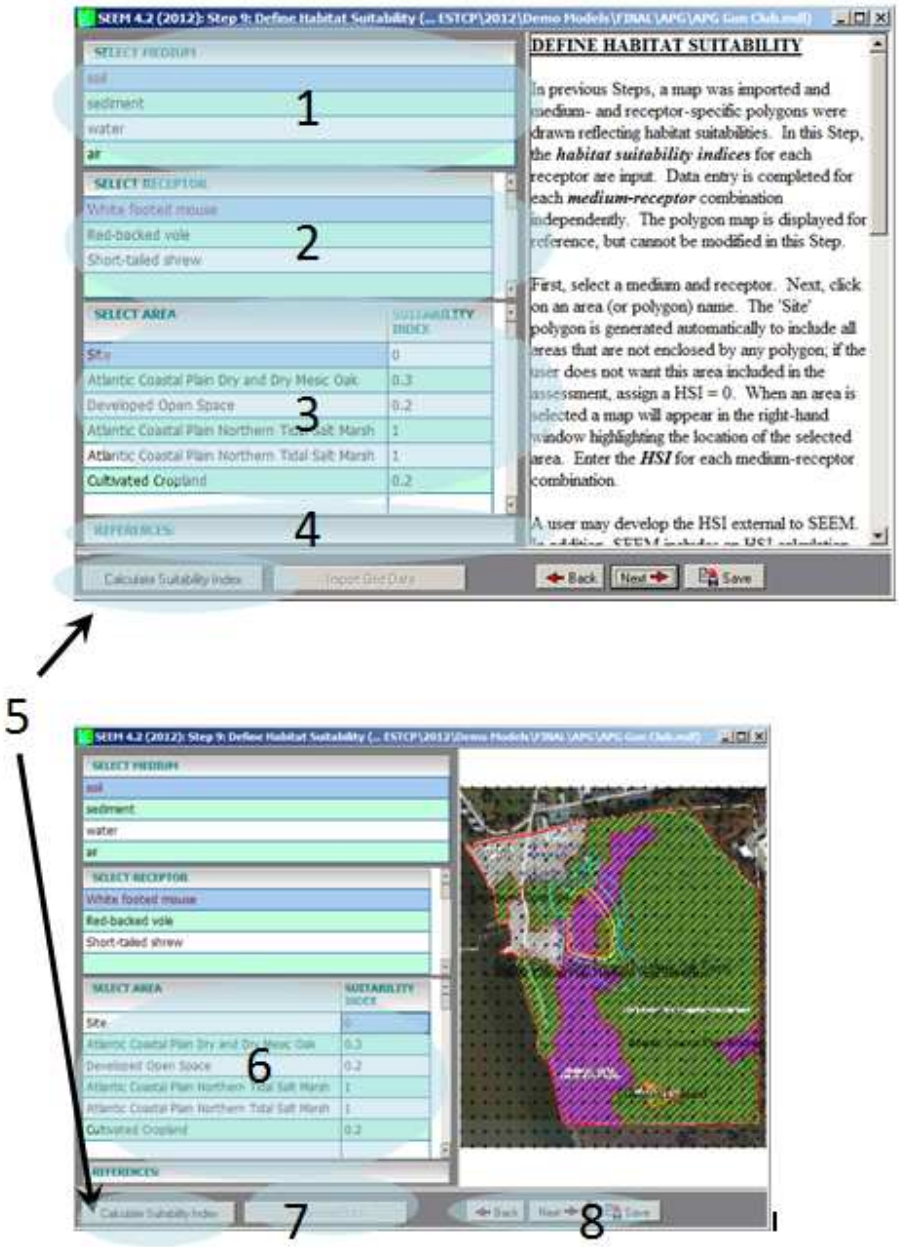


Figure 18. Adding habitat suitabilities

First, select a medium (**1**) and receptor (**2**)[22]. Next, click on an area (polygon or grid cell) name (**3 & 6**). In the same way that the chemical concentration entry screen toggled between guidance and an interactive map, the HSI screen will also display a map and the specific polygon or cell

[22] Each combination may have an entirely different polygon or grid design and what is high quality habitat for one species, may be poor habitat for another species.

when a name is selected. A 'Site' polygon is also generated automatically to include all areas that are not enclosed by any polygon; if the user does not want this area included in the assessment, assign a HSI = 0. Enter the ***HSI*** for each medium-receptor combination directly in the appropriate input cell (**3**). HSI values are decimals between 0 and 1 with 1 representing perfect habitat for the selected species. ***References*** may be entered for tracking the source of each HSI (**4**).

A user may develop the HSI outside of SEEM. In addition, SEEM includes an HSI calculation tool developed by Kapustka, et al. 2005[23]. In order to apply the tool, select a polygon from the list of names selected previously (**3**). To access the calculator, click on ***calculate suitability index (5)***. Users can toggle back to the guidance by clicking on the map or in the area labeled **(6)**. The ***Import Grid Data*** **(7)** button functionality has been replaced by another file management tool called SEEM XL Utility. Appendix B summarizes the use of this utility to import data directly from Excel. To advance, move to the previous slide and save click on the respective buttons at the bottom of this screen **(8)**.

When a user clicks on ***calculate suitability index*** **(5)**, the window that opens includes three primary tabs: ***equations*** (**10**), ***input variables (11)*** and ***calculated variables*** (**12**). The ***Equation*** tab stores the programming code that underlies an HSI for a given species (Figure 19). The ***Input Variables*** tab is the primary data entry window for estimating an HSI (Figure 20). The required inputs are described and the final HSI is estimated. Finally, the ***calculated variables*** tab is used to review intermediate HSI calculations (Figure 21). Each of these tabbed windows is displayed below. Figure 22 provides an image of the home screen for the HSI calculator.

Equation Tab

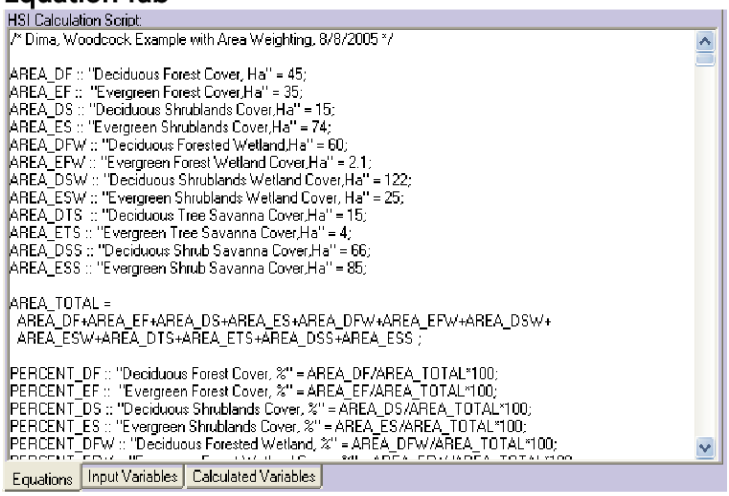


Figure 19. Equation tab – calculate HSI

[23] The US Geological Service (USGS) compiled a number of habitat suitability models. The user should review and decide if any specific model is appropriate for use at a given site. The models can be found on the USGS website: http://www.nwrc.usgs.gov/wdb/pub/hsi/hsiindex_bynumber.htm

Input Tab

VARIABLE	DESCRIPTION	VALUE
AREA_DF	Deciduous Forest Cover, Ha	45
AREA_EF	Evergreen Forest Cover,Ha	35
AREA_DS	Deciduous Shrublands Cover,Ha	15
AREA_ES	Evergreen Shrublands Cover,Ha	74
AREA_DFW	Deciduous Forested Wetland,Ha	60

Equations | Input Variables | Calculated Variables

Figure 20. Input Tab – calculate HSI

Calculation Tab

VARIABLE	DESCRIPTION	VALUE
AREA_TOTAL		548.1
PERCENT_DF	Deciduous Forest Cover, %	8.21
PERCENT_EF	Evergreen Forest Cover, %	6.386
PERCENT_DS	Deciduous Shrublands Cover, %	2.737
PERCENT_ES	Evergreen Shrublands Cover, %	13.5
PERCENT_DFW	Deciduous Forested Wetland, %	10.95

