

US EPA ARCHIVE DOCUMENT

DATA COLLECTION FOR THE HAZARDOUS WASTE IDENTIFICATION RULE

SECTION 13.0 ECOLOGICAL RECEPTORS AND HABITATS

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Under Contract No. 68-W-98-085

U.S. Environmental Protection Agency
Office of Solid Waste
Washington, DC 20460

October 1999

ACKNOWLEDGMENTS

A number of individuals have been involved with the collection of ecological receptor and habitat data. David Cozzie and Stephen Kroner of the U.S. Environmental Protection Agency (EPA), Office of Solid Waste (OSW), provided overall technical direction and review throughout this work.

Steve Beaulieu of Research Triangle Institute (RTI) was the task leader for this work. He developed the methodology for the collection of ecological receptor and habitat data. Other RTI staff members who contributed to this report include: Aimée Harmon, Joan McLean, and Andrea Thomas; Jerry Conrad, who developed GIS methodologies; Linda Andrews, who processed the data; Kathy Restivo, who performed the editorial review; and Sharon Pressley, who provided publication support.

DISCLAIMER

The work presented in this document has been funded by the U.S. EPA. Mention of trade names or commercial products does not constitute endorsement or recommendation for use by the Agency.

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13.0 Ecological Receptors and Habitats

The Hazardous Waste Identification Rule 1995 (HWIR95) proposed ecological risk assessment procedures that included separate assessment modules for terrestrial and aquatic sites. During the HWIR95 review and comment period, one of the significant issues raised about these modules was the need to include a variety of terrestrial and aquatic habitats that would reflect the natural variation of the sites being assessed. Thus, in the final HWIR modeling system, the ecological exposure module assesses exposure in 14 different terrestrial habitats, including upland, wetland, and waterbody margin habitats, and 8 different aquatic habitats, including cold and warm water streams, lakes, ponds, and wetlands. These habitats cover all types of ecosystems except those associated with estuarine and marine waters, which are explicitly excluded from the HWIR analysis.

Table 13-1 lists the variables collected and passed to the HWIR modeling system to describe terrestrial habitats and receptors across the 201 HWIR sites. Data collection methods are briefly summarized in this table along with the section which discusses the corresponding methodology in detail. To document collection of these variables, Section 13.1 describes the development of and rationale for the 14 representative terrestrial habitats; Section 13.2 describes the development of food webs and the selection of receptor species for each habitat; Section 13.3 explains the delineation of habitats at each site using the HWIR geographic information system (GIS); Section 13.4 describes the placement of receptor home ranges; and Section 13.5 describes the GIS programs and database processing necessary to export the variables shown in Table 13.1 to the HWIR modeling system. The aquatic habitats are described in Section 11.0, "Aquatic Food Web Data Collection," and in the Aquatic Food Web Module documentation.

13.1 Development of Representative Terrestrial Habitats

The representative habitats are defined for each site by the following site layout file inputs to the ecological exposure module: HabGroup, which indicates whether a habitat type is terrestrial, aquatic, or wetland; HabType, a string variable that gives the descriptive name of the habitat; and HabIndex, which assigns an index number to each habitat type.

The concept of habitat was chosen as the appropriate level of differentiation for the spatial element of the ecological risk assessments. In this context, the term habitat implies a level of detail and specificity that is meaningful for the exposure scenario at a particular facility site, but does not require extensive biological inventory or field investigation for identification or delineation.

The terrestrial habitats address areas inhabited by land-based receptors. In addition to land-based mammals, birds, and herpetofauna, these receptors include some species that spend

Table 13-1. Parameters Collected

Code	Description	Units	Section
HabGroup	group in which habitat type is attributed: 1 = terrestrial, 2 = aquatic, 3 = wetland	not applicable	13.1.4
HabIndex	index of habitat type	unitless	13.1.4
HabNumRange	number of ranges per habitat	unitless	13.5.2
HabRangeRecIndex	receptor index associated with each home range (a single receptor)	unitless	13.5.1
HabRangeRecType	type of receptor (e.g., herbivert, omnivert, small mammal, small bird)	not applicable	13.5.1
HabType	type of representative habitat (e.g., grassland, pond, wetland)	not applicable	13.1.4
NumEcoRing	number of eco rings	unitless	13.3.2
NumHabGroup	number of general groups into which habitat types are placed	unitless	13.1.
NumReceptor	complete receptor list across all habitat types	unitless	13.2.2
NumTrophicLevel	number of possible trophic levels	unitless	13.2.1
ReceptorIndex	indices assigned to each receptor	unitless	13.2.2
RecTrophicLevel	trophic level into which each receptor falls	not applicable	13.2.1
GIS - Based Parameters			
EcoRingHabIndex	index of habitat contained within ecoring (1 = 0 - 1km; 2 = 1 - 2 km)	unitless	13.5.2
EcoRingNumHab	number of habitats contained within each eco ring	unitless	13.5.2
HabArea	area of habitat	m ²	13.5.2
HabNumWBNRch	number of WBN reaches that impact habitat range	unitless	13.5.2
HabRangeAreaFrac	fraction of range that falls within habitat	fraction	13.5.2
HabRangeFishWBNIndex	index of WBN containing fishable reaches that impact habitat range	unitless	13.5.2
HabRangeLWSIndex	local watershed indices associated with each habitat range	unitless	13.5.2
HabRangeLWSSubAFrac	fraction of contributing LWS subarea	fraction	13.5.2
HabRangeLWSSubAIndex	index of contributing subarea in local watershed indices associated with each habitat range	unitless	13.5.2

(continued)

Table 13-1. (continued)

Code	Description	Units	Section
HabRangeNumLWSSubA	contributing subarea in local watershed indices associated with each habitat range	unitless	13.5.2
HabRangeNumSISrc	number of surface impoundments that intersect habitat range	unitless	13.5.2
HabRangeNumWBNRch	number of WBN reaches found within habitat range	unitless	13.5.2
HabRangeNumWSSub	number of watersheds that impact habitat range	unitless	13.5.2
HabRangeWBNIndex	index of WBN that impacts habitat range	unitless	13.5.2
HabRangeWBNRchIndex	index of WBN reaches that impact habitat range	unitless	13.5.2
HabRangeWSSubFrac	fraction of habitat range impacted by watershed	fraction	13.5.2
HabRangeWSSubIndex	index of watershed that impacts habitat range	unitless	13.5.2
HabWBNIndex	index of WBN that impacts habitat range	unitless	13.5.2
HabWBNRchFrac	fraction of habitat range impacted by aquatic	fraction	13.5.2
HabWBNRchIndex	index of WBN reaches that impact habitat	unitless	13.5.2
HRangeFishWBNRchInde	index of WBN fishable reaches that impact habitat range	unitless	13.5.2
HRangeNumFishWBNRch	number of fishable reaches that cross habitat range	unitless	13.5.2
NumHab	number of habitats selected for site simulation	unitless	13.5.2
NumHabType	number of habitat types represented at the site	unitless	13.5.2

significant time in the water, such as the bullfrog or the snapping turtle, and some that derive all or most of their food from the water, such as the osprey or the muskrat. Based on these species' biology and potential routes of exposure, they are more appropriately assessed as terrestrial receptors than as aquatic receptors. In order to assess their exposure, however, the aquatic element of their habitat must be included; therefore, the 14 terrestrial habitats include waterbody margin habitats such as stream corridors and pond margins. A discussion of aquatic receptor species and their habitats (e.g., fish and benthic organisms living in streams, lakes, or ponds) is presented in Section 11.0 of the data collection documentation and Section 11.0 of the module documentation.

13.1.1 Goals for Development of Representative Habitats

The primary goal for development of ecological risk assessment habitats is to provide a framework for incorporating characteristics of site location into the assessment methodology. The biological and ecological characteristics of site location (i.e., the habitat) determine the organisms likely to be present and affect the potential mechanisms for exposure to constituents of potential ecological concern (CPEC). Therefore, consideration of site habitat enhances the

effectiveness of the risk assessment. The representative habitats should be general enough to encompass all potential habitats in the United States because the sites included in the assessment are distributed throughout the continental United States (CONUS). Although currently existing facilities probably occur in a limited number of habitat types, this approach allows the representative habitats to be applied in the future and potentially to other populations of sources.

Second, the representative habitats act as a composite reflection of site-specific spatial data for each HWIR site. The GIS includes several layers of site data that affect exposure, such as land use, cover type, elevation, and surface waterbodies; the representative habitats effectively combine these data layers and make a statement about the receptors and exposure scenarios likely to occur there. Therefore, the habitats should be compatible with available GIS data.

Third, the level of refinement or degree of detail delimiting the habitats should be consistent with data availability and selected endpoints. For the HWIR analysis, the selected endpoints are survival of receptor species populations. Accordingly, habitats should be distinguished at a level that affects receptor species' exposure and, in particular, at a level that affects the species included in the analysis. The HWIR receptor species are those for which sufficient exposure factor, uptake, and benchmark data are available; therefore, habitat characteristics that determine these species' presence or absence at a site should form the basis of the habitat classification. For example, differentiating between coniferous and deciduous forests was considered, but based on the available receptor species, these two habitats would both include the same or similar receptors. Furthermore, available plant uptake factors do not distinguish between coniferous and deciduous forest species. No benefit would be derived from describing separate coniferous and deciduous forest habitats; thus, a single forest habitat was included.

13.1.2 Criteria for Defining Representative Habitats

Based on these goals, classification criteria were established for defining the representative habitats. The criteria for delimiting representative habitats should consist of parameters that determine or affect the occurrence of receptor species. In general, habitat affects which species are present at a site by providing essential resources such as food, shelter, nesting sites or materials, and appropriate sites for behaviors such as courtship, mating, roosting, or hibernation. Therefore, criteria that describe the physical setting in terms of these resources were chosen. The criteria developed for the representative habitats were based on a survey of existing ecological classifications (Bailey, 1996; Bourgeron and Engelking, 1994; Cowardin et al., 1979; Davis and Simon, 1995; Demarchi, 1996; Drake and Faber-Langendoen, 1997; Federal Geographic Data Committee, 1997; Kuchler, 1964; Omernik, 1987; Sawyer and Keeler-Wolf, 1995; Shafale and Weakley, 1990; U.S. Department of Agriculture [USDA] Forest Service, 1994; U.S. Fish and Wildlife Service [FWS], 1998a; Viereck and Elbert, 1991; Weakley et al., 1998; Whitney, 1985).

13.1.2.1 Criteria for Terrestrial and Wetland Habitats. The primary criteria for terrestrial and wetland habitats are soil moisture and vegetation structure. Soil moisture, or degree of saturation, affects soil chemistry, general vegetation structure, and habitat suitability. Soil moisture is differentiated based on the three following categories:

- # terrestrial–well-aerated, nonsaturated soils;
- # intermittently flooded–periodically saturated or inundated but aerated for some periods during the growing season; and
- # permanently flooded–saturated or inundated throughout most years.

Vegetation structure refers to the stature, spacing, and relative stem size of the dominant vegetation. It describes the primary producers and indicates the appropriateness of the habitat for use by major trophic levels. Generally accepted categories of vegetation structure are grasses, herbs, shrub/scrub, forest, and woodland. Each category has dominant vegetation with distinct height and density that, in turn, supports a distinct suite of fauna.

An additional criterion considered for inclusion was the presence or absence of a soil substrate. This criterion differentiates sites that support vegetation versus those that do not; however, it is assumed for risk assessment that all terrestrial and wetland sites have a soil substrate. Terrestrial sites without a soil substrate are assumed to be industrial sites that do not support ecological communities and, therefore, do not warrant ecological risk assessment. Natural areas lacking a soil substrate (e.g., rock outcrops) are assumed to be relatively small inclusions within a habitat and, thus, are not the focus of this risk assessment.

The criteria are quite general and do not include many of the abiotic parameters often associated with ecological classification systems such as latitude, climate, topography, elevation, or soil type. Vegetation type, however, is directly affected by these abiotic parameters and, therefore, often used as a general indicator of many abiotic characteristics. Moreover, in consideration of the goal to develop habitats that reflect current risk assessment methods and data availability, the selected criteria do not incorporate parameters beyond the reach of available methods. For example, available data for bird species are not adequate to differentiate between the effects on birds that inhabit mesic forests versus birds that inhabit temperate rain forests. Nor are data available to differentiate between plant uptake in these two forest types. Consequently, defining habitats in terms of climatic differences would not be useful.

In addition, criteria describing the current conditions at a site were chosen over those that reflect potential or climax natural communities. Although potential natural vegetation is useful for some resource management activities, exposure pathways were determined by existing habitat conditions. Existing vegetation structure and physiognomy are visually discernible and easily determined through remote imagery interpretation. Data on existing hydrologic conditions also are readily available.