Equations | Input Variables | Calculated Variables

Figure 21. Calculation tab – calculate HSI

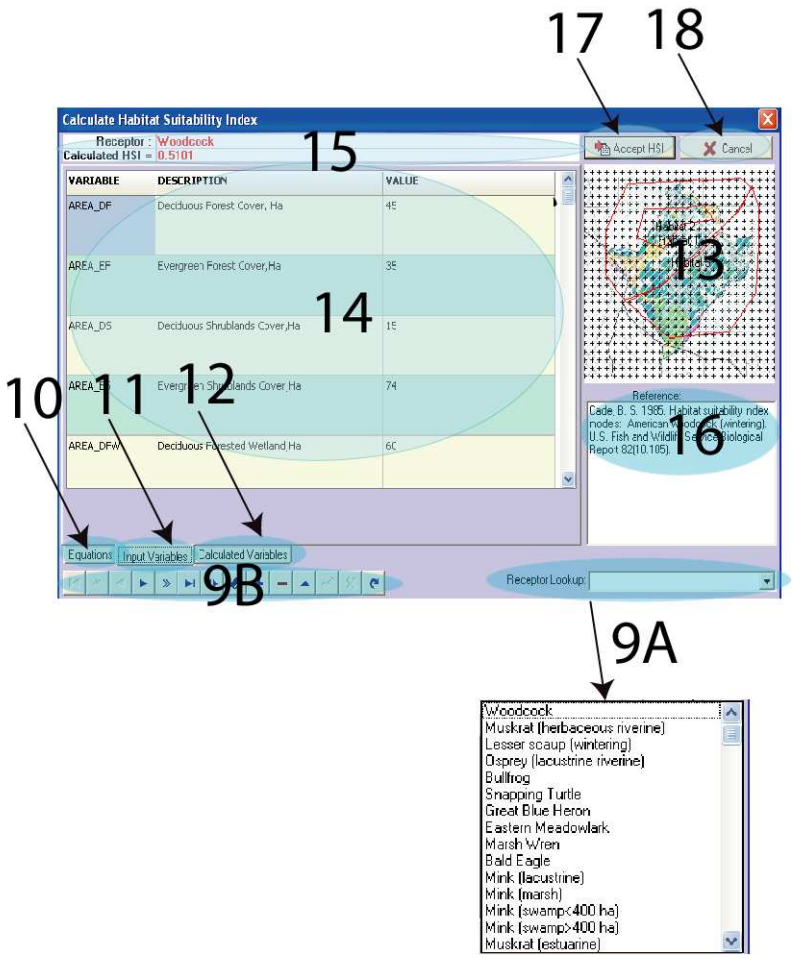


Figure 22. Home Screen for HSI calculation

In the ***equation tab***, the core programming for underlying the HSI is presented (Figure 19). Generally, users should have no need to access this tab during model operation. Advanced users may wish to modify an equation or use existing programming to create a new HSI.

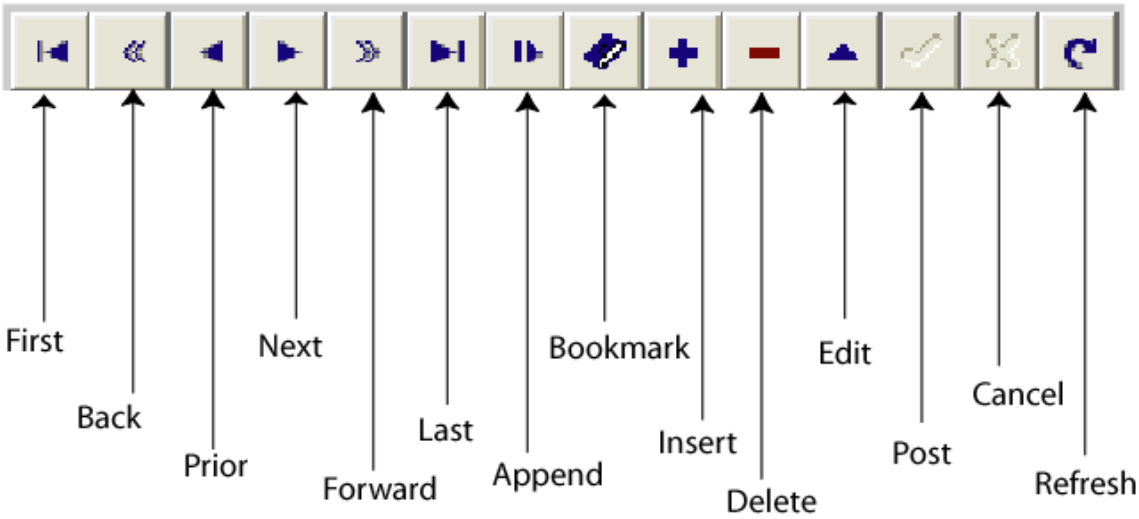
The ***input variables tab*** is the primary user access point to the HSI calculator (Figure 20). This tab displays the required variables and the input cells for each variable. Enter the site-specific values into the appropriate cells. The ***calculated variables tab*** presents the results of the intermediate HSI calculations and the final calculated HSI value (Figure 21).

Click on input variables. An HSI is comprised of an equation that tallies the status of various attributes of the habitat that define habitat suitability for a specific species or species group. The equations are species and habitat specific. For example, some species may seek habitat with tree densities > X and canopy cover of > Y. In the lower right-hand corner of the HSI screen, click on ***Receptor Lookup*** (**9A**). Users may also navigate using the forward and reverse arrow keys (**9B**) (Figure 22). The scrolling list includes all of the species with an established HSI equation; additional species/equations will be added as they become available.

Users may also enter site-specific equations (discussed below) (**10**). In some cases substituting the equation for a species with similar habitat requirements, but lacking an HSI may facilitate site analysis. Select the appropriate species (**9A**). Once the HSI equation has been selected for a particular receptor, enter the site-specific values for each of the variables on the ***input variables*** tab (**11 & 14**). The supporting and final calculations are displayed on the ***calculated variables*** tab (**12**). The active polygon is displayed on the insert map (**13**) and, consistent with the other input screens, users may enter reference information for the HSI; references for the provided HSI equations are already included in the calculator but additional text may be appended (**16**). Click ***Accept HSI*** to assign the estimated HSI to the selected polygon (**17**). To exit the HSI calculator without accepting an HSI calculation, click *Canc*el (**18**). Figure 23 provides a close up view of the navigation buttons on the HSI calculator.

When HSIs have been entered for all medium-receptor combinations, then click ***Next*** to continue with data entry. In some cases, User's experience difficulty if an HSI is entered first and then a User decides to use the HSI calculator to replace the value. SEEM will continue to use the originally entered HSI unless the user clicks another row in the HSI entry table. Click – Accept HSI within the calculator, then navigate back to Step 9. Locate the new HSI cell, and click on the next HSI in the table. This will lock the new HSI value in.

Appendix A presents instructions for entering new HSI records.



First – go to the first database record;
Back –returns to the prior record when accessing database randomly;
Prior – one record back;
Next – one record forward;
End – go to the database end;
Bookmark – create bookmark on the current record or select previous bookmark to return to;
Insert – insert new record;
Delete – delete current record;
Edit – start editing database;
Post – write editing in the database (it is also done automatically when you just edited the data);
Cancel – undo changes just done;
Refresh – refresh database view (if somebody else corrected database in multitasking mode the new changes will appear after this)

Figure 23. Habitat suitability index calculator – key to navigation buttons for receptor lookup

3.11 Step 10: Define Modeling and Report Parameters

SEEM estimates exposure to a population of individuals rather than a 'representative' individual. The user defines the size of the population assessed. The user is responsible for selecting a reasonable population size given the size and available habitat limitations. In this step, the user selects the ***model population size***[24] to be assessed for each receptor and selects the ***report options*** (Figure 24). A number of SEEM outputs are available. Depending on the information needs of each user, some options may be more applicable than others.

Highlight a species of interest. Enter the population size (**1**). Repeat for each receptor.

Check/select all of the preferred output/report options (**2**).

Click ***Next*** to continue to the last step.

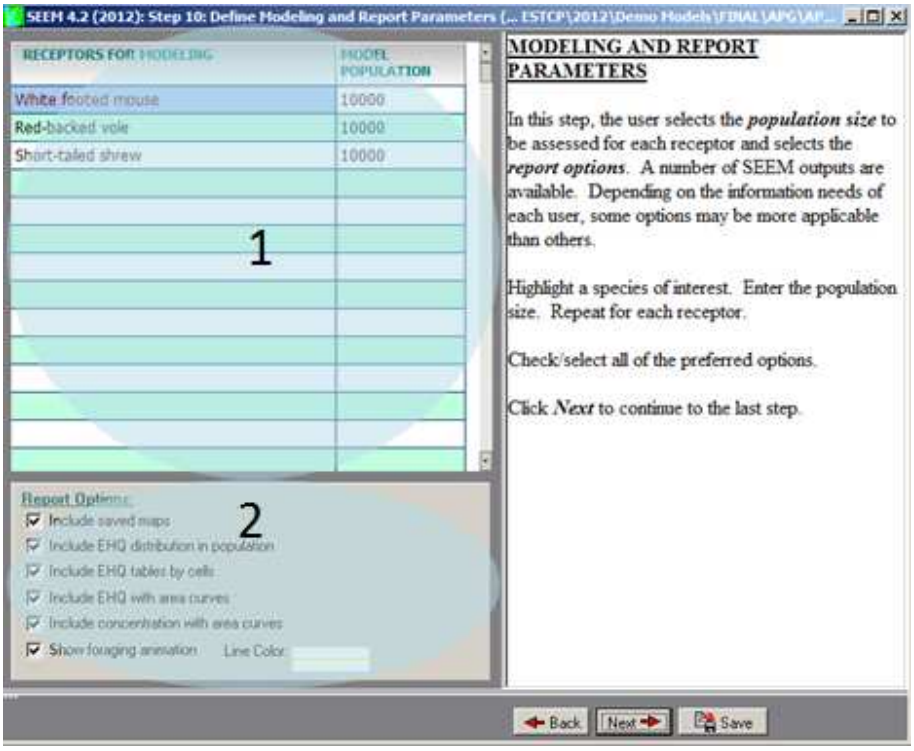


Figure 24. Defining modeling parameter and Report preferences

[24] The model population size is not indented to capture the true population size. When using these types of models it is important to understand how the 'population' might be influenced by chemicals in the environment. Whereas running the model for the true number of individuals in an area would yield a snapshot of exposure, running the model for that group for many days would provide a better exposure estimate. Ultimately, the same goal will be accomplished whether a small population is run for a large number of days or a large population is run for a small number of days. We recommend running the model with a large 'modeled' population for a large number of days.