In addition to the general classifications cited in Section 13.1.2, primary sources for development of wetland habitats include Christensen et al., 1988; Damman and French, 1987; Glaser, 1987; Gosselink and Turner, 1978; Kadlec and Knight, 1996; Larsen, 1982; Mitsch and Gosselink, 1993; Niering, 1985; Norquist, 1984; Sharitz and Gibbons, 1982; Verry, 1997; Windell et al., 1986; and Winter, 1989.

13.1.2.2 Criteria for Waterbody Margin Habitats. Using the waterbody margin habitats in the exposure assessment for terrestrial receptors allows inclusion of freshwater aquatic plants and prey items that are part of the terrestrial receptor food chain. A brief review of the literature supports the use of two criteria, energy/flow and size, as a simple but effective classification approach. Although aquatic classifications in general consist of more complex divisions, most include these two criteria at their basic levels. The energy/flow criterion distinguishes between still water and flowing water, and the size criterion addresses the intrinsic differences between large and small systems such as net primary production, diversity of habitat, and length and complexity of food webs. No commonly used size cutoffs were found in the literature. For lakes versus ponds, the waterbody margin habitats use the U.S. Environmental Protection Agency's (EPA's) Environmental Monitoring and Assessment Program (EMAP) 10-ha cutoff for small versus large lakes. For streams versus rivers, the generally accepted stream order concept was considered, and stream order 5¹ was initially proposed as a cutoff between streams (small flowing waterbodies) and rivers (large flowing waterbodies). It became evident, however, that modeled constituent concentrations in streams larger than stream order 5 are effectively diluted to an undetectable level. Therefore, streams and rivers of order 5 or less are included in a single habitat, and those of order 6 and 7 are not included in the ecological exposure assessment.

References consulted for the development of the waterbody margin habitats include the habitat classifications cited in Section 13.1.2 as well as Davis and Simon (1995), USDA (1998), and Caduto (1990).

13.1.3 Regionalization

Consideration was given to using one of the many national scale ecological classification systems developed during the past few decades. In particular, Bailey's ecoregions were assessed for relevance to the HWIR risk assessment (Bailey, 1996). Even the finest level of Bailey's classification, the section, does not indicate the physical parameters that determine exposure pathways, however. For example, the Everglades Section (Section 411A) or the Sierra Nevada Foothills Section (Section M261F) each includes a broad diversity of natural communities such as forests, grasslands, uplands, wetlands, and developed areas. Each of these natural communities would exhibit a different exposure scenario; therefore, they should not be treated as a single geographic entity (e.g., a Bailey's section) for exposure assessment. Thus, although the representative habitats described in the following section are general, they differentiate types of vegetation structure and gross water regimes on a site-based level and, consequently, are more relevant and useful than available regionalized classification systems. (Bailey's ecoregions are used in the HWIR analysis to express regional distribution of receptor species; see Section 13.2.2.2 for further discussion.)

13.1.4 Descriptions of the Representative Habitats

Based on these classification criteria, 14 terrestrial, wetland, and waterbody margin habitats were developed for classifying the 201 sites included in the HWIR risk assessment.

¹ The Strahler (1957) Stream ordering system is used throughout this document.

Table 13-2 presents an overview of the representative habitats. Detailed descriptions of the habitats are presented in the sections that follow. (Note that the examples given in the descriptions are not taken from any particular classification system. They are not definitive or exhaustive and are intended only to suggest visual illustrations of the range of the natural communities included.)

Grasslands—Grasslands are dominated by grasses or other herbaceous vegetation and lack shrub and tree layers. In most cases, vegetation height is between a few inches and more than a meter. Grasslands generally lack woody vegetation. Individual species may be annual or perennial. Grasses are often persistent (i.e., some aboveground vegetative structure persists throughout the year). Forbs (nongrass herbaceous species) may or may not be persistent. Grasslands provide foraging, grazing, and hunting habitat for species at all trophic levels; offer cover and nesting habitat for passerine and ground birds and for small mammals; and support a varied community of insects and other arthropods. Examples include the following:

- # prairies,
- # rangelands (southwestern United States),
- # power cuts,
- # mountain meadows, and
- # grassy balds (southern Appalachians).

Table 13-2. Ecological Risk Assessment Representative Habitats for Terrestrial Receptors

Terrestrial Habitats	
#	Grasslands
#	Shrub/scrub
#	Forests
#	Crop fields and pastures
#	Residential
Wetland Habitats	
#	Intermittently flooded grasslands
#	Intermittently flooded shrub/scrub
#	Intermittently flooded forests
#	Permanently flooded grasslands
#	Permanently flooded shrub/scrub
#	Permanently flooded forests
Waterbody Margin Habitats	
#	Rivers/streams
#	Lakes
#	Ponds

Shrub/Scrub—Shrub/scrub habitats are dominated by multistemmed woody vegetation about 3 m high or less. Trees may be present but are widely spaced. Vegetation is deciduous or evergreen. Shrub/scrub communities can be dense to impenetrable (e.g., dune scrub) or can consist of a mosaic of widely spaced patches of shrub/scrub with herbaceous cover in between (e.g., chaparral). In either case, the shrubs provide cover, forage, and nesting habitat. Extensive areas of shrub/scrub support large mammals such as bears. Many shrub/scrub habitats are fire-maintained and succeed to forests if fire is suppressed. Examples include the following:

- # California coastal scrub,
- # aspen/oak/willow scrublands (north central United States),
- # sagebrush steppe,
- # sandhill scrub (southeastern United States),
- # scrub oak/mountain mahogany community,
- # mid-Atlantic dune thickets,
- # desert cactus/scrub,
- # chaparral,
- # heath balds (southern Appalachians),
- # rhododendron slopes (southern Appalachians), and
- # juniper shrublands (midwestern United States).

Forests—Forests are communities dominated by tree species (i.e., single-stemmed woody species that grow to more than 3 m in height). Forests also can have shrub layers and herbaceous ground cover and, therefore, provide more structural diversity than grassland or shrub/scrub habitats. This habitat includes deciduous, evergreen, and mixed forests. Natural communities known as woodlands, in which trees are widely scattered throughout a grassland, also are included in this habitat type. Forests provide hunting and foraging habitat as well as nesting and cover for all trophic levels. Large forest areas can support several large mammal species, such as mountain lions, coyotes, bear, elk, and lynx, in their respective ecoregions. Examples include the following:

- # deciduous oak woodlands (western United States),
- # mixed mesic hardwood forests,
- # temperate rain forests (northwestern United States),
- # aspen groves,
- # mixed spruce/hardwood boreal forests,
- # beech/maple forests,
- # xeric scrub oak forests,
- # evergreen oak woodlands (western United States),
- # longleaf pine savannas,
- # sprucefir/hemlock forests (coastal northwestern United States),
- # cove forests (southern Appalachians),
- # maritime forests (southeastern United States),
- # ponderosa pine Sierran forests, and
- # loblolly pine plantations.

Crop Fields and Pastures—This habitat includes actively farmed crop fields and pastures and fallow fields. It is generally characterized by crop monocultures or pasture grass species. These habitats provide forage for herbivores and omnivores of all sizes. Fields and pastures also provide cover for nests and dens for a wide variety of mammals and birds. Pastures are included here rather than with grasslands because available land use data classify crop fields and pastures together as agricultural land.

Residential—This habitat is characterized by houses, lawns, landscaped areas, and streets. Much of the vegetation is not native, and the habitat is very patchy. This patchiness and the proximity of human activity limit the receptors using these areas (e.g., deer, rabbits, racoons, small mammals).

Rivers/Streams—Rivers and streams are waterbody margin systems characterized by flowing water, stream order 5 or lower. The river/stream habitat includes the stream itself as a source of food, as well as adjacent land such as stream banks, natural levees, and flood plains directly associated with the stream. Vegetation adjacent to streams can include grasses and forbs, scrub/shrub, or forests. This habitat supports receptors that depend on the stream for feeding (e.g., muskrats) and reproduction (e.g., amphibians).

Lakes—This habitat includes large waterbody margin systems (surface area greater than 10 ha) characterized by standing water. It includes deep water and shallow areas as well as lake shores and immediately surrounding areas directly associated with and/or affected by the lake. Lake margin substrates include sandy beaches, rocky shores, mud flats, and/or distinct banks. Vegetation surrounding lakes may be grasses and forbs, shrub/scrub, or forests. Lake habitats support receptors that depend on the lake for food (e.g., osprey) or reproduction (e.g., amphibians).

Ponds—This habitat includes small aquatic systems (surface area of 10 ha or less) characterized by standing water. Pond habitats can include deep water and shallow areas, although they are generally shallow compared to lakes. The habitat also includes pond margins and immediately surrounding areas directly associated with or affected by the pond. Vegetation surrounding ponds may be grasslands, shrub/scrub, or forests. In general, ponds support a different suite of terrestrial species than lakes because of their smaller surface area and the smaller size and lower diversity of prey. Terrestrial wildlife receptors for ponds are species that depend on the pond for food or reproduction (e.g., amphibians).

Intermittently Flooded Forests—Intermittent flooding implies a seasonal flood regime that allows for drying and oxygenation of the soil, particularly during the growing season. The dominant vegetation comprises tree species, but this habitat also includes herb and shrub layers. Therefore, it supports a complex food web. Forested wetland habitats, particularly those dominated by mast producing species (e.g., oak and hickory), support different bird and mammal species than nonforested wetland habitats. This habitat type includes a particularly wide range of vegetative communities, including plant communities with exceptionally high species diversity (e.g., wet savannas and pine flatwoods). Some have relatively low wildlife diversity (e.g., arroyos), while others have fairly high faunal diversity (e.g., riverine forests). Seasonal flooding

causes periodic soil saturation, thus affecting the behavior of contaminants as well as wildlife use of the habitat. Examples include the following:

- # spruce bogs,
- # arroyo thickets,
- # wet conifer forests,
- # pine flatwoods,
- # longleaf pine savannas,
- # bottomland hardwood forests,
- # Atlantic white cedar swamps, and
- # riverine forests.

Intermittently Flooded Shrub/Scrub—In this habitat, the dominant vegetation is shrubs. Intermittent flooding implies a seasonal flood regime that allows for drying and oxygenation of the soil, particularly during the growing season. This habitat supports similar trophic levels and functional groups as the terrestrial shrub/scrub habitats, but seasonal flooding causes periodic soil saturation, thus affecting the behavior of contaminants as well as wildlife use of the habitat. Some intermittently flooded shrub/scrub wetlands, most notably pocosins, are extremely dry during significant portions of some years. Fire is an important element in many intermittent shrub/scrub wetlands. Examples include the following:

- # cranberry bogs,
- # pocosins, and
- # alder thickets.

Intermittently Flooded Grasses/Forbs—The dominant vegetation in this habitat is emergent herbaceous species. In some cases, grasses are dominant; in others, forbs or a mix of grasses and forbs dominates. The flood regime is generally seasonal, allowing for drying and oxygenation of the soil, particularly during the growing season. This habitat type supports similar trophic levels and functional groups as terrestrial grasslands, but seasonal flooding causes periodic soil saturation, thus affecting the behavior of contaminants as well as wildlife use of the habitat. Some intermittently flooded grass/forb wetlands are fire-maintained. Examples include the following:

- # upland hard pan pools,
- # stream heads and springs,
- # vernal pools,
- # prairie potholes,
- # wet meadows, and
- # spray cliffs or waterfall ledges.

Permanently Flooded Forests—This habitat includes forested habitats where inundation may fluctuate, but soil remains saturated to flooded throughout most years. A lack of soil oxygenation limits vegetative species. Many of these habitats are commonly known as swamps. This habitat includes canopy and subcanopy layers and possibly a shrub layer. Inundation limits the herbaceous layer. This habitat provides food and cover to an especially wide variety of

vertebrates and invertebrates. Permanently flooded wetlands are assumed to support benthic fauna and fish as well as aquatic, emergent, and facultative vegetation; therefore, they support a complex food web including both terrestrial and aquatic fauna. Examples include the following:

- # cypress swamps,
- # tupelo (gum) swamps,
- # hardwood swamp forests,
- # forested pond and lake edges, and
- # Atlantic white cedar forests.

Permanently Flooded Shrub/Scrub—These habitats are dominated by shrub species; inundation may fluctuate, but soil remains saturated to flooded throughout most years. A lack of soil oxygenation limits vegetative species. Shrub/scrub habitats tend to be densely vegetated, thus providing greater cover than many forest or grass/forb habitats. They provide food and cover for a significant number of avian species. Permanently flooded wetlands are assumed to support benthic fauna and fish as well as aquatic, emergent, and facultative vegetation; therefore, they support a complex food web including both terrestrial and aquatic fauna. Examples include the following:

- # vegetated pond and lake edges,
- # mountain seeps,
- # northern shrub bogs,
- # beaver ponds, and
- # willow/alder swamps.