3.12 Step 11: User Input is Finished

The last step provides users with the opportunity to close and exit the guided input (Figure 25). When a user clicks ***finish*** for a model that has not been previously saved, SEEM will open a standard dialog for saving inputs in an external file.

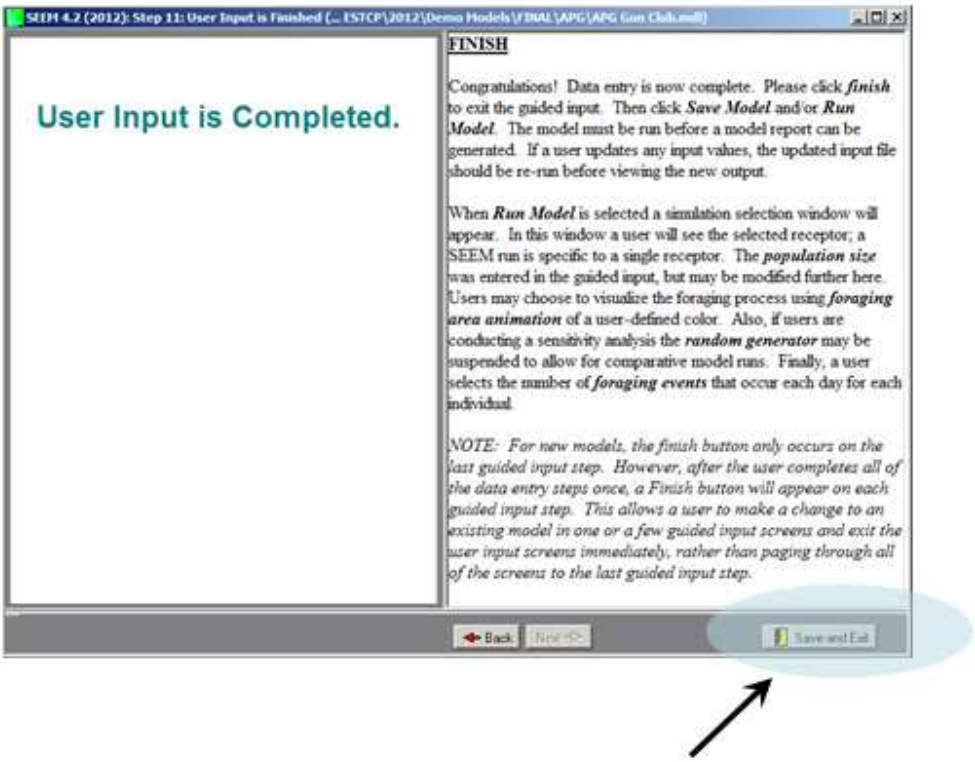


Figure 25. Completion of data entry – Final input screen

To save updated existing files with a different name click ***Save and Exit*** from the home screen and either choose a new file name or choose to over write the existing file[25].

Recently, an Excel macro called SEEM XL was created to facilitate data input reviews and modification of inputs for sensitivity analyses. The macro operates within SEEM and allows a user to import existing SEEM files (.mdl). The data for each guided input step are displayed on separate Excel worksheets. A subset of those data are available for modification/editing within

[25] NOTE: For new models, the finish button only occurs on the last guided input step. However, after the user completes all of the data entry steps once, a Finish button will appear on each guided input step. This allows a user to make a change to an existing model in one or a few guided input screens and exit the user input screens immediately, rather than paging through all of the screens to the last guided input step. Pressing 'Finish' automatically saves the updated data in the associated external file. Closing the input form without pressing 'Finish' will not save the changes to the external file content and the updated data will be lost.

the XL tool. Upon completion the modified data are exported back into an .MDL file that can be read within the SEEM program. The utility does not currently allow modification of the drawn polygons – only the assigned values for the polygons. A detailed description of SEEMXL and the capabilities of the macro is provided in Appendix B.

3.13 Run Model

After all of the required inputs have been entered, the user may run the model (Figure 26). A SEEM model run is specific to a receptor, however the model will run for all chemicals in the data set. The receptor that will be run is the active receptor appearing in the receptor window at the top of the home screen in SEEM. To change the receptor to be run, select a new receptor from those entered/available in the specific dataset by using the pull-down menu. In SEEM a model run and report generation are two separate user-initiated activities. When a new dataset is completed or an existing dataset is updated, the model must be re-run to update the Report. Within a dataset, the report generator will compile the model run for each receptor (and chemical) allowing users to access all outputs for receptors with complete model runs.

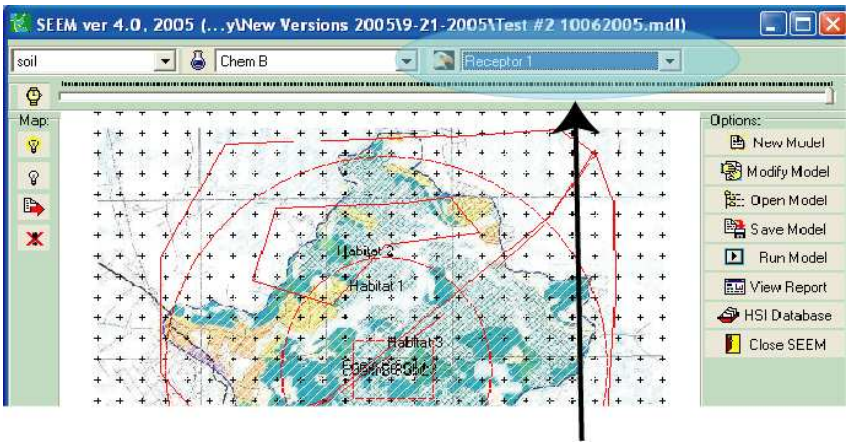


Figure 26. Running the model

When ***Run Model*** is selected a simulation selection window will appear (**1**) (Figure 27). In this window a user will see the selected receptor; a SEEM run is specific to a single receptor (**1**). The ***model population size***[26] was entered in the guided input, but may be modified further here (**2**). Users may choose to visualize the foraging process using ***foraging area animation (3)*** and a user- defined color for the foraging boundaries (Line Color) (**6**). In addition, a user may choose to suspend the random number generator. The starting seed number may be held constant

[26] The model population size is not indented to capture the true population size. When using these types of models it is important to understand how the 'population' might be influenced by chemicals in the environment. Whereas running the model for the true number of individuals in an area would yield a snapshot of exposure, running the model for that group for many days would provide a better exposure estimate. Ultimately, the same goal will be accomplished whether a small population is run for a large number of days or a large population is run for a small number of days. We recommend running the model with a large 'modeled' population for a large number of days.

(uncheck **3** & **complete 4)** or may be random; holding the starting number constant would aid in sensitivity analyses and comparative model runs, for example (**3**). Finally, a user selects the number of ***foraging events*** that occur each day for each individual (**5**).

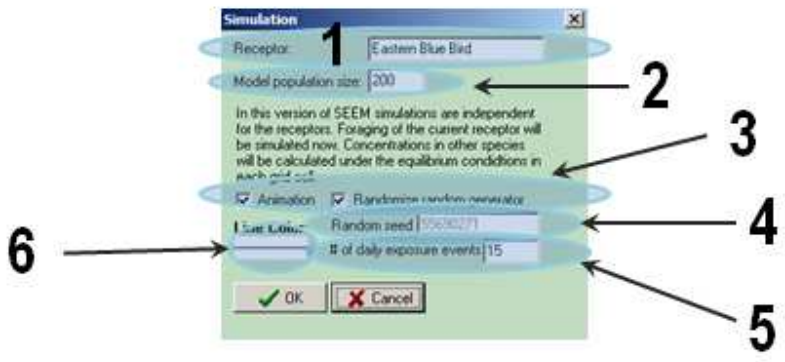


Figure 27. Simulation window for running the model

When all of the Simulation options have been reviewed and selected, click Ok to run the model. A status bar across the top of the model home screen tracks the progress of the run (Figure 28). The time required to complete a model run depends on the number of individuals in the population, the number of daily foraging events, the number of days selected for the model run, and the computer processor speed. A meter is provided to allow a user to track modeling progress.

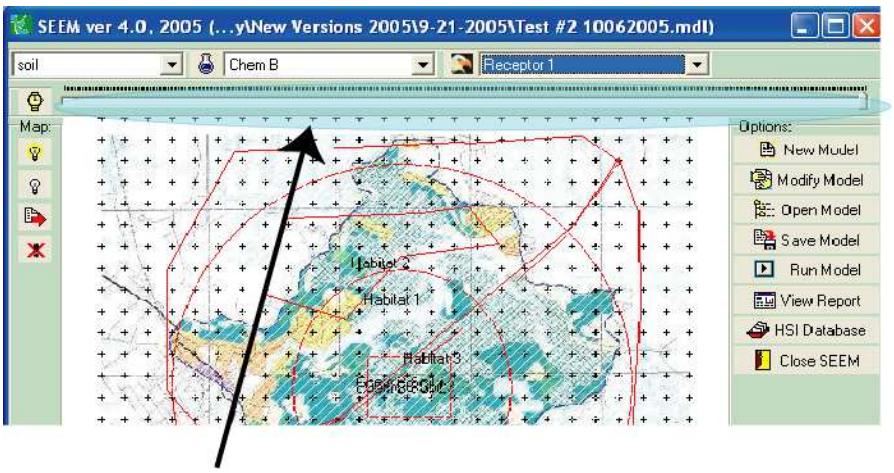


Figure 28. Model run progress bar

3.14 Data Analysis and Reporting

3.14.1 SEEM Report

SEEM provides users with a report generation option for assembling and summarizing model results. The report is generated using Microsoft Excel©. In order to generate a report, the model file/data should be run by SEEM. In the event that a user enters the required input data, but does not run the model, an informational pop-up will appear reminding the user to run the model.