Permanently Flooded Grasses/Forbs—These habitats are dominated by emergent grasses and herbaceous species. Inundation may fluctuate, but soil remains saturated to flooded throughout most years. A lack of soil oxygenation limits vegetative species. Some of these habitats are commonly known as marshes. This habitat provides food and cover for a significant number of avian species; in some instances, vegetation is not persistent, and therefore, is apparent only in the growing season. Permanently flooded wetlands are assumed to support benthic fauna and fish as well as aquatic, emergent, and facultative vegetation; therefore, they support a complex food web including both terrestrial and aquatic fauna. Examples include the following:

- # brackish marshes,
- # freshwater marshes,
- # sphagnum bogs,
- # sedge bogs,
- # vegetated pond and lake margins, and
- # fens.

13.2 Food Webs and Receptor Groups

The ecological exposure module uses the representative habitats to determine the receptor species likely to be present at a site and then calculates receptor doses based on the diet items

(plants, prey, and water) expected to be present in the habitat. Receptor variables in the ecological exposure models are ReceptorName, a string variable that gives the descriptive species name; ReceptorIndex, which assigns an index number to each receptor species; and ReceptorType which describes the trophic behavior of the receptor (e.g., predator, omnivert, herbivert). This section describes the methods by which receptor groups were developed for each habitat. The basis of the methodology is the construction of food webs for the habitats. The food webs describe the trophic levels, eating strategies, and faunal classes included in each habitat. Receptors are then selected to represent these components of the food web. Section 13.2.1 describes the food webs, and Section 13.2.2 presents the receptor groups for each habitat.

13.2.1 Food Webs

Food webs were developed to assess the feeding strategies and trophic level interactions that characterize the representative habitats. Figures 13-1 and 13-2 present generalized food webs for terrestrial receptors in terrestrial and aquatic ecosystems. Wetland ecosystems are assumed to have a food web similar to either an aquatic or terrestrial ecosystem, depending on its water regime. The three intermittently flooded wetland habitats are characterized by infrequent inundation and do not support aquatic communities; therefore, their food web is assumed to be described by the general terrestrial food web. The three permanently flooded wetland habitats are characterized by long-term inundation and support aquatic communities including fish, benthic organisms, and aquatic plants. Thus, their food web is assumed to be similar to the aquatic habitat food web.

The food webs were developed based on generally accepted concepts about food webs and natural community dynamics (Anderson, 1997; Begon and Mortimer, 1981; Caduto, 1990; Davis and Simon, 1995; Kadlec and Knight, 1996; Sample et al., 1997; Schoener, 1989; Schoenly and Cohen, 1991; Suter, 1993; Tanner, 1978; U.S. EPA, 1993a, 1994a). The food webs serve two primary purposes: they illustrate potential exposure pathways, and they facilitate the selection of receptor species to be associated with each habitat. The webs are designed to illustrate the particular taxa and functional groups (or feeding strategies) that each habitat comprises. Based on the trophic levels, taxa, and functional groups in the food webs, receptor species are identified to produce a receptor group for each representative habitat. The receptor groups reflect their respective habitat's food web and, thus, provide an effective suite of receptors for assessing exposure.

13.2.1.1 Terrestrial Habitat Food Web. As illustrated in Figure 13-1, the terrestrial food web includes primary producers (vascular plants) and three faunal trophic levels. Trophic level 1 (T1) consists of species that consume only plants (i.e., the herbivores) and that are potential prey for higher trophic level species. T1 species include small or large mammals, herpetofauna, invertebrates, and birds. The soil community is a subset within T1 and includes invertebrate soil organisms that live in direct contact with soil, thus reflecting a unique exposure pathway. Within the HWIR analysis, the soil community is assumed to be T1, although the dynamics within soil communities are, in fact, very complex and include herbivores, omnivores, and carnivores at several trophic levels. This complexity is beyond the reach of the HWIR models and available supporting data.

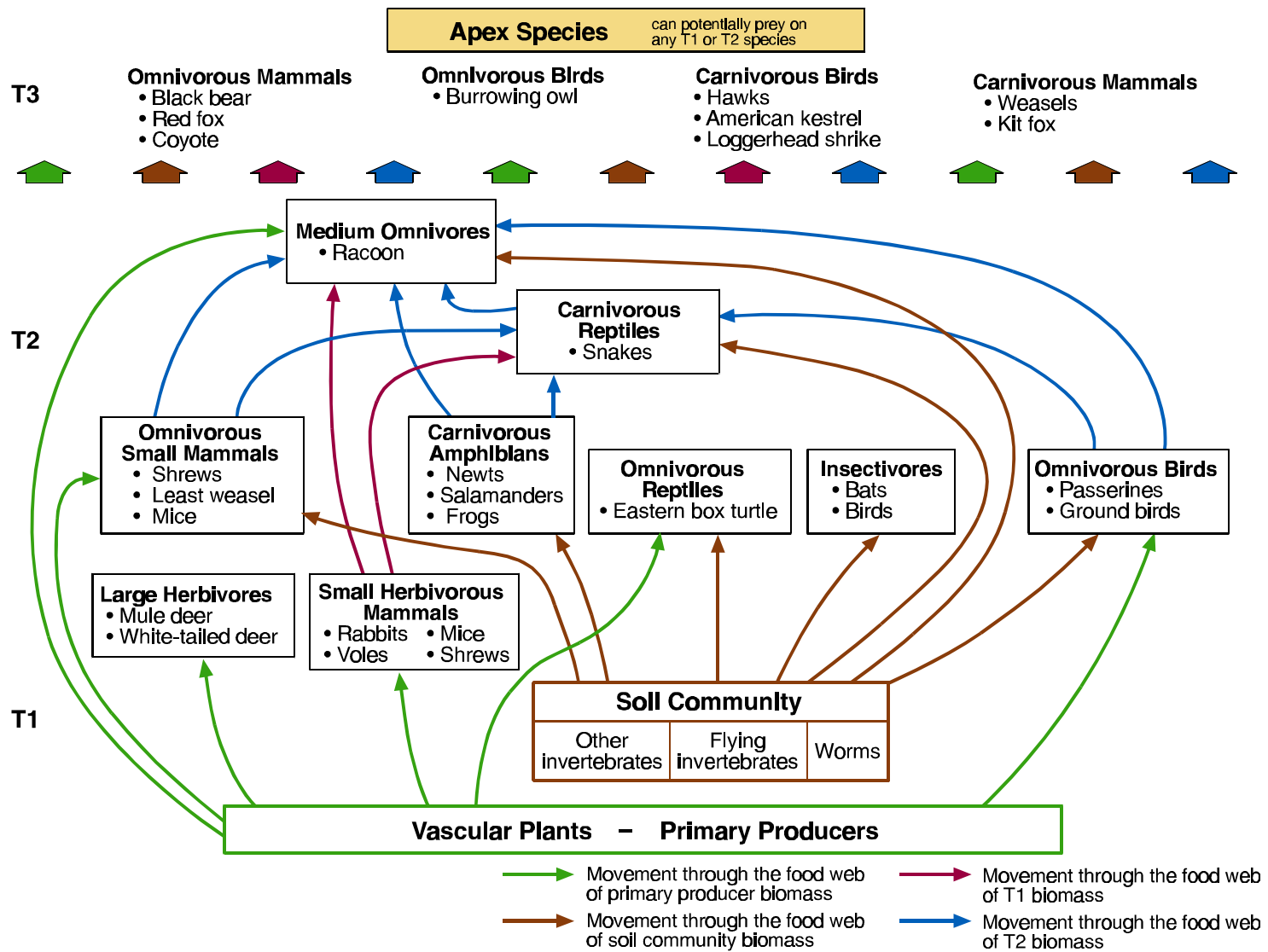


Figure 13-1. Terrestrial food web, including example receptors.

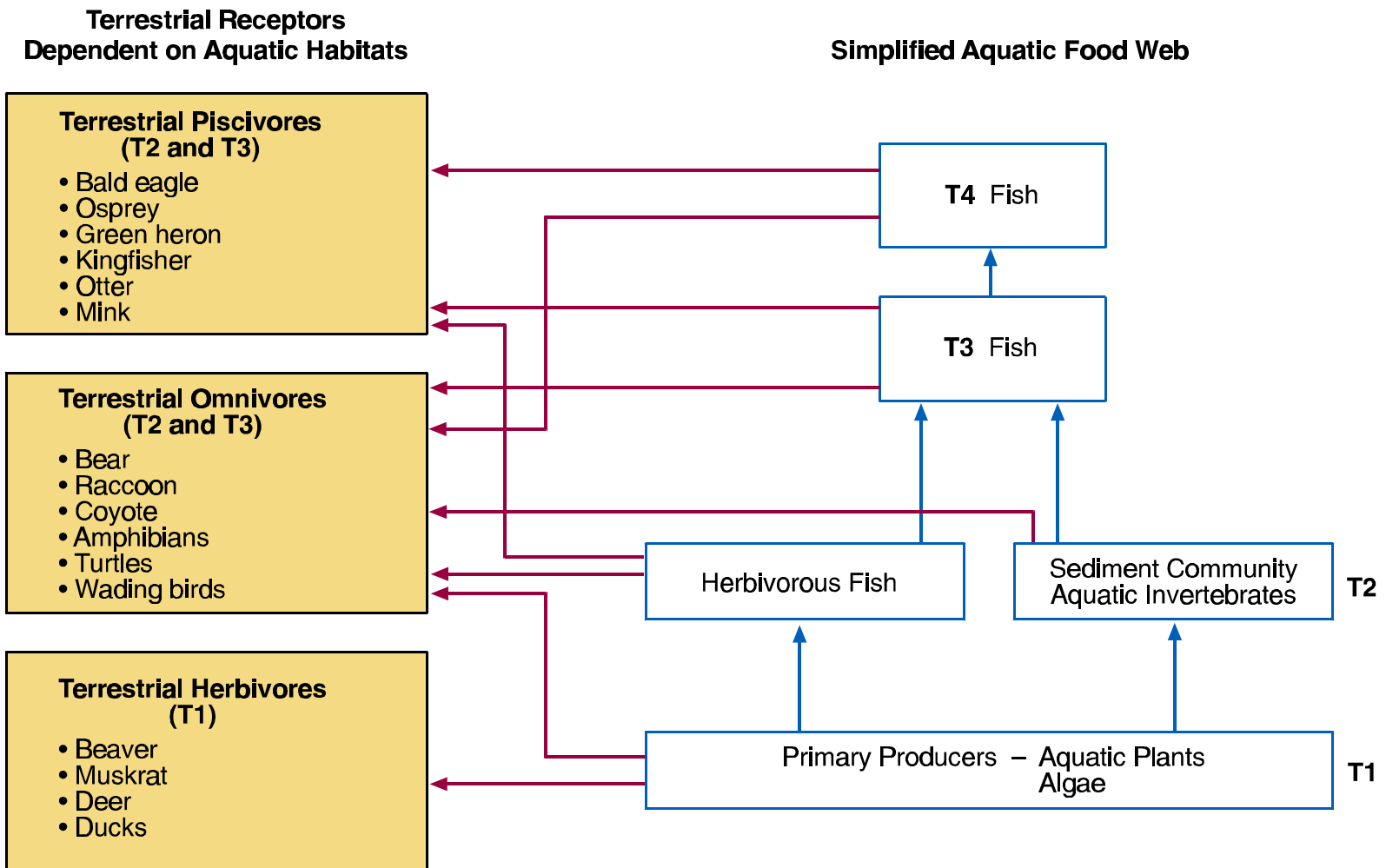


Figure 13-2. Interface between terrestrial receptors and aquatic food web, including example receptors.

Trophic level 2 (T2) includes species that consume plants and/or animals (herbivores, omnivores, and carnivores) and that are also prey to other carnivores or omnivores. These species can be from any faunal class, functional group, or size range. As shown in Figure 13-1, T2 species include a particularly wide array of small- to medium-sized omnivorous mammals, birds, and herpetofauna. T2 carnivores include, for example, reptiles and small amphibians that eat benthic organisms, other invertebrates, and small amphibians and mammals. These carnivores are, in turn, food for numerous larger predators in both trophic levels 2 and 3. Opportunistic feeders in T2, such as raccoons, increase the complexity of the web by feeding on virtually any T1 or T2 prey.

Trophic level 3 (T3) consists of apex species, or those that do not have any predators (other than humans) in the given habitat. Apex species also include a variety of sizes and classes of receptors, such as large mammals (black bears) and small raptors (Cooper's hawks). It could be argued that many of these species are not, in fact, true apex species because their eggs or young may be consumed by other species. For the HWIR analysis, however, species for which the adults are not a regularly consumed prey item are considered apex or T3 species.