Once the model has been run, click on ***View Report*** from the main Options menu. A report options window will appear (Figure 29). First, ***select the receptor*** to summarize (**1**). A report in SEEM is specific to a receptor and a chemical combination. Therefore, also choose a ***chemical*** for the report (**2**). Users may also choose the content of the report (3). A full report includes a summary of saved maps, tabular summaries, population distributions of EHQs and concentration with area curves. Inputs are generated in the report facilitating quality control reviews. Any maps saved during operation of the map-based viewer (discussed below) are generated in the Report.

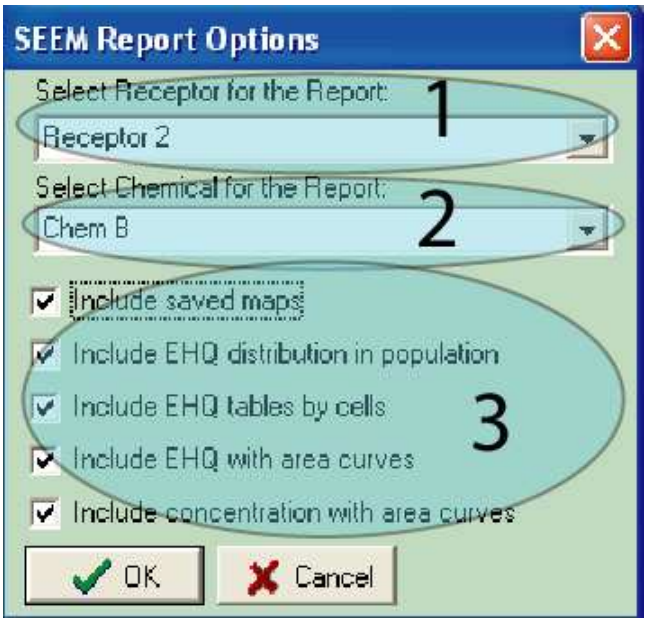


Figure 29. Report option selection

A progress bar is provided to track the progress of the report generator (Figure 30). The progress bar presents the progress by report page. The required time to complete the report generation will depend on the complexity and size of the model dataset.

When the report viewer completes report generation, Microsoft Excel will open and display the results across multiple worksheets.

A user can abort a model run by clicking .

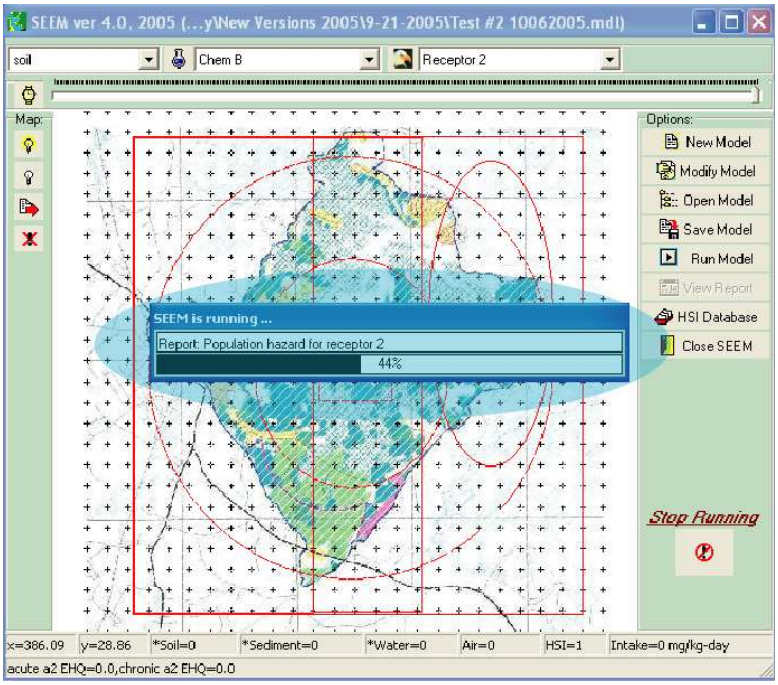


Figure 30. Report generation progress bar

3.14.2 Map-based Viewer

In addition to the SEEM report, users may also apply user-specified criteria to each of the exposure values to screen the site (Figure 31) (left-hand side of home screen). As discussed previously, SEEM translates site characteristics into a fixed grid using area-weighted averaging. The result is a landscape of cells, each with an HSI and media concentration(s). Based on these values users may enter criteria and identify cells that meet or exceed those criteria. The criteria may be applied to any of the following:

- Ecological Hazard Quotients for current recipient and chemical;
- Daily intake of current chemical;
- Concentration of current chemical; and,
- Habitat suitability index for current recipient.

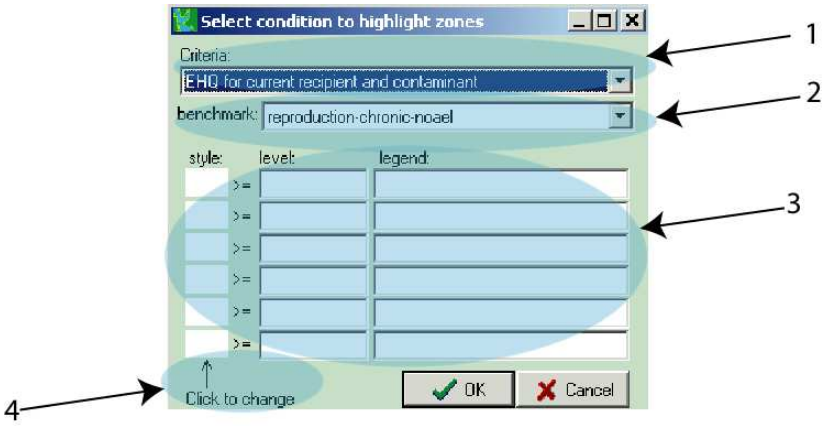


Figure 31. Conditional map based query

Users define the criteria (must be entered in increasing order) and select the input to be reviewed (Figure 32). For example, a user may select the ecological hazard quotient (EHQ) and elect to evaluate three EHQ ranges: <1, 1-2 and >2. The viewing tool will highlight the cells that meet each of these criteria in a unique way. It is important to note that the calculations evaluated in this viewing tool are independent of habitat suitability. The doses are calculated for a specific receptor based solely on the soil (sediment & water) concentrations and the prey items concentrations. Population results are presented in the Viewer only. Users may also wish to evaluate how the position of the largest EHQs compares to the position of the most suitable habitat. This tool can be employed to answer those questions. The user can run the tool for the EHQ criteria first, and then re-run the tool to evaluate HSI's on the same map. This allows a user to identify cells where an elevated EHQ is co-located with a high HSI. In addition, this tool can evaluate soil concentrations compared to soil screening values. The tool provides an important function in conjunction with the population evaluation viewers.

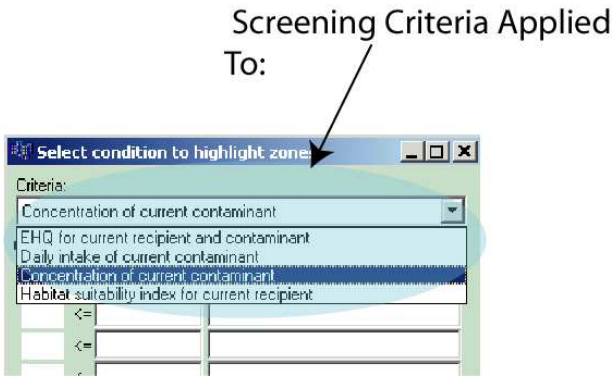


Figure 32. Screening criteria options

To access this tool, click on from the main model menu. The user is provided with a suite of options. First, select the parameter to be screened **(1)**. The criteria may be applied to the

ecological hazard quotients, the daily intake of current chemical, the concentration of the current chemical, or the habitat suitability index for the current receptor. Next, select the parameter specific entry type if applicable **(2)**. In the EHQ comparison, the user may select the benchmark underlying the EHQ calculation for the comparison and for the chemical concentration, the user may select the medium for comparison.

In the final entry area **(3)**, a user enters the actual comparative criteria in increasing order, e.g. target EHQs, HSI's, or media screening criteria (ECO Soil Screening Levels, sediment ERLs etc.). SEEM can accommodate up to six different ranges of criteria, e.g. EHQ<1, EHQ 1-5, EHQ>5, etc. For each criterion the user may enter a legend text description and select a unique shading pattern and color to distinguish each criterion from the others **(4)**. After providing all inputs, click Ok and cells that meet each criterion will be highlighted consistent with the selected format.

An example of the output of an analysis of EHQs across a landscape is provided below. In this sample dataset, the high HSI's are located in the upper left-hand corner and lower HSI's are located in the lower right-hand corner.

After running this viewer, the user may clear the screen by clicking , or the user may save the specific view/map by clicking . When saved, a map will appear in the View Report. Finally, the user can clear all saved maps by clicking .

Note also that as you run the cursor over the map grid there is a real-time display along the bottom of the model screen that summarizes cell-specific information including: cell coordinates (x,y) **(5)**, media chemical concentrations **(6)**, habitat suitability indices **(7)**, doses/intake **(8)**, and ecological hazard quotients **(9)** (Figure 33).

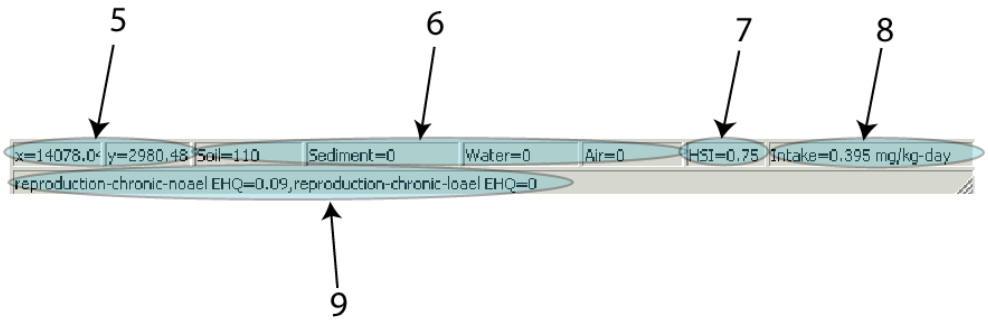


Figure 33. Status bar on model home screen

3.14.3 SEEM Data Output/Figures

SEEM generates three primary types of figures:

SEEM Output: Concentration with Area Curves (OUT_Area_____)

SEEM Output: Ecological Hazard Quotient with Area Curves (OUT__EHQ_Area____)

SEEM Output - Population_Plots _(OUT_Popul_Plot____)

<u>SEEM Output: Concentration with Area Curves (OUT_Area_____)</u>

The area with concentration curve provides users with a view of the data in terms of geographic cover (Figure 34). The figure is developed by ranking the concentration data from high to low and then sequentially averaging each point/group with the next. The result provides the user with information regarding the coverage of concentrations that may be problematic to wildlife. While the figure does not examine concentrations that are next to one another necessarily, the data do provide users with a sense of the geographic scale of the different concentrations.

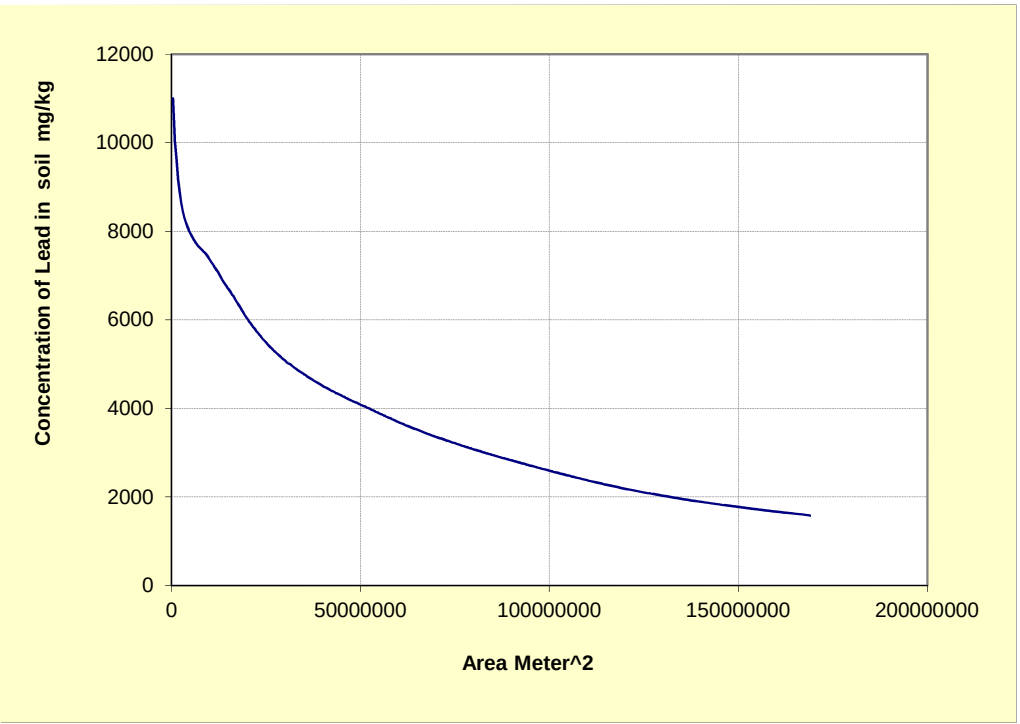


Figure 34. Example of an Area v Concentration Curve (OUT_Area_____)

In some cases the remedial requirements may be specified by the areal coverage of a concentration greater than a specified value (Figure 35). An example is provided below:

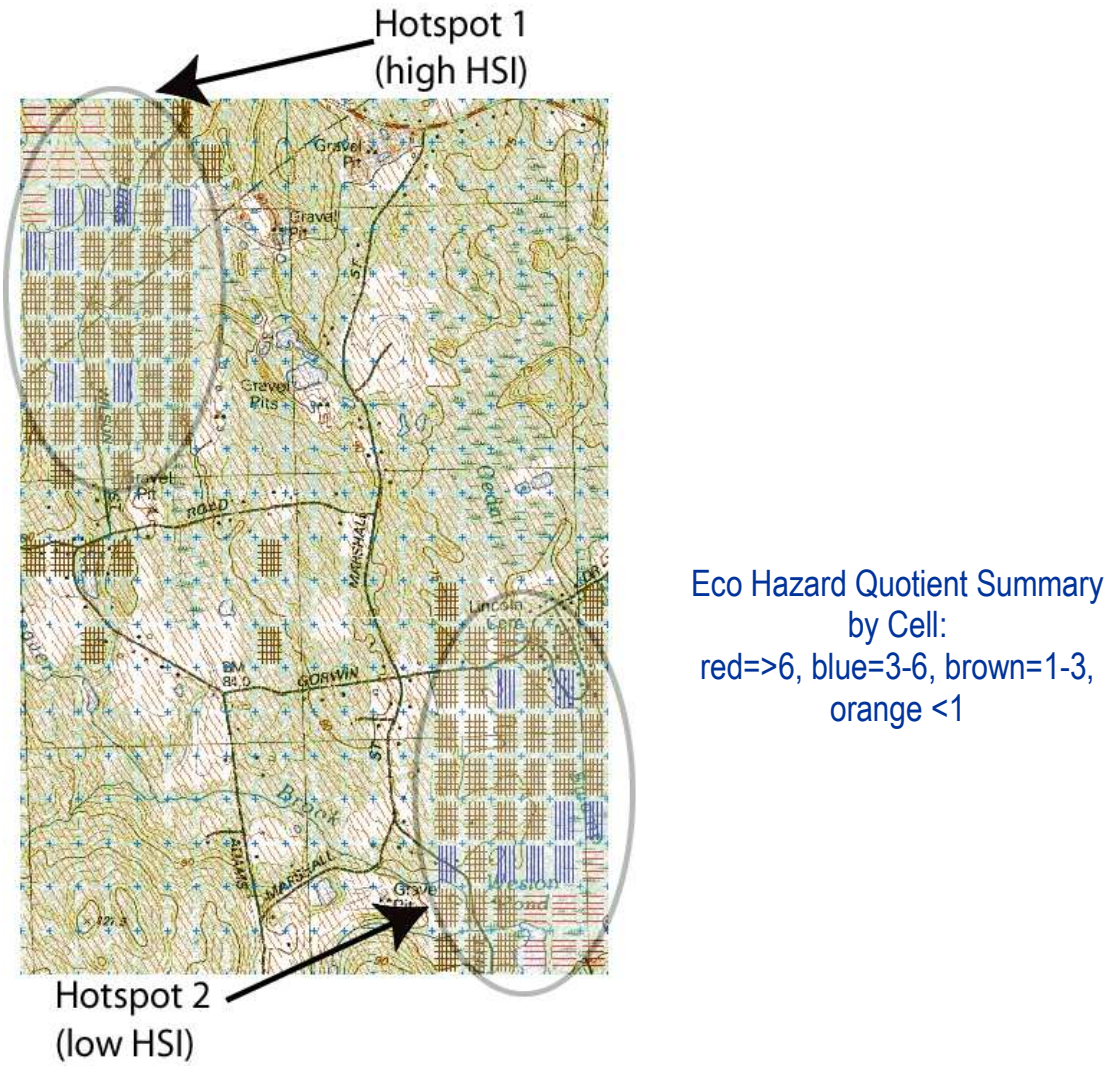


Figure 35. Example of map output specifying screening criteria exceedances

SEEM Output: Ecological Hazard Quotient with Area Curves (OUT__EHQ_Area____)

Another output figure is the EHQ versus Area Curve (Figure 36). An example of this output is:

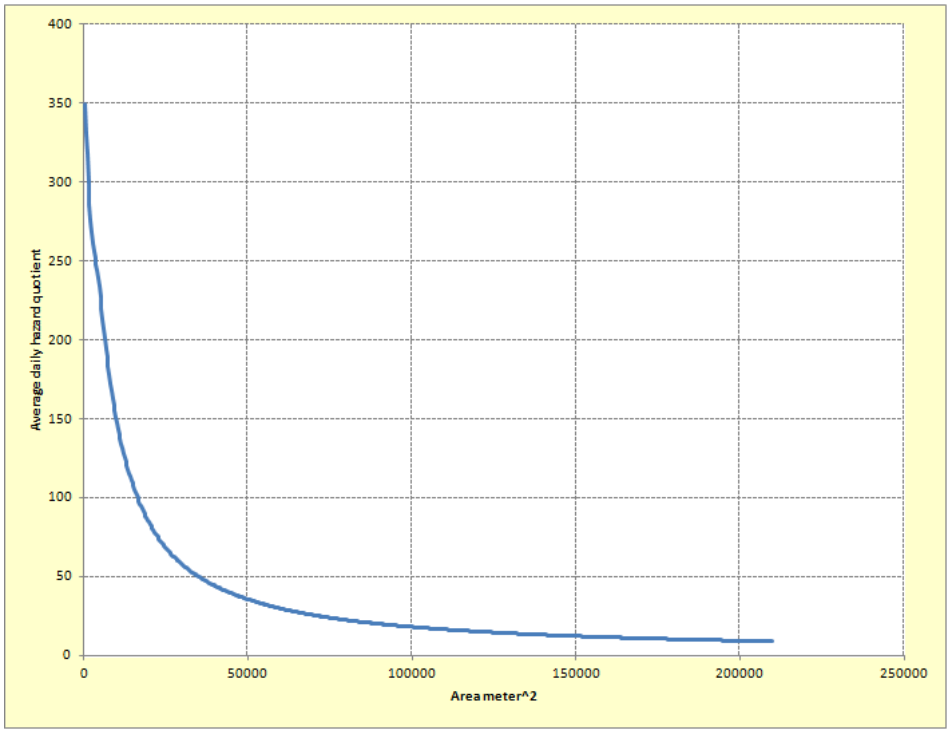


Figure 36. Example of an Area v EHQ Curve (OUT_Area_EHQ_____)

SEEM Output - Population_Plots _(OUT_Popul_Plot____)

The primary summary figure for SEEM is the population – Environmental Hazard Quotient curve (Figures 37a and 37b). It includes a summary of maximal and average exposures for the toxicity reference values entered. These curves summarize the exposure of all of the individuals in the modeled population. Two examples of the population – EHQ curves are provided below. In one example a species employs the random walk foraging strategy, while in the other example the species forages from a nest.

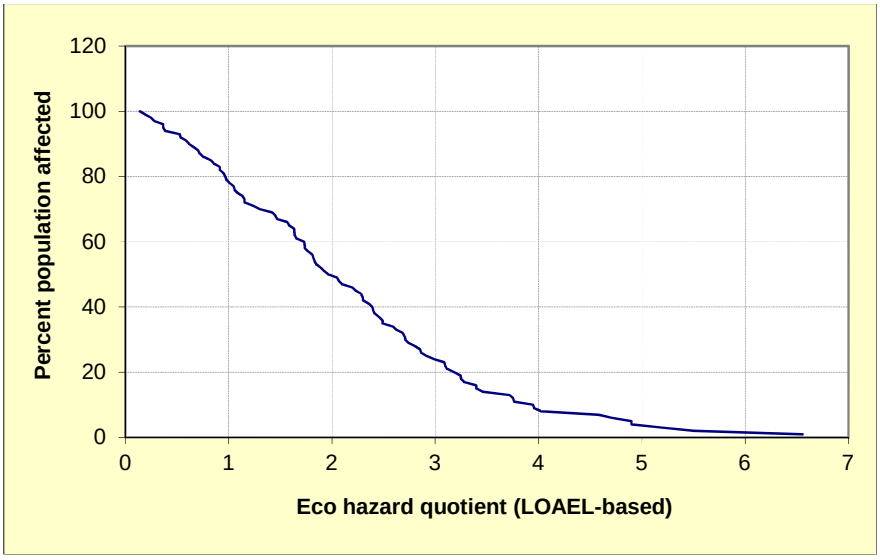


Figure 37a. Example Output - Baseline – Random Walk

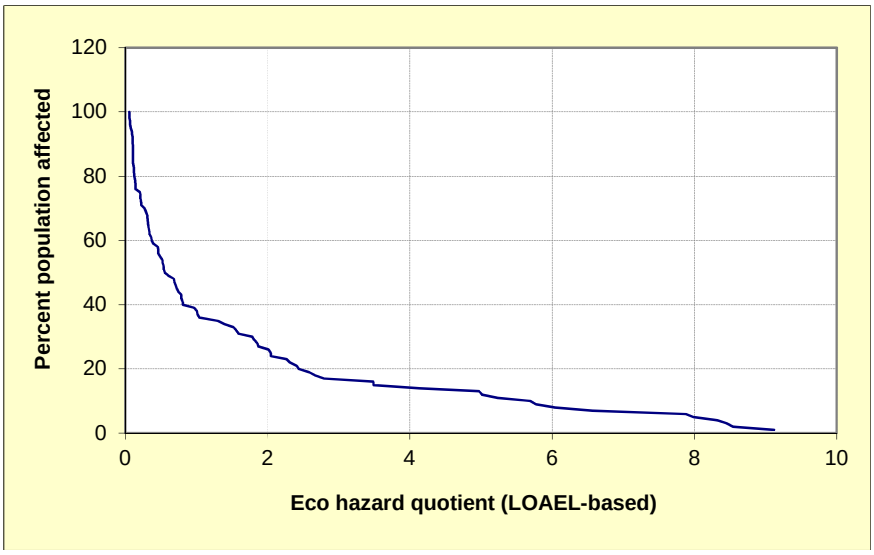


Figure 37b. Example Output - Baseline – nesting/local

4 UNCERTAINTY

General Uncertainties

As is the case with any model, simplifying assumptions are employed. SEEM is designed to answer large questions regarding the interaction of wildlife with chemicals accounting for habitat preferences across a landscape. As Stephens and Krebs (1986) describe, foraging behaviors are extremely complex and may involve the interaction of energy expended, energy gained, availability of prey, behaviors such as search versus stay in different area and discrimination among prey items. SEEM cannot capture all of the complexities of biological activities. However, working with the model, users can begin to explore more of the complexities in foraging behavior. For example, varying the number of foraging events per day could be used to examine different levels of effort in combination with variable HSI's. The magnitude of the foraging radius might also be used as a surrogate for effort – the larger the radius the greater the area over which a receptor must forage. While SEEM does not incorporate a direct assessment of caloric needs, quitting rates and energy cost-benefit analysis for different prey items, modification of the available inputs can allow modelers to ask and begin to answer questions beyond the basic exposure analysis.

The original design of SEEM was based on a fixed grid of cells. The current version retains this grid for internal calculations, however users may draw polygons to characterize the chemistry and habitat suitability of the study area. As noted previously in this Manual, the polygon data are translated into the intersected cells using area weighted averaging of all polygons that intersect a given cell. The result visually is that some foraging areas appear to fall outside of the study area (map) when the foraging areas are visualized. Figure 38 below highlights this issue.

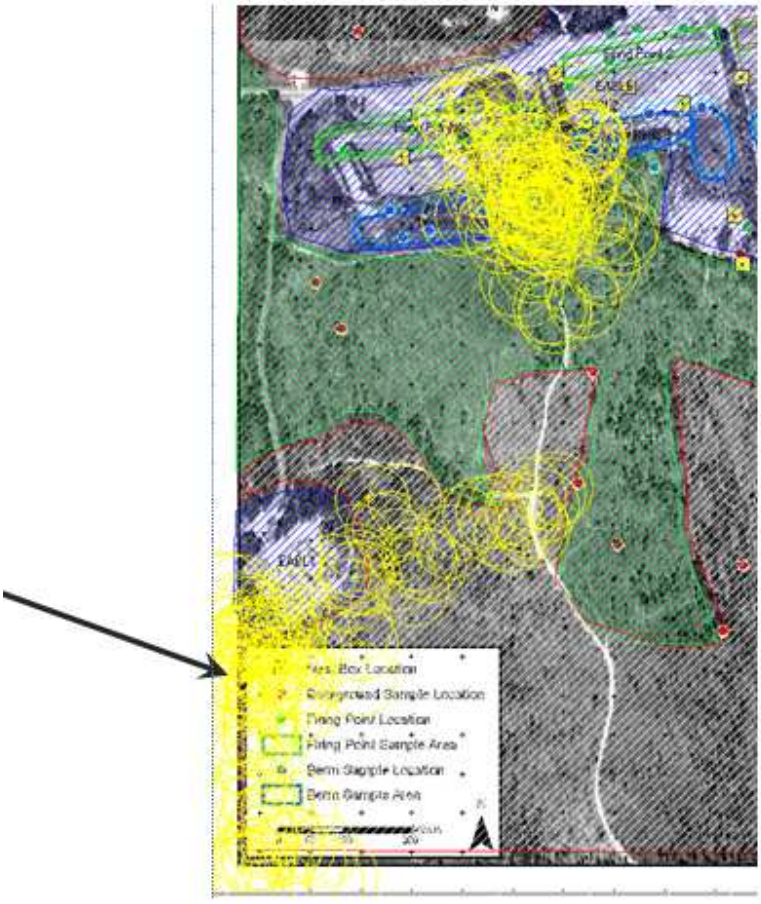


Figure 38. Example of potential uncertainty in image processing

The arrow points at foraging areas that extend beyond the base map. This is because the base map include a boundary beyond the image and because the polygon data are averaged to give values to the grid cells below. The grid boundary is at the edge of the image – in this case a white border. To avoid this issue, the image should be imported without a boundary. Receptors may forage in any grid cell with a habitat suitability greater than 0.

<u>Version 4.2.1 Notes</u>

With each subsequent version of SEEM, SEEM standalone becomes more stable and more user friendly. However, some issues remain and new issues may arise as the platforms are updated and the model is used more often. We are aware of a few issues that remain in the latest version. We are in the process of transitioning to a GIS-based platform for the model. The standalone version works well, but the GIS platform will increase the power of the model and allow for greater spatial integration.