13.2.1.1.1 Faunal Classes. The food webs also reflect an array of faunal classes—mammals, birds, reptiles, and amphibians. Faunal class distinctions are useful because species within similar groups are known to respond similarly to environmental disturbance. It is, therefore, important for the exposure characterization to include representative species from different organizational groups to ensure that all potential pathways and responses are addressed. Generally speaking, in CONUS, these major faunal classes occur throughout all trophic levels (with the exception of amphibians in T3); however, exposure and toxicological data are not necessarily available for representative species in all classes at all trophic levels. Therefore, not all potential compartments are represented in the food web. In particular, herbivorous (T1) herpetofauna and birds are not included, and T3 reptiles are not represented in the terrestrial habitat food web, although they are included in aquatic habitats (see Section 13.2.2).

13.2.1.1.2 Functional Groups. The term functional group refers to general types of feeding strategies—herbivore, carnivore, omnivore, or insectivore. These functional groups experience different exposure based on the composition of their respective diet. Therefore, the terrestrial food web was constructed to include these different groups in appropriate positions. Herbivores are synonymous with T1 and occur at that level only. Insectivores, a special case of carnivore, are included in T2; insectivores are generally not top predators, so they are not represented in T3. Omnivores are well-represented in both T2 and T3. Each of the functional groups reflects a unique exposure pathway recognized by the risk model. As described in the ecological exposure module documentation, the module estimates an exposure dose for each receptor species based on its dietary composition; insectivores are exposed through ingestion of invertebrates, carnivores are exposed through ingestion of small mammals and herpetofauna, and so on.

13.2.1.2 Food Web for Aquatic Habitats. Although the representative terrestrial habitats were designed to address exposure in areas inhabited by land-based receptors, some of the species that would be exposed to contaminants in these habitats, such as ospreys or muskrats, derive all or most of their food from the water. Additional receptors, such as bullfrogs or

snapping turtles, also spend significant time in the water. Based on these species' biology and potential routes of exposure, they are more appropriately addressed as terrestrial than as aquatic receptors. To assess their exposure, however, the aquatic element of their habitat must be included; therefore, the 14 terrestrial habitats include 3 waterbody margin habitats: stream/river corridors, pond margins, and lake margins. These habitats include both an aquatic component and a terrestrial component, but they are used to assess exposure only for terrestrial species. Figure 13-2 illustrates the interface between these terrestrial receptors and the aquatic habitats upon which they depend. Further descriptions of the habitats are presented in Section 13.1. A discussion of aquatic receptor species and their habitats (e.g., fish and benthic organisms living in streams, lakes, or ponds) is presented in Section 11.0 of the data collection documentation and Section 11.0 of the module documentation.

The waterbody margin habitats allow for the assessment of exposure through ingestion of sediment, aquatic plants, benthic filter feeders, and fish. For receptors in these habitats that feed strictly on aquatic food items, the food web is assumed to be relatively simple, consisting of the four-compartment aquatic food web directly linked to the terrestrial receptor (see Figure 13-2). For example, the osprey eats fish almost exclusively and, thus, is an apex predator at the top of the simplified aquatic food web. The osprey takes prey from the T2, T3, and T4 aquatic compartments. For omnivores and more opportunistic species in the waterbody margin habitats, the food web is essentially the same as that for strictly terrestrial species but with an added component of aquatic prey as potential food items. Many of these species (e.g., raccoon or black bear) are equally successful whether or not aquatic habitats are available. At sites where aquatic prey are available, however, these exposure pathways present unique exposure scenarios.

13.2.2 Receptor Groups

A receptor group is a suite of wildlife species chosen to characterize the exposure scenarios for a particular representative habitat. To adequately reflect potential exposure scenarios, the receptor group should represent all of the faunal classes, trophic levels, and feeding strategies that the habitat comprises. Receptor groups were drawn from the species contained in the wildlife exposure factors database; these are species for which at least the minimum required toxicological and exposure data are available (see Section 12.0 for a description of the wildlife exposure factors database). As such, the species composition of the receptor groups is based on available data as well as on species distribution and habitat information. The exposure factor database was populated with the intent to represent an array of habitats, trophic levels, and feeding strategies. In a few cases, additional species were specifically sought to fill regional data gaps. For example, the mule deer was added to the database to include a large herbivore in some of the regions where the white-tailed deer is not distributed.

To develop the habitat receptor groups, each species in the wildlife exposure factors database was categorized by general faunal class, functional group, and trophic level. Then, the species were assigned to habitats in which they could potentially be exposed. Species were assigned to habitats in which they are documented to ingest food or water based on normally expected feeding behavior. Table 13-3 lists all of the receptor species and notes their faunal class (mammal, bird, reptile, or amphibian), their functional group (herbivore, omnivore, carnivore, or

Table 13-3. Terrestrial Wildlife Receptors

Species	Scientific Name	Class ¹	Functional Group ²	Trophic Level ³	Habitats ⁴	References
Alligator snapping turtle	<i>Macrolemys temminckii</i>	R	O	T3	St, P, L, PFF	Lane and Mitchell, 1997 Conant and Collins, 1991
American kestrel	<i>Falco sparverius</i>	B	C	T2	G, F, C, R	Terres, 1980 U.S. EPA, 1993b Lane and Fischer, 1997 Stokes and Stokes, 1996
American robin	<i>Turdus migratorius</i>	B	O	T2	G, S, F, C, R	Terres, 1980 U.S. EPA, 1993b Stokes and Stokes, 1996
American woodcock	<i>Scolopax minor</i>	B	O	T2	G, S, F, C, St, IFG, IFS, IFF, PFG, PFS, PFF	Terres, 1980 U.S. EPA, 1993b Stokes and Stokes, 1996
Bald eagle	<i>Haliaeetus leucocephalus</i>	B	C	T3	St, P, L, PFF, PFS, PFG	Terres, 1980 U.S. EPA, 1993b Stokes and Stokes, 1996
Beaver	<i>Castor canadensis</i>	M	H	T1	St, P, L, PFF, PFS, PFG	Stokes and Stokes, 1986 Whitaker, 1997 Jenkins and Busher, 1979
Belted kingfisher	<i>Ceryle alcyon</i>	B	O	T2	St, P, L, PFF, PFS, PFG	Terres, 1980 U.S. EPA, 1993b Stokes and Stokes, 1996
Black bear	<i>Ursus americanus</i>	M	O	T3	S, F, St, P, L, IFS, IFF, PFS, PFF	Schaefer and Sargent, 1990 Stokes and Stokes, 1986 Whitaker, 1997

(continued)

Table 13-3. (continued)

Species	Scientific Name	Class ¹	Functional Group ²	Trophic Level ³	Habitats ⁴	References
Black-tailed jackrabbit	<i>Lepus californicus</i>	M	H	T1	G, S, C	Whitaker, 1997 Sample et al., 1997 MacMahon, 1985
Bullfrog	<i>Rana catesbeiana</i>	A	O	T2	St, P, L, IFG, IFF, PFG, PFF	Conant and Collins, 1991 U.S. EPA, 1993b Martof et al., 1980 Behler and King, 1979
Burrowing owl	<i>Speotyto cunicularia</i>	B	O	T2	G, C	Terres, 1980 Sample et al., 1997 Stokes and Stokes, 1996
Canada goose	<i>Branta canadensis</i>	B	H	T1	P, L	Terres, 1980 U.S. EPA, 1993b Niering, 1985 Stokes and Stokes, 1996
Cerulean warbler	<i>Dendroica cerulea</i>	B	I	T2	F, PFF	Evans and Fischer, 1997 Terres, 1980 Stokes and Stokes, 1996
Cooper's hawk	<i>Accipiter cooperi</i>	B	C	T3	F, C, R	Terres, 1980 Sample et al., 1997 Stokes and Stokes, 1996
Coyote	<i>Canis latrans</i>	M	O	T3	G, S, F, C, IFS, IFF, PFS, PFF	Bekoff, 1977 Sample et al., 1997 Whitaker, 1997 Stokes and Stokes, 1986

(continued)

Table 13-3. (continued)

Species	Scientific Name	Class ¹	Functional Group ²	Trophic Level ³	Habitats ⁴	References
Deer mouse	<i>Peromyscus maniculatus</i>	M	O	T2	G, S, F, C	Whitaker, 1997 U.S. EPA, 1993 Stokes and Stokes, 1986
Eastern newt	<i>Notophthalmus viridescens</i>	A	C	T2	F, P, IFG, IFS, IFF, PFG, PFS, PFF	Martof et al., 1980 U.S. EPA, 1993 Conant and Collins, 1991 Niering, 1985 Behler and King, 1979
Eastern cottontail rabbit	<i>Sylvilagus floridanus</i>	M	H	T1	G, S, F, C, R, IFG, IFS, IFF	Stokes and Stokes, 1986 Chapman et al., 1980 Whitaker, 1997
Eastern box turtle	<i>Terrapene carolina</i>	R	O	T2	All habitats	Martof et al., 1980 U.S. EPA, 1993b Sutton and Sutton, 1985 Conant and Collins, 1991
Flatwoods salamander	<i>Ambystoma cingulatum</i>	A	C	T2	R, P, IFG, IFS, IFF, PFG, PFS, PFG	Palis, 1997 Martof et al., 1980 Conant and Collins, 1991 Behler and King, 1979
Gopher frog	<i>Rana capito</i>	A	C	T2	G, S, F, P, IFG, PFG	Palis and Fischer, 1997 Conant and Collins, 1991 Behler and King, 1979
Great blue heron	<i>Ardea herodias</i>	B	O	T2	St, P, L, IFG, PFG, PFS, PFF	Terres, 1980 U.S. EPA, 1993b Stokes and Stokes, 1996 Niering, 1985

(continued)

Table 13-3. (continued)

Species	Scientific Name	Class ¹	Functional Group ²	Trophic Level ³	Habitats ⁴	References
Great Basin pocket mouse	<i>Perognathus parvus</i>	M	O	T2	G, S	Whitaker, 1997 Sample et al., 1997
Green heron	<i>Butorides virescens</i>	B	O	T2	St, P, L, PFG, PFS, PFF	Terres, 1980 Sample et al., 1997 Stokes and Stokes, 1996 Niering, 1985
Green frog	<i>Rana clamitans melanotar</i>	A	O	T2	St, L, P, IFG, IFS, IFF, PFG, PFS, PFF	Martof et al., 1980 U.S. EPA, 1993b Conant and Collins, 1991 Niering, 1985 Behler and King, 1979
Herring gull	<i>Larus argentatus</i>	B	O	T2	St, P, L, PFG, PFS	Terres, 1980 U.S. EPA, 1993b Stokes and Stokes, 1996
Kit fox	<i>Vulpes velox</i>	M	C	T3	G, S	McGrew, 1979 Sample et al., 1997 MacMahon, 1985 Whitaker, 1997
Least weasel	<i>Mustela nivalis</i>	M	C	T2	G, F, C, IFG, IFF, PFG	Whitaker, 1997 Stokes and Stokes, 1986
Lesser scaup	<i>Aythya affinis</i>	B	O	T2	P, L, PFG, PFF	Terres, 1980 U.S. EPA, 1993b Stokes and Stokes, 1996
Little brown bat	<i>Myotis lucifugus</i>	M	I	T2	C, R, P, L	Whitaker, 1997 Sample et al., 1997

(continued)

Table 13-3. (continued)

Species	Scientific Name	Class ¹	Functional Group ²	Trophic Level ³	Habitats ⁴	References
Loggerhead shrike	<i>Lanius ludovicianus</i>	B	C	T2	G, S, F, C	Hall et al., 1997 Terres, 1980 Stokes and Stokes, 1996
Long-tailed weasel	<i>Mustela frenata</i>	M	C	T2	G, F, C	Sutton and Sutton, 1985 Sample et al., 1997 Stokes and Stokes, 1996
Mallard	<i>Anas platyrhynchos</i>	B	O	T2	St, P, L, PFG, PFS, PFF	Terres, 1980 U.S. EPA, 1993b Stokes and Stokes, 1996 Niering, 1985
Marsh wren	<i>Cistothorus palustris</i>	B	C	T2	IFG, IFS, PFG, PFS	Terres, 1980 U.S. EPA, 1993b Stokes and Stokes, 1996 Niering, 1985
Meadow vole	<i>Microtus pennsylvanicus</i>	M	H	T1	G, C, R, IFG	Whitaker, 1997 U.S. EPA, 1993b Stokes and Stokes, 1986
Mink	<i>Mustela vison</i>	M	C	T2	St, P, L, PFG	Niering, 1985 U.S. EPA, 1993b Whitaker, 1997 Stokes and Stokes, 1986
Mule deer	<i>Odocoileus hemionus</i>	M	H	T1	G, S, F, IFG, IFS, IFF, PFG, PFS, PFF	Whitaker, 1997 Sample et al., 1997 Anderson and Wallmo, 1984 Whitney, 1985

(continued)

Table 13-3 (continued)

Species	Scientific Name	Class ¹	Functional Group ²	Trophic Level ³	Habitats ⁴	References
Muskrat	<i>Ondatra zibethicus</i>	M	H	T1	St, P, L	Niering, 1985 U.S. EPA, 1993b Stokes and Stokes, 1986 Willner et al., 1980 Whitaker, 1997
Northern water snake	<i>Nerodia sipedon</i>	R	C	T2	St, P, L, PFG, PFS, PFF	Martof et al., 1980 U.S. EPA, 1993b Conant and Collins, 1991 Niering, 1985 Behler and King, 1979
Northern bobwhite	<i>Colinus virginianus</i>	B	O	T2	G, S, F, C	Terres, 1980 U.S. EPA, 1993b Stokes and Stokes, 1986
Osprey	<i>Pandion haliaetus</i>	B	C	T3	ST, P, L, PFG, PFS	Terres, 1980 U.S. EPA, 1993b Stokes and Stokes, 1986
Painted turtle	<i>Chrysemys picta</i>	R	O	T2	St, P, L	Niering, 1985 U.S. EPA, 1993b Conant and Collins, 1991 Behler and King, 1979
Pine vole	<i>Microtus pinetorum</i>	M	H	T1	G, F, IFF	Whitaker, 1997 Sample et al., 1997
Prairie vole	<i>Microtus ochrogaster</i>	M	H	T1	G, C	Whitaker, 1997 U.S. EPA, 1993b

(continued)

Table 13-3. (continued)

Species	Scientific Name	Class ¹	Functional Group ²	Trophic Level ³	Habitats ⁴	References
Raccoon	<i>Procyon lotor</i>	M	O	T2	All habitats	Lotze and Andersen, 1979 U.S. EPA, 1993b Whitaker, 1997 Stokes and Stokes, 1986
Racer	<i>Coluber constrictor</i>	R	C	T2	G, S	Behler and King, 1979 U.S. EPA, 1993b Conant and Collins, 1991 Martof et al., 1980
Red fox	<i>Vulpes vulpes</i>	M	O	T3	G, S, F, C, IFG, IFS, IFF, PFG, PFS, PFF	Whitaker, 1997 U.S. EPA, 1993b Stokes and Stokes, 1986
Red-tailed hawk	<i>Buteo jamaicensis</i>	B	C	T3	G, S, C, R	Terres, 1980 U.S. EPA, 1993b Stokes and Stokes, 1996
River otter	<i>Lutra canadensis</i>	M	C	T2	St, PFS, PFG	Whitaker, 1997 U.S. EPA, 1993b Niering, 1985 Stokes and Stokes, 1986
Short-tailed shrew	<i>Blarina brevicauda</i>	M	O	T2	G, F, C, R, IFG, PFG	Whitaker, 1997 U.S. EPA, 1993b Stokes and Stokes, 1986
Short-tailed weasel	<i>Mustela erminea</i>	M	C	T2	G, F, C	King, 1983 Sample et al., 1997 Whitaker, 1997

(continued)

Table 13-3. (continued)

Species	Scientific Name	Class ¹	Functional Group ²	Trophic Level ³	Habitats ⁴	References
Snapping turtle	<i>Chelydra serpentina</i>	R	O	T3	L, P	Martof et al., 1980 U.S. EPA, 1993b Behler and King, 1979 Conant and Collins, 1991
Southern hognose snake	<i>Heterodon simus</i>	R	C	T2	F, C	Behler and King, 1979 Jordan, 1998 Martof et al., 1980 Conant and Collins, 1991
Spotted sandpiper	<i>Actitis macularia</i>	B	C	T2	ST, P, L, PFF	Terres, 1980 U.S. EPA, 1993b Stokes and Stokes, 1996
Tree swallow	<i>Tachycineta bicolor</i>	B	O	T2	G, S, C, R, IFG, PFG	Terres, 1980 Sample et al., 1997 Stokes and Stokes, 1996
Western meadowlark	<i>Sturnella neglecta</i>	B	O	T2	G, S, C	Terres, 1980 Sample et al., 1997 Stokes and Stokes, 1996

(continued)

Table 13-3. (continued)

Species	Scientific Name	Class ¹	Functional Group ²	Trophic Level ³	Habitats ⁴	References
White-tailed deer	<i>Odocoileus virginianus</i>	M	H	T1	G, S, F, St, P, L, IFG, IFS, IFF	Whitaker, 1997 Stokes and Stokes, 1986 Smith, 1991

¹ Class: A = amphibian, B = bird, M = mammal, R = reptile.

² Functional group: C = carnivore, H = herbivore, I = insectivore, O = omnivore.

³ Trophic level: T1 = prey, not a predator; T2 = both a predator and prey; T3 = a top predator, not prey.

⁴ Habitats:

- G = grasslands
- S = shrub/scrub
- F = forests
- C = crop fields and pastures
- R = residential
- St = streams/rivers
- P = ponds
- L = lakes
- PFG = permanently flooded grasslands
- PFS = permanently flooded shrub/scrub
- PFF = permanently flooded forests
- IFG = intermittently flooded grasslands
- IFS = intermittently flooded shrub/scrub
- IFF = intermittently flooded forests.

insectivore), and their trophic level. Tables 13-4 to 13-17 present habitat-specific receptor groups.

13.2.2.1 Assumptions for Habitat Assignment and Feeding Behavior

Characterization. Information on species habitats was of two types. EPA's *Wildlife Exposure Factors Handbook* (U.S. EPA, 1993b) and Sample and colleagues' complementary compilation of wildlife exposure factors (Sample et al., 1997) are principal sources of wildlife exposure factor data. In some cases, these data include information on the habitat where exposure data were recorded. These data document the particular habitat where observations were made on one or a few individuals; the data are not intended to describe the full range of potential habitats for any species. Therefore, additional sources were consulted for more general habitat information. These additional sources include a wide array of field guides, nature guides, and wildlife encyclopedias as well as species-specific monographs that describe the habitats known to be frequented or used by the species.

The terminology used to describe wildlife habitats in the source references varies considerably, as would be expected. Although the representative habitat types are quite general and are named with common descriptive terms, these terms are not used consistently in the literature. Therefore, professional judgment was used to correlate the habitat terminology found in the literature with the representative habitat types. Although some interpolation was employed in certain cases, a species was not assigned to a habitat unless such assignment was supported by a reference or firsthand knowledge. Anomalous sitings or casual occurrences (sometimes reported for birds) were not included.

Wetland habitats, in particular, raised questions about habitat assignments. Sources of habitat information for wetland species rarely refer to the degree or frequency of flooding when describing wetland habitats. Therefore, it was difficult to differentiate between species using intermittently flooded as opposed to permanently flooded wetland habitats. In many cases, the food or prey items attributed to a species were used as an indicator; for example, if a source reported that a species fishes in wetland habitats, the species was assigned to the appropriate permanently flooded wetland habitat, which, by definition, supports fish. Due to the predominant use in the source literature of terms such as swamps and marshes, which imply a relatively long flood duration, fewer species were assigned to the intermittently flooded wetland habitats. Furthermore, intermittently flooded wetlands are generally less discernable from surrounding uplands than are permanently flooded wetlands and, thus, are reported less frequently in general wildlife habitat sources. These differences are reflected in the smaller receptor groups for the intermittent wetlands.

Similar data interpretation methods were used to qualitatively characterize each species' diet, to establish its trophic levels, and to populate the terrestrial food web compartments for each habitat. A wide range of sources were consulted for information on feeding habits, including primary sources for wildlife exposure factors (U.S. EPA, 1993b; Sample et al., 1997), species monographs, zoological profiles, and field guides. All dietary items reported as commonly eaten were included in the characterizations. Information from species monographs and zoological profiles was emphasized over field guides. In general, dietary information from the various sources was quite consistent.

Table 13-4. Terrestrial Wildlife Receptors for Grasslands

Mammals	Birds	Herpetofauna
Meadow vole - H, T1	American robin - O, T2	Eastern box turtle - O, T2
Prairie vole - H, T1	American woodcock - O, T2	Gopher frog - C, T2
Pine vole - H, T1	Northern bobwhite - O, T2	Racer - C, T2
Black-tailed jackrabbit - H, T1	Western meadowlark - O, T2	
Mule deer - H, T1	Burrowing owl - O, T2	
Raccoon - O, T2	Loggerhead shrike - C, T3	
Great Basin pocket mouse - O, T2	American kestrel - C, T3	
Deer mouse - O, T2	Red-tailed hawk - C, T3	
Short-tailed shrew - O, T2	Tree swallow - I, T2	
Coyote - O, T3		
Red fox - C, T3		
Kit fox - C, T3		
Long-tailed weasel - C, T3		
Short-tailed weasel - C, T3		
Least weasel - C, T2		
Eastern cottontail rabbit - H, T1		
White-tailed deer - H, T1		

Functional group: C = carnivore, H = herbivore, I = insectivore, O = omnivore.

Trophic level: T1 = is prey, is not a predator; T2 = both a predator and prey; T3 = a top predator, not prey.

Table 13-5. Terrestrial Wildlife Receptors for Shrub/Scrub

Mammals	Birds	Herpetofauna
Black-tailed jackrabbit - H, T1	Tree swallow - I, T2	Eastern box turtle - O, T2
Deer mouse - O, T2	American robin - O, T2	Gopher frog - C, T2
Eastern cottontail rabbit - H, T1	American woodcock - O, T2	Racer - C, T2
Great Basin pocket mouse - O, T2	Northern bobwhite - O, T2	
Mule deer - H, T1	Western meadowlark - O, T2	
Raccoon - O, T2	Loggerhead shrike - C, T3	
Coyote - O, T3	Red-tailed hawk - C, T3	
Red fox - C, T3		
Kit fox - C, T3		
Black bear - O, T3		
White-tailed deer - H, T1		

Functional group: C = carnivore, H = herbivore, I = insectivore, O = omnivore.

Trophic level: T1 = is prey, is not a predator; T2 = both a predator and prey; T3 = a top predator, not prey.

Table 13-6. Terrestrial Wildlife Receptors for Forests

Mammals	Birds	Herpetofauna
Black bear - O, T3	American robin - O, T2	Eastern newt - C, T2
/Pine vole - H, T1	American woodcock - O, T2	Eastern box turtle - O, T2
Mule deer - H, T1	Northern bobwhite - O, T2	Gopher frog - C, T2
Raccoon - O, T2	Cerulean warbler - I, T2	Southern hognose snake - C, T2
Deer mouse - O, T2	Cooper's hawk - C, T3	
Short-tailed shrew - O, T2	Loggerhead shrike - C, T3	
Coyote - O, T3	American kestrel - C, T3	
Red fox - C, T3		
Long-tailed weasel - C, T3		
Short-tailed weasel - C, T3		
Least weasel - C, T2		
Eastern cottontail rabbit - H, T1		
White-tailed deer - H, T1		

Functional group: C = carnivore, H = herbivore, I = insectivore, O = omnivore.

Trophic level: T1 = is prey, is not a predator; T2 = both a predator and prey; T3 = a top predator, not prey.

Table 13-7. Terrestrial Wildlife Receptors for Crop Fields and Pastures

Mammals	Birds	Herpetofauna
Meadow vole - H, T1	American robin - O, T2	Eastern box turtle - O, T2
Prairie vole - H, T1	American woodcock - O, T2	Southern hognose snake - C, T2
Black-tailed jackrabbit - H, T1	Northern bobwhite - O, T2	
Raccoon - O, T2	Western meadowlark - O, T2	
Deer mouse - O, T2	Burrowing owl - O, T2	
Short-tailed shrew - O, T2	Loggerhead shrike - C, T3	
Coyote - O, T3	American kestrel - C, T3	
Red fox - C, T3	Red-tailed hawk - C, T3	
Long-tailed weasel - C, T3	Tree swallow - I, T2	
Short-tailed weasel - C, T3	Cooper's hawk - C, T3	
Least weasel - C, T2		
Eastern cottontail rabbit - H, T1		
Little brown bat - I, T2		

Functional group: C = carnivore, H = herbivore, I = insectivore, O = omnivore.

Trophic level: T1 = is prey, is not a predator; T2 = both a predator and prey; T3 = a top predator, not prey.

Table 13-8. Terrestrial Wildlife Receptors for Residential Habitats

Mammals	Birds	Herpetofauna
Meadow vole - H, T1	American robin - O, T2	Flatwood salamander - C, T2
Raccoon - O, T2	Tree swallow - I, T2	Eastern box turtle - O, T2
Short-tailed shrew - O, T2	American kestrel - C, T3	
Eastern cottontail rabbit - H, T1	Red-tailed hawk - C, T3	
Little brown bat - I, T2	Cooper's hawk - C, T3	

Functional group: C = carnivore, H = herbivore, I = insectivore, O = omnivore.

Trophic level: T1 = is prey, is not a predator; T2 = both a predator and prey; T3 = a top predator, not prey.

Table 13-9. Terrestrial Wildlife Receptors for River/Stream Habitats

Mammals	Birds	Herpetofauna
Beaver - H, T1	Belted kingfisher - C, T3	Alligator snapping turtle - O, T3
Raccoon - O, T2	Great blue heron - O, T2	Eastern box turtle - O, T2
River otter - C, T2	Green heron - C, T2	Bullfrog - O, T2
Mink - C, T3	American woodcock - O, T2	Green frog - C, T2
Muskrat - H, T1	Mallard - O, T2	Northern water snake - C, T2
Black bear - O, T3	Spotted sandpiper - I, T2	Painted turtle - O, T2
	Osprey - C, T3	
	Bald eagle - C, T3	
	Herring gull - O, T2	

Functional group: C = carnivore, H = herbivore, I = insectivore, O = omnivore.

Trophic level: T1 = is prey, is not a predator; T2 = both a predator and prey; T3 = a top predator, not prey.

Table 13-10. Terrestrial Wildlife Receptors for Pond Habitats

Mammals	Birds	Herpetofauna
Beaver - H, T1	Belted kingfisher - C, T3	Snapping turtle - O, T3
Raccoon - O, T2	Great blue heron - O, T2	Alligator snapping turtle - O, T3
Little brown bat - I, T2	Green heron - C, T2	Eastern box turtle - O, T2
Mink - C, T3	Bald eagle - C, T3	Bullfrog - O, T2
Muskrat - H, T1	Mallard - O, T2	Green frog - C, T2
Black bear - O, T3	Spotted sandpiper - I, T2	Northern water snake - C, T2
	Osprey - C, T3	Painted turtle - O, T2
	Canada goose - H, T1	Eastern newt - C, T2
	Lesser scaup - O, T2	Flatwood salamander - C, T2
	Herring gull - O, T2	Gopher frog - C, T2

Functional group: C = carnivore, H = herbivore, I = insectivore, O = omnivore.

Trophic level: T1 = is prey, is not a predator; T2 = both a predator and prey; T3 = a top predator, not prey.

Table 13-11. Terrestrial Wildlife Receptors for Lake Habitats

Mammals	Birds	Herpetofauna
Beaver - H, T1	Belted kingfisher - C, T3	Snapping turtle - O, T3
Raccoon - O, T2	Great blue heron - O, T2	Alligator snapping turtle - O, T3
Little brown bat - I, T2	Green heron - C, T2	Eastern box turtle - O, T2
Mink - C, T3	Bald eagle - C, T3	Bullfrog - O, T2
Muskrat - H, T1	Mallard - O, T2	Green frog - C, T2
Black bear - O, T3	Spotted sandpiper - I, T2	Northern water snake - C, T2
	Osprey - C, T3	Painted turtle - O, T2
	Canada goose - H, T1	
	Lesser scaup - O, T2	
	Herring gull - O, T2	

Functional group: C = carnivore, H = herbivore, I = insectivore, O = omnivore.

Trophic level: T1 = is prey, is not a predator; T2 = both a predator and prey; T3 = a top predator, not prey.

Table 13-12. Terrestrial Wildlife Receptors for Intermittently Flooded Grasslands

Mammals	Birds	Herpetofauna
Meadow vole - H, T1	Great blue heron - O, T2	Bull frog - O, T2
Mule deer - H, T1	American woodcock - O, T2	Eastern box turtle - O, T2
Raccoon - O, T3	Marsh wren - C, T2	Gopher frog - C, T2
Short-tailed shrew - O, T2	Tree swallow - I, T2	Eastern newt - C, T2
Red fox - C, T3		Flatwood salamander - C, T2
Least weasel - C, T2		Green frog - C, T2
Eastern cottontail rabbit - H, T1		
White-tailed deer - H, T1		

Functional group: C = carnivore, H = herbivore, I = insectivore, O = omnivore.

Trophic level: T1 = is prey, is not a predator; T2 = both a predator and prey; T3 = a top predator, not prey.

Table 13-13. Terrestrial Wildlife Receptors for Intermittently Flooded Shrub/Scrub

Mammals	Birds	Herpetofauna
Coyote - O, T3	American woodcock - O, T2	Green frog - C, T2
White-tailed deer - H, T1	Marsh wren - C, T2	Eastern box turtle - O, T2
Black bear - O, T3		Eastern newt - C, T2
Eastern cottontail rabbit - H, T1		Flatwood salamander - C, T2
Mule deer - H, T1		
Raccoon - O, T3		
Red fox - C, T3		

Functional group: C = carnivore, H = herbivore, I = insectivore, O = omnivore.

Trophic level: T1 = is prey, is not a predator; T2 = both a predator and prey; T3 = a top predator, not prey.

Table 13-14. Terrestrial Wildlife Receptors for Intermittently Flooded Forests

Mammals	Birds	Herpetofauna
Black bear - O, T3	American woodcock - O, T2	Eastern box turtle - O, T2
White-tailed deer - H, T1		Bullfrog - O, T2
Mule deer - H, T1		Flatwood salamander - C, T2
Raccoon - O, T3		Green frog - C, T2
Coyote - O, T3		Eastern newt - C, T2
Red fox - C, T3		
Least weasel - C, T2		
Pine vole - H, T1		
Eastern cottontail rabbit - H, T1		

Functional group: C = carnivore, H = herbivore, I = insectivore, O = omnivore.

Trophic level: T1 = is prey, is not a predator; T2 = both a predator and prey; T3 = a top predator, not prey.

Table 13-15. Terrestrial Wildlife Receptors for Permanently Flooded Grasslands

Mammals	Birds	Herpetofauna
Meadow vole - H, T1	Bald eagle - C, T3	Green frog - C, T2
Beaver - H, T1	Belted kingfisher - C, T3	Eastern box turtle - O, T2
Mink - C, T3	Great blue heron - O, T2	Gopher frog - C, T2
River otter - C, T2	Green heron - C, T2	Northern water snake - C, T2
Mule deer - H, T1	Herring gull - O, T2	Bullfrog - O, T2
Raccoon - O, T2	Lesser scaup - O, T2	Eastern newt - C, T2
Short-tailed shrew - O, T2	Marsh wren - C, T2	Flatwood salamander - C, T2
Red fox - C, T3	Mallard - O, T2	
Least weasel - C, T2	Tree swallow - I, T2	
	Osprey - C, T3	

Functional group: C = carnivore, H = herbivore, I = insectivore, O = omnivore.

Trophic level: T1 = is prey, is not a predator; T2 = both a predator and prey; T3 = a top predator, not prey.

Table 13-16. Terrestrial Wildlife Receptors for Permanently Flooded Shrub/Scrub

Mammals	Birds	Herpetofauna
Coyote - O, T3	Bald eagle - C, T3	Green frog - C, T2
Beaver - H, T1	Belted kingfisher - C, T3	Eastern box turtle - O, T2
Black bear - O, T3	Great blue heron - O, T2	Northern water snake - C, T2
River otter - C, T2	Green heron - C, T2	Eastern newt - C, T2
Mule deer - H, T1	Herring gull - O, T2	Flatwood salamander - C, T2
Raccoon - O, T3	American woodcock - O, T2	
Red fox - C, T3	Marsh wren - C, T2	
	Mallard - O, T2	
	Osprey - C, T3	

Functional group: C = carnivore, H = herbivore, I = insectivore, O = omnivore.

Trophic level: T1 = is prey, is not a predator; T2 = both a predator and prey; T3 = a top predator, not prey.

Table 13-17. Terrestrial Wildlife Receptors for Permanently Flooded Forests

Mammals	Birds	Herpetofauna
Black bear - O, T3	Bald eagle - C, T3	Alligator snapping turtle - O, T3
Beaver - H, T1	American woodcock - O, T2	Eastern box turtle - O, T2
Mule deer - H, T1	Belted kingfisher - C, T3	Bullfrog - O, T2
Raccoon - O, T3	Cerulean warbler - I, T2	Flatwood salamander - C, T2
Coyote - O, T3	Green heron - C, T2	Green frog - C, T2
Red fox - C, T3	Spotted sandpiper - I, T2	Eastern newt - C, T2
Least weasel - C, T2	Lesser scaup - O, T2	Northern water snake - , T2
	Mallard - O, T2	
	Great blue heron - O, T2	

Functional group: C = carnivore, H = herbivore, I = insectivore, O = omnivore.

Trophic level: T1 = is prey, is not a predator; T2 = both a predator and prey; T3 = a top predator, not prey.

13.2.2.2 Regionalization of Receptor Groups. Because the HWIR analysis is a national scale analysis, the receptor groups must be applicable to sites located throughout the CONUS. National applicability was achieved primarily by using species with wide geographic distributions. In addition, information on the geographic distribution of each receptor species was included in the site layout data, thus restricting the model to assessing exposure for only those species documented to occur in the region where each site was located. This regional component was based on Bailey's ecoregions (Bailey, 1996). The distribution pattern for each receptor species was correlated with geographic sections from Bailey's classification. Digitized Bailey's section data were included in the HWIR GIS, and as each site was assessed, only those species documented to occur in the section where the site was located were included in the exposure assessment.

To facilitate the regionalization of receptor groups, an attempt was made to represent each food web compartment with either nationally distributed species or an array of species that represent most CONUS regions. For example, the eastern cottontail rabbit and the black-tailed jackrabbit were both included in the grasslands receptor group in order to provide a small mammalian herbivore in temperate regions of the eastern United States as well as in the drier western regions. In some cases, adequate exposure and toxicological data were not available for complementary species. In particular, the amphibians and reptiles of the western states are not as well-represented; however, all faunal classes and feeding strategies are represented by at least one receptor at each trophic level for all CONUS regions.

Complete regional coverage was based on certain assumptions about species occurrence. Most importantly, it was assumed that receptor species occur in their assigned representative habitats regardless of a site's position in the landscape. Thus, if a forest habitat is delineated at a site, all the species included in the forest receptor group and occurring in that particular region are assumed to be present. In fact, it is probably unlikely that all of the receptor species, particularly those less adapted to human impacts and development, would be present. Moreover, when the habitat patches at a site are small, it is questionable whether the entire receptor group would use the habitat. For example, the black bear is included in the forest habitat receptor group; but, even within its normal distributional range, it is unlikely to occur in developed or industrialized areas or areas that consist of small habitat patches. Exposure doses were adjusted to account for the proportion of a species' required home range provided at a site; however, no adjustment was made to account for differences in species diversity in small versus large habitat patches or in disturbed versus undisturbed areas.

13.3 Habitat Delineation

The habitats occurring at each HWIR site were identified and delineated based on mapped land use and wetland and other waterbody data. Terrestrial habitats were delineated based on digitized Anderson land use categories (Anderson et al., 1976) available from the EPA's Geographic Information Retrieval and Analysis System (GIRAS) (U.S. EPA, 1994b); a combination of National Wetland Inventory (U.S. FWS, 1998b), GIRAS, and Reach File Version 3.0 Alpha Release (RF3-Alpha) (U.S. EPA, 1994c) data were used to delineate wetlands; and RF3-Alpha (U.S. EPA, 1994c) and Digital Elevation Model (DEM) (USGS, 1990) data were used to delineate waterbody margin habitats. Section 5.0 provides a discussion of the selection, downloading, and processing of these data sets. Digitized land use features, wetlands, and waterbodies were generated in the HWIR GIS as described in Section 5.0; these data layers then provided the basis for the manual delineation of representative habitats at each site using a GIS delineation tool. The following subsections document the manual delineation procedures used for terrestrial, wetland, and waterbody margin habitats.

13.3.1 Hand-Delineation Protocols

A program was implemented in ArcView allowing hand delineation of habitats at each site. The delineators used the digitized spatial features at each site as the initial indicators for the placement and boundaries of habitats. Additional protocols were developed to combine patches of like habitat at a single site into one contiguous polygon and to eliminate very small isolated patches that would not provide useful habitat. The basis for these protocols is the assumption that wildlife receptors in disturbed landscapes, such as those in which HWIR sites are most likely to be located, will travel from patch to patch to forage and feed. Most developed areas of CONUS consist of a mosaic of different vegetation communities. In many cases, the individual habitat patches that make up this mosaic are not large enough to support a significant food web. When combined with similar patches in the landscape, however, these patches can provide the necessary habitat to support the food webs and receptors developed for the HWIR analysis. Thus, in order to indicate receptor movement throughout each habitat type, patches of like habitat were connected, or bridged, in the delineation process. Consideration was given to barriers to movement, such as waterbodies or industrial areas.

When a single small patch of a particular habitat type occurred at a site, the delineators checked the surrounding area outside the area of interest (AOI) for additional habitat of the same type. If none existed within a reasonable distance, the single isolated patch was subsumed in its adjacent habitat type. In these cases, the assumption was made that a small isolated habitat patch would not effectively support receptor species.

13.3.1.1 Technical Description of GIS Habitat Delineation Tool. The habitat delineation tool was developed to eliminate the need for habitats to be digitized by GIS staff and, thus to save many hours of labor. The ESRI product ArcView was used to develop the tool for several reasons: it is easy to use, it was already in use in other aspects of the HWIR project, and it is PC-based and could be used on the delineator's computers. The basic concept of the tool was to allow users to easily assemble different layers of GIS data for a given site and delineate habitat areas with a minimal amount of training. Two different scripts were written to be run from within the ArcView GIS software. The first script would start a dialog box that would prompt the user for a site identification number (see Figure 13-3).

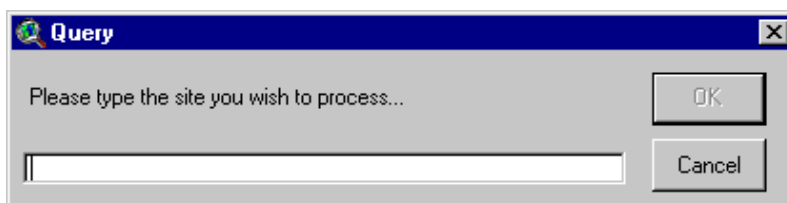


Figure 13-3. Initial dialog box for delineation tool.

Once entered, the script would load and symbolize the different GIS data layers needed for habitat delineation:

- # site location;
- # AOI;
- # waste management unit (WMU);
- # GIRAS land use;
- # delineated waterbodies—rivers, lakes, and wetlands;
- # NWI wetlands;
- # RF3 waterbodies;
- # managed areas;
- # 2-m DEM contours; and
- # preprocessed habitat grid.

Habitats were delineated by selecting grid cells and coding them with one of the 12 habitat codes. Because most habitats were based on the GIRAS land use data, the grid was preprocessed and attributed with habitat codes based on a crosswalk from the GIRAS land use types. This gave the delineators a starting point and sped up the process because they did not have to delineate all habitats from scratch (see Figure 13-4). (See Section 13.3.2 and Table 13-7 for further discussion of the land use-to-habitat crosswalk.)

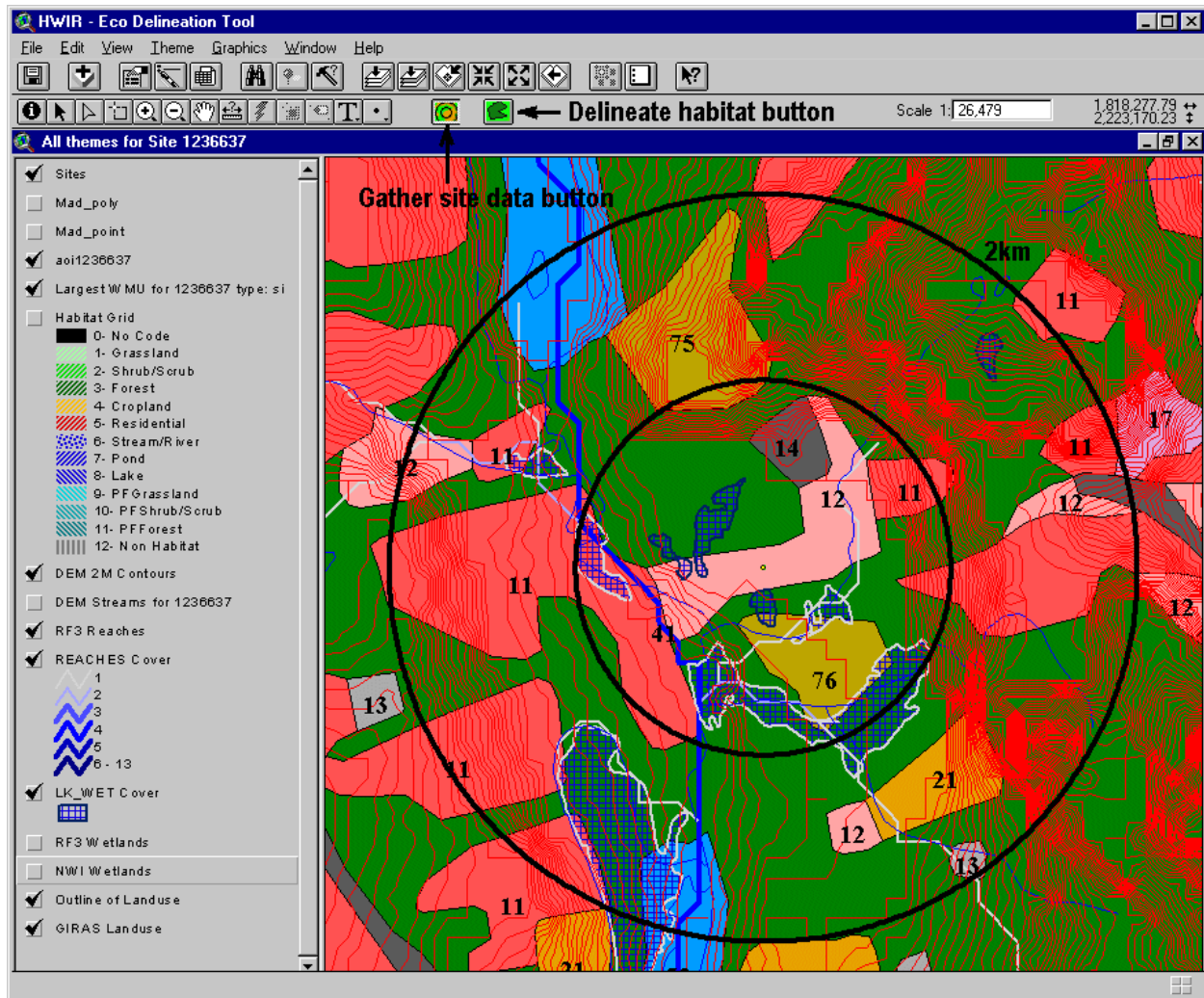


Figure 13-4. Preprocessed habitat codes.

Once the layers were loaded and symbolized, the user could turn them on or off depending on which layers were needed for delineation. Habitats were then delineated in the second script. By pressing a button, the user was prompted to select a group of grid cells and a habitat code from a drop-down list (see Figure 13-5). Because this process worked by changing attributes on grid cells rather than by defining vector polygons, the program ran very quickly, even over a network.

13.3.2 Terrestrial Habitat Delineation

Habitats were delineated at each site within a defined area of interest. For purposes of making risk management decisions, OSW decided to evaluate ecological risks within a 0-1 kilometer radius, a 1-2 kilometer radius, and across the site. These different areas for evaluation are designated by the variable NumEcoRing. It should be noted that risks calculated for habitats that overlap both distance rings are attributed to each ring.

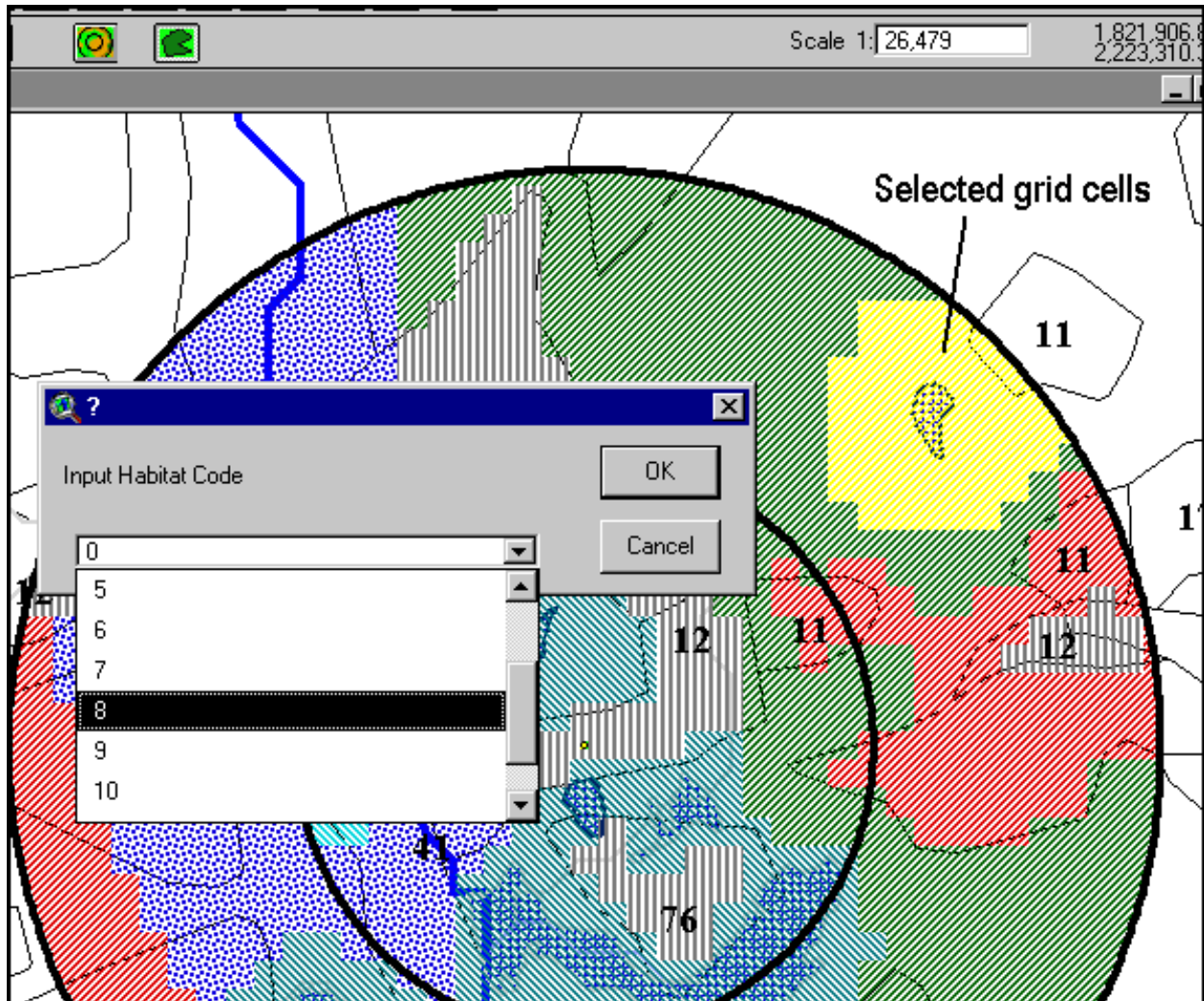


Figure 13-5. Delineation tool habitat code drop-down list.

To delineate the terrestrial habitats at each WMU site, the representative habitat types were correlated with Anderson land use categories. The Anderson Land Use Classification, developed by the USGS, assigns land use descriptors to areas that are distinguishable in satellite and other remotely sensed data. Digitized Anderson land use data are readily available through GIRAS and, therefore, provide a useful tool for locating habitats. GIRAS provides comprehensive digital land use data for the conterminous United States originally collected by the USGS and then converted into the ARC/INFO GIS format by EPA. GIRAS land use/land cover (LU/LC) data delineate land use patterns with respect to vegetation (e.g., rangelands, forests), human activity (e.g., residential, agricultural), and waterbodies (e.g., streams, lakes, wetlands). Although these data are 15 to 25 yr old and, therefore, do not reflect current conditions in some locations, the GIRAS data set is the most complete and current national data set available. A full description of GIRAS data and methods for use in the HWIR analysis is presented in Section 7.0.

The Anderson land use codes correlate reasonably well with the representative terrestrial habitats, and a simple crosswalk between the two classifications is possible for most categories (see Table 13-17). Because the land use classification and the habitats were developed for different purposes and use different terminology, however, certain assumptions and subjective decisions were necessary to correlate the two. In general, the land use categories reflect a finer level of detail (24 categories as compared to 14 habitats) and are based on human activities and land use rather than on purely biotic and abiotic criteria. The land use categories also include five categories for tundra and two for perennial ice and snow, none of which is relevant to WMU sites, and four aquatic and two wetland categories, which are overridden for the HWIR analysis by spatial data specific to wetlands and surface waterbodies (see Sections 13.3.2 and 13.3.3).

Table 13-18. Crosswalk: Anderson Land Use Codes and Ecological Receptor Habitats

Anderson Land Use Code	Habitat (HabType)
1 Urban or Builtup Land	
11–Residential	Residential
12–Commercial and services	Nonhabitat
13–Industrial	Nonhabitat
14–Transportation, communications, and utilities	Included in largest adjacent habitat
15–Industrial and commercial complexes	Nonhabitat
16–Mixed urban or builtup land	Nonhabitat
17–Other urban or builtup land	Residential
2 Agricultural Land	
21–Cropland and pastures	Crop fields/pastures
22 –Orchards, groves, vineyards, nurseries, and ornamental horticultural areas	Residential
23–Confined feeding operations	Nonhabitat
24 –Other agricultural land	Default to largest adjacent or proximate agricultural polygon
3 Rangeland	
31–Herbaceous rangeland	Grassland
32–Shrub and brush rangeland	Shrub/scrub
33–Mixed rangeland	Default to proximate rangeland habitat

(continued)

Table 13-18. (continued)

Anderson Land Use Code	Habitat (HabType)
4 Forest	
41–Deciduous forest land	Forest
42–Evergreen forest land	Forest
43–Mixed forest land	Forest
5 Water	
51–Streams and channels	Stream/river habitats delineated based on DEM and RF3 data
52–Lakes (GIRAS data used to delineate lakes or ponds only if NWI data are not available)	
Lakes =/<10 ha	Pond
Lakes >10 ha	Lake
53–Reservoirs (GIRAS data used to delineate lakes or ponds only if NWI data are not available)	
Lakes =/<10 ha	Pond
Lakes >10 ha	Lake
54–Bays and estuaries	Not included in HWIR analysis
6 Wetland (GIRAS data used to delineate wetlands only if NWI data are not available)	
61–Forested	Permanently flooded forest
62–Nonforested	Permanently flooded grassland
7 Barren Lands	
71–Dry salt flats	Shrub/scrub
72–Beaches	(Refer to adjacent surface waterbody type)
73–Sandy areas other than beaches	Shrub/scrub
74–Bare exposed rock	Nonhabitat
75–Strip mines, quarries, gravel pits	Nonhabitat
76–Transitional areas	Nonhabitat
77–Mixed barren land	Nonhabitat
8 Tundra	
Not applicable	
9 Perennial Snow or Ice	
Not applicable	

Anderson land use categories for industrial and commercial uses were assumed to lack the soil and vegetation communities necessary to support wildlife and are delineated as nonhabitat. One agricultural category, confined feeding operations, and the unvegetated barren land categories are also delineated as nonhabitat because these areas would not be expected to provide food or water for receptors.

Figures 13-6 and 13-7 show an example of terrestrial habitat delineation based on land use codes. Figure 13-6 shows an example site with the land use data, and Figure 13-7 shows the site with the resultant habitat delineation.

13.3.2.1 Crosswalk Inconsistencies. Certain inconsistencies between the Anderson land use classification and the HWIR representative habitats raise the possibility of double coverage or omission of certain areas. In most of these cases, the mapped Anderson land use category encompasses more than one HWIR habitat type, yet no data exist to further identify habitats within a single mapped land use category. Inconsistencies between the Anderson land use codes and the representative habitats are discussed on a category-specific basis here. Many of the inconsistencies were resolved based on decision rules using the largest adjacent or proximate similar land use polygon as the default. These decision rules are based on the assumption that the predominant land use in an area is likely to exert the greatest influence on receptors occurring in the vicinity. Therefore, when the habitat designation for a polygon could not be determined with certainty, data from the largest adjacent or proximate polygon were used.

11-Residential. Anderson land use code 11 corresponds with the residential habitat type. The land use code definition, however, notes that high-density as well as low-density housing areas are included. The residential habitat is intended to cover areas where lawns, gardens, and landscaped areas provide habitat for species such as passerine and ground birds and small mammals. The high-density residential areas included in land use code 11 probably do not provide such habitat. The GIRAS data, however, give no indication about whether an area mapped as land use code 11 is high- or low-density residential. Lacking any distinguishing data, all areas mapped as land use code 11 were delineated as residential habitats.

14-Transportation, Communication, and Utilities. Anderson land use code 14 covers industrial areas but also includes several land use types characterized by open green space, such as highway right-of-ways, airport runway areas, and utility line power cuts and pipelines. These areas provide habitat described by the grassland habitat. Therefore, the predominant adjacent land use was used as an indicator of habitat type. Areas mapped as land use code 14 were treated as nonhabitat if the largest adjacent polygon's classification was industrial or commercial in nature. All other polygons classified as Anderson land use code 14 were delineated as grassland habitat.

16-Mixed Urban or Builtup Land. Anderson land use code 16 was applied when more than one-third of an area consists of mixed urban or builtup uses that cannot be separated from each other at mapping scale. This land use is largely industrial or commercial but can include farmsteads intermixed with industrial or commercial uses. Farmsteads presumably include farmhouses and their immediate surroundings and correspond to the residential habitat type. Because of the variable nature of mixed categories, a precise habitat assignment was difficult to

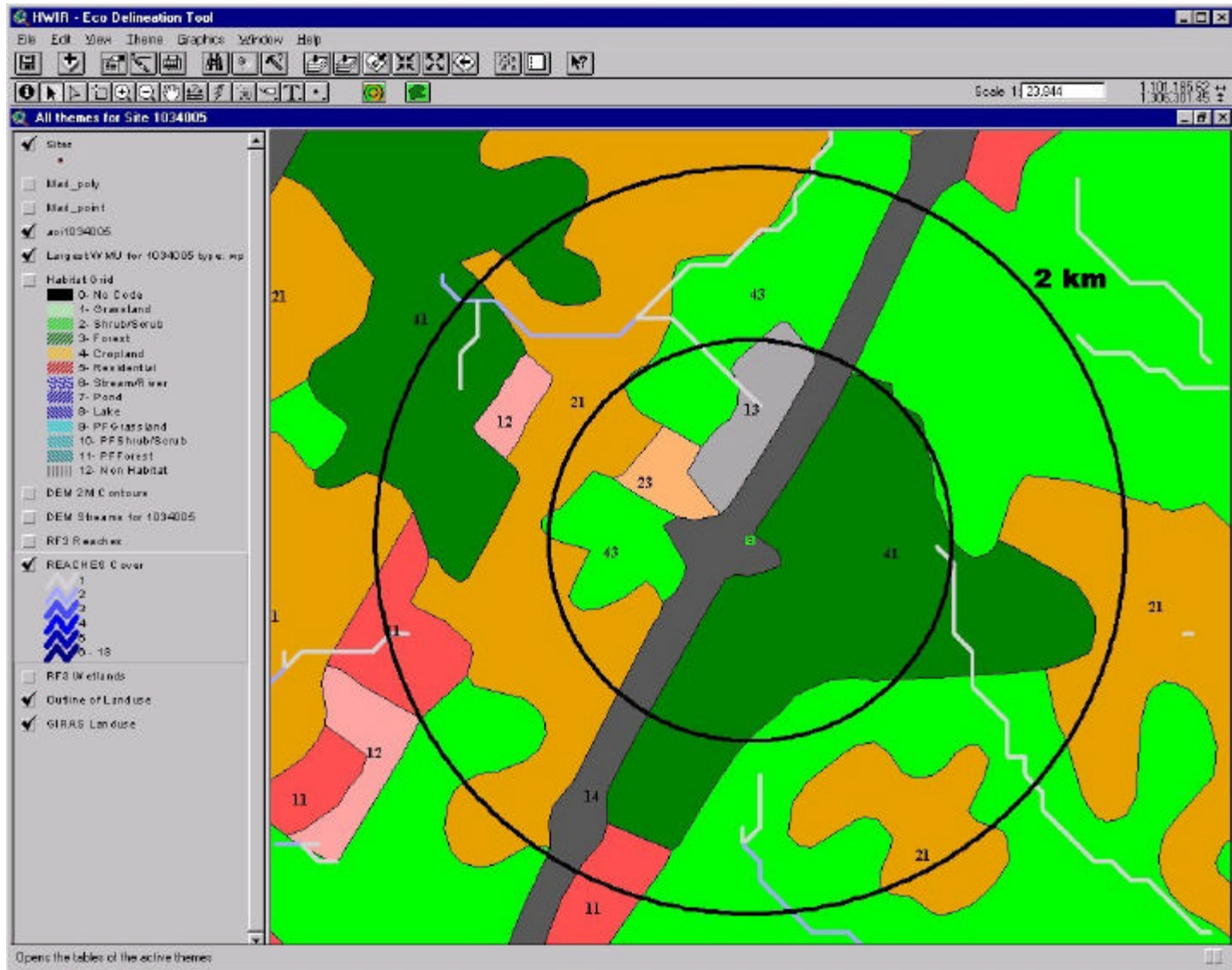


Figure 13-6. Example delineation of terrestrial habitats–land use data.

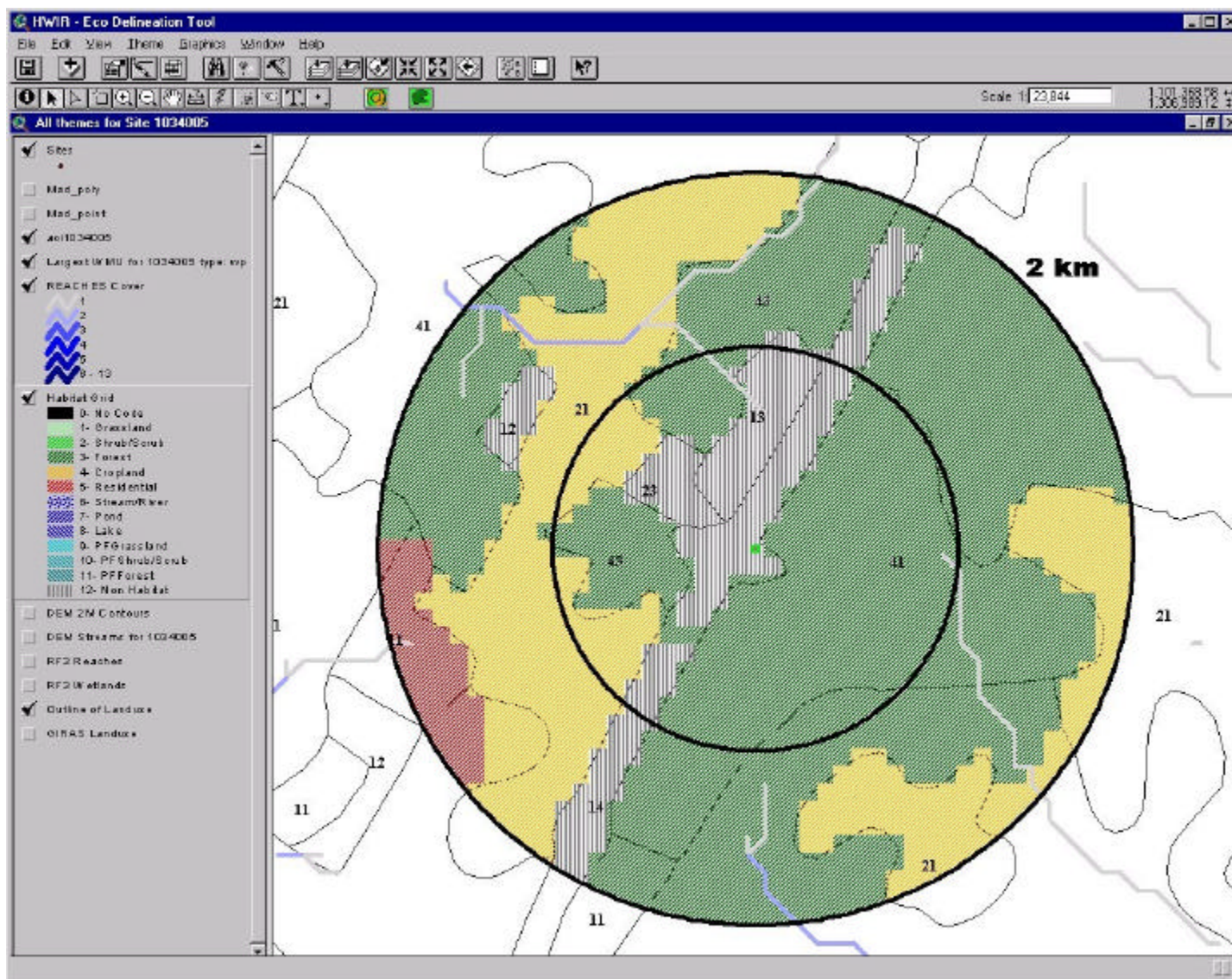


Figure 13-7. Example delineation of terrestrial habitats.

make. Therefore, these areas were classified as nonhabitat, which was anticipated to be appropriate for most cases.

17–Other Urban or Builtup Land. This category is defined as typically consisting of golf driving ranges, zoos, parks, and the undeveloped portions of golf courses and ski resorts (e.g., portions other than buildings and parking areas). Most of these areas are characterized by grass, lawns, and landscape plantings and are best categorized as residential habitats. The undeveloped portions of ski resorts are a notable exception; such areas are probably best classified as grassland or forest. Because this particular land use was unlikely to occur in HWIR study sites, Anderson land use code 17 polygons were delineated as residential.

21–Cropland and Pasture. This Anderson land use classification does not distinguish between crop fields and pastures. Pasture vegetation generally consists of a variety