The issues that we are aware of include:

a. Map Geometry. For certain base maps the values of the top row of CC and HSI grid cells are calculated incorrectly. They are off by about 4% from what they should be. The issue is due to the specifications of the image file imported. The problem arises when a user selects an image file that scales to non-integer length and width. SEEM doesn't currently correct for this issue. This issue is fixed by using a base map which is drawn to proper scale with integer values for the North-South and East-West dimensions. For example, this error occurs one model because the map length in North-South is 1510 meters, but the length in East-West is 1166.81818181818. If the user selected a 1500×1200 meter map there would not be an issue. We suggest that users import proper orthophotos from say USGS or Pictometry which have a pixel size of exactly 10 meters. This will eliminate this issue.

b. The minimize button does not work.

c. If a user adds two new receptors in step 4, but then goes back and renames the first receptor added, SEEM will crash. The workaround if a receptor requires renaming is to go to the next step, then go back.

d. SEEM occasionally crashes with an "OLE error" when generating reports. This seems to occur with newer versions of Excel and when a user is doing anything in the Excel window while the report is being written. The workaround is to just leave SEEM/Excel alone until the report is finished generating.

e. SEEM occasionally becomes unstable (though doesn't entirely crash) after drawing polygons and saving changes. Error message is "External Exception." Changes are not saved and the polygon drawing tool no longer works until the program is restarted. Seems to occur when a user draws one polygon, draws another which may nearly overlap, then goes back and selects the previous polygon to make changes such as name, color, etc. The error is very intermittent. Restarting the model resolves this issue.

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APPENDIX A

CREATING A NEW HSI CALCULATOR RECORD

CREATING A NEW HSI CALCULATOR RECORD

The development of HSIs is a time-consuming process requiring the assembly of experts on a particular species to reach consensus about the habitat features most important to that species. For users wishing to add HSI equations to the database, general guidance on the process is provided below. Also, working with an existing HSI and modifying the equation as necessary will provide users with a starting point.

When constructing an HSI equation and defining the variables, editorial functions are available. These may be accessed by pressing the right mouse button when the target text is highlighted. Choose "Edit" to initiate the editor from which additional options may be accessed such as different fonts, styles and colors. Each equation must be finished with a semicolon ";". There are three types of variables in an HSI equation. They include: the definition of an input variable, the definition of a calculating variable and the definition of a lookup variable. Each are introduced below.

A. Definition of "Input variable" i.e. a variable representing a characteristic of the habitat – the input is a simple numeric value. The input variable is defined as:

Variable :: "Extended Comment on the Variable" = Value;

The "Variable" refers to a name which will be used in an equation verbatim (e.g. V2, V3), whereas the "Extended comment on the Variable" is any string of text enclosed within "" that defines the variable, e.g., description, units. The extended comment is not required to complete an equation, however a variable and a value are: Variable = Value;

B. Definition of "Calculating variable" i.e. a value that is the result of a mathematical equation/expression – the input variables are used to calculate a 'calculating variable'. The calculating variable is defined as:

Variable :: "Extended Comment on the Variable" = Expression; Or
Variable = Expression;

This variable is analogous to the simple input variable, but a mathematical expression is used instead of simple value. Any previously defined variable can be used in the expression. Example:

```
A=2;
B=2;
C=(A*B)^0.5;
```

As the result of this script C=2 (if we replace "C=(A*B)^0.5" with "C=SQRT(A*B)" the result will be the same)

C. Definition of "Lookup Variable", i.e. a categorical variable defined by a selection of multiple choice options. The lookup variable is defined as:

```
Variable :: "Extended Comment on the Variable" =
  ? "Option 1" = Value1
  ? "Option 2" = Value2
  …
  ? "Last Option" = Last_Value;
```

In this case, "Value1",…"Last_Value" are simple numbers like 3.14, 1e10 etc. "Option 1", "Option 2", etc. are descriptions of the value to assist the user in value selection. This text appears in the SEEM pull-down menu. When a user chooses, an "Option" a corresponding value will be applied in the model. For example,

A=? "choice 1" = 1 ? "choice 2" = 2 ? "choice 3"=3;
B=A+3;

If the user selects "choice 2" from the corresponding combo box in the SEEM interface, the value of variable A becomes 2, and B then =5. This example also demonstrates that extended descriptions/comments for variables and using separate lines for each option is not necessary.

Reviewing New Programming

There are 3 Tabs in the HSI calculation dialog: "Equations", "Input Variables" and "Calculated Variables". Move through each tab to confirm that the programming is functioning correctly.

When a change is made in the script, those scripts should be automatically interpreted and all variables should be recalculated. All calculations are repeated automatically also when a value is changed on the "Input Variables" page of the tabbed dialog. If a script has mistakes, error messages will be generated.

APPENDIX B

SEEM XL UTILITY – USER'S GUIDE

Microsoft© Excel© Data Utility

In the latest release of SEEM, programmers added a Microsoft© Excel© data utility (SEEMXL). The utility was added to serve the following purposes:

Provide easy access to input data through the commonly used spreadsheet program Excel;

Allow users to cut and paste chemical data and habitat suitability indices into the model file;

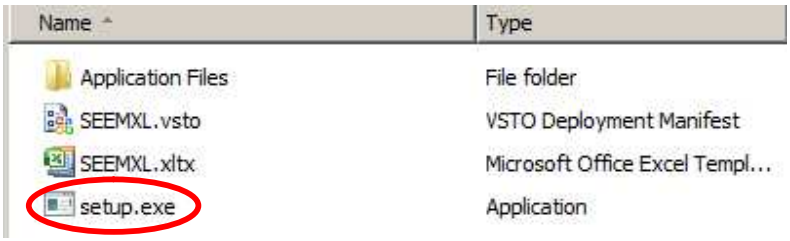
Facilitate data quality control reviews; and,

Increase the efficiency of changing select input parameters in order to evaluate model sensitivity and variability.

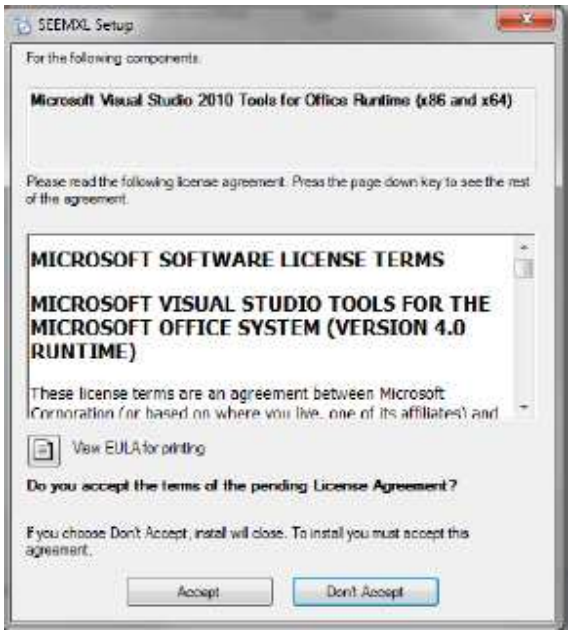
Within Excel, users can modify existing SEEM model files. SEEM remains the primary model development vehicle, while the Excel tool only operates on existing SEEM files.

Setup

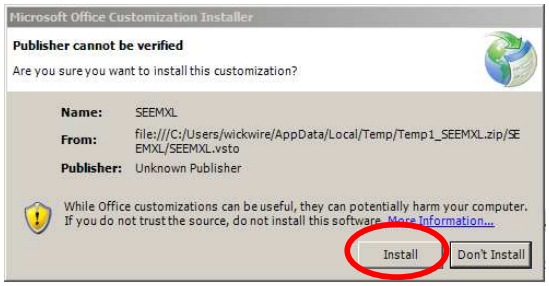
The SEEMXL data utility is distributed in a .zip file. After extracting the zip file, the user clicks on the setup.exe file to initiate installation.



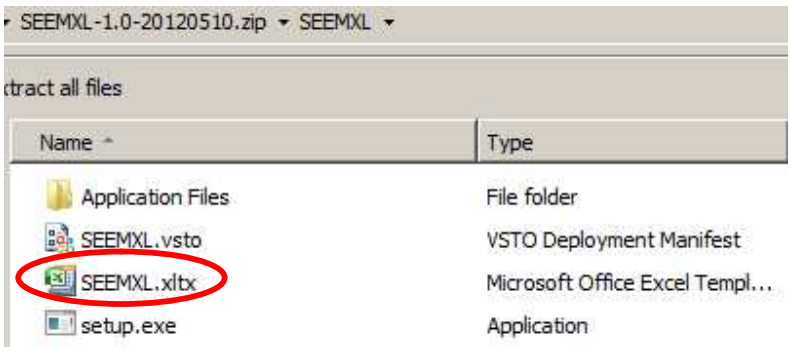
If not already installed, a window may appear for the EULA for Microsoft Visual Studio 2010 Tools for Office Runtime, click Accept.



After this installation, the computer will require a reboot and SEEMXL installation will resume automatically. Because the utility has been custom developed for use with SEEM, the software is not publisher verified and an installation warning may appear – see below. To continue to install the utility, click Install.



Once installed, the program is accessed by returning to the original program folder and clicking on SEEMXL.XLTX to open the utility.



Application of Utility

SEEMXL operates in the same way as an Excel Workbook; standard Excel functionality[27] is accessible when working on a SEEM model file The one exception is a new tab under which the user will find an Import, Export and Saving toolbar specific to the Utility. The utility does not interact directly with SEEM but serves as an interface between the SEEM modeling file (.MDL file) and Excel functionality. Although the Excel file itself can be saved, the primary model file is the .MDL file. Excel files are not compatible with SEEM directly. The utility converts an existing .MDL file generated in SEEM, into an Excel file allowing editing of certain inputs and once editing is completed, the utility will re-convert the Excel file back to an .MDL file for direct use in the SEEM model. The utility will not work on .MDL files with grid site area.

The steps involved in using the SEEM Utility include:

1) Create a new model file within the SEEM Program or locate an MDL file created during a previous session of SEEM modeling.

2) Open the SEEM Utility. At this step there are two options. (1) The most common will be to import an active MDL file for review and editing. To import an MDL, click Import MDL, locate the file and click Open. Data from the MDL will populate the nine worksheets. (2) In some cases, a user may have started the review of an existing MDL, saved the Excel file and returned to complete the review at a later time. In this case the user would open the Excel file and continue to edit and review. To import an MDL, click Import MDL, locate the file and click Open. Data from the MDL will populate the nine worksheets.

3) There are ten worksheets in the SEEM utility. They generally mirror the guided input steps in SEEM. Review of the actual drawn polygons or modification of the polygons is not possible within this utility. Editing of polygon locations, number and names occurs within the SEEM model. Within each worksheet, a subset of the entered data may be modified. Column headers in red indicate data that may be changed in the tool. The tool also does not run SEEM. The focus is on displaying the data in an easy to review format and allowing editing of variable, key input data. Users cannot add rows to any worksheet. One of the key functions in the SEEM tab is 'SAVE changes' a user must save changes (to the MDL – saving to an Excel file works the same way as any Excel saving function) in order to Export those changes back to SEEM.

[27] User's must have Excel installed on the machine used for SEEM Modeling.

4) The **Model** worksheet presents background data on the file and model run. There are no inputs that can be modified in the SEEM utility on this worksheet.

5) On the **Seasons** worksheet, users may modify the number of days in each season. In order to modify the names of the seasons and number of seasons, users will need to return to SEEM.

	B	C
1	Name	Days
2	Winter	92
3	Spring	91
4	Summer	91
5	Autumn	91

6) The **Chemicals** worksheet cannot be modified in the Excel utility.

	B	C
1	Name	CAS
2	Lead	7439-92-1

7) The **Food Items** worksheet summarizes the names of food items, the chemicals applicable to each, tissue concentration and medium concentration and a bioaccumulation factor (BAF). The tissue concentration, medium concentration and BAF may all be modified in the Excel utility. Note that when a tissue concentration and medium concentration are entered a BAF will automatically be calculated, over-writing any BAF entered previously.

	C	D	E	F	G	H
1	Name	Chemical	CAS	TissueConcentration	MediumConcentration	BAF
2	plants	Lead	7439-92-1	0	0	0.0388
3	insects	Lead	7439-92-1	0	0	23.8301
4	earthworms	Lead	7439-92-1	0	0	3.342

8) The **Receptors** worksheet summarizes the movement inputs specific to each receptor assessed in the study. The user may modify the population size, migration type and foraging distance. There are two migration types available to SEEM users – the options can be selected using a drop-down box for each receptor.

	B	C	D	E	F	G
1	Name	PopulationSize	MigrationType	ForagingDistance	TerrestrialHabitat	WaterHabitat
2	Vole	10000	free ranging foraging	16	TRUE	FALSE
3	Shrew	10000	free ranging foraging	35	TRUE	FALSE
4	Mouse	100	free ranging foraging	20	TRUE	FALSE

9) The **Diet** worksheet specifies the diet items by each receptor, the ingestion rate specific to the receptor and diet item and the percent of each type of diet item in the diet of each receptor. The ingestion rate and diet proportion may be changed in the Excel Utility. For the more complex changes involving seasonal-specific values, please initiate these changes within the SEEM guided input in the primary model.

	D	E	F	G	H
1	Receptor	DietItem	IngestionRate	Season	DietProportion
2	Vole	plants	0.17	Winter	1
3	Vole	plants	0.17	Spring	1
4	Vole	plants	0.17	Summer	1
5	Vole	plants	0.17	Autumn	1
6	Vole	soil	0.00408	Winter	1
7	Vole	soil	0.00408	Spring	1
8	Vole	soil	0.00408	Summer	1
9	Vole	soil	0.00408	Autumn	1

10) The **Migration** worksheet captures an advanced modeling feature accessed within the model from the Diet guided input tab. A user can modify the insite probability from the Utility Tool. Outsite probability is automatically calculated when the user saves changes.

	C	D	E	F
1	Receptor	Season	InsiteProbability	OutsiteProbability
2	Vole	Winter	1	0
3	Vole	Spring	1	0
4	Vole	Summer	1	0
5	Vole	Autumn	1	0
6	Shrew	Winter	1	0
7	Shrew	Spring	1	0
8	Shrew	Summer	1	0
9	Shrew	Autumn	1	0

11) The **Benchmarks** worksheet summarizes the benchmarks selected for use in the model. Users may modify the benchmark name and the actual benchmark value by receptor and chemical combination.

	D	E	F	G	H
1	Receptor	Benchmark	Chemical	CAS	TRV
2	Vole	NOAEL	Lead	7439-92-1	4.7
3	Vole	LOAEL	Lead	7439-92-1	40.7
4	Shrew	NOAEL	Lead	7439-92-1	4.7
5	Shrew	LOAEL	Lead	7439-92-1	40.7
6	Mouse	NOAEL	Lead	7439-92-1	4.7
7	Mouse	LOAEL	Lead	7439-92-1	40.7

12) The **Habitat Polygons** worksheet displays the polygon-specific data related to habitat suitability. The SEEM Utility does not facilitate modification of the actual drawn polygons, but allows users to modify the name and habitat suitability index (HSI) value for existing polygons. Names of polygons must be unique. To add or remove polygons, users should return to the drawing tool within the program's guided input.

	E	F	G	H	I	J
1	Layer	SubLayer	Site	SiteData	HabitatPolygonName	HSI
2	sediment	Habitat Suitability	Shrew	1	Nonriverine Swamp and Wet Hardwo	1
3	sediment	Habitat Suitability	Shrew	1	Distrubed/Successional Shrub Regen	1
4	sediment	Habitat Suitability	Shrew	1	Developed Low Intensity	1
5	sediment	Habitat Suitability	Shrew	1	Evergreen Plantation or Managed Pine	1
6	sediment	Habitat Suitability	Shrew	1	Road	1
7	sediment	Habitat Suitability	Shrew	1	Evergreen Plantation or Managed Pine	1
8	sediment	Habitat Suitability	Shrew	1	Dry and Dry Mesic Oak Forest	1
9	sediment	Habitat Suitability	Shrew	1	Dry and Dry Mesic Oak Forest	1
10	sediment	Habitat Suitability	Shrew	1	Road	1
11	sediment	Habitat Suitability	Shrew	1	Evergreen Plantation or Managed Pine	1
12	sediment	Habitat Suitability	Shrew	1	Developed Open Space	1
13	sediment	Habitat Suitability	Shrew	1	Dry and Dry Mesic Oak Forest	1
14	sediment	Habitat Suitability	Shrew	1	Small Backwater River Floodplain Fore	1
15	sediment	Habitat Suitability	Shrew	1	Evergreen Plantation or Managed Pine	1
16	sediment	Habitat Suitability	Shrew	1	Small Backwater River Floodplain Fore	1
17	sediment	Habitat Suitability	Shrew	1	Dry and Dry Mesic Oak Forest	1

13) The last worksheet in the SEEM Utility Tool focuses on the **Chemical Polygons** concentrations. Consistent with the habitat worksheet, the SEEM Utility does not facilitate modification of the actual drawn chemical polygons, but allows users to modify the name, chemical concentrations and bioavailability adjustment factor for existing polygons. Names of polygons must be unique. To add or remove polygons, users should return to the drawing tool within the program's guided input.

	E	F	G	H	I	J	K	L
1	Layer	SubLayer	Site	SiteData	SiteAdjFactor	ChemicalPolygonName	ChemicalConcentration	BioavailabilityAdjustment
2	soil	Chemical Concentrations	Lead	270	1	0-25 Percentile	270	1
3	soil	Chemical Concentrations	Lead	270	1	25-50 Percentile	1200	1
4	soil	Chemical Concentrations	Lead	270	1	50-75 Percentile	3000	1
5	soil	Chemical Concentrations	Lead	270	1	75-95 Percentile	20000	1
6	soil	Chemical Concentrations	Lead	270	1	95-100 Percentile	130000	1

For advanced GIS users, a standalone SEEM GIS Integration tool is available upon request. Because it requires GIS software and knowledge of GIS functionality, it is not distributed with the primary software and Excel Utility.

14) Upon completion of all changes, click **save changes** in the SEEM tab and then click **export mdl**. Users can either create a new mdl file (recommended) or save over the original file.

APPENDIX C

REVIEWER REPORTING FORM

SEEM REVIEW REPORTING FORM

DATE:	
NAME:	
ORGANIZATION:	
EMAIL ADDRESS:	
SEEM VERSION NUMBER & DATE:	

ERROR REPORTING		
ERROR ID	**DESCRIPTION**	**LOCATION OR OCCURRED WHEN**

SUGGESTIONS

PLEASE RETURN TO:
Exponent, Attn: Ted Wickwire, 1 Clock Tower Place, Suite 150, Maynard, MA 01754 **or** Fax to: (978) 461-4699 OR Email: wickwire@exponent.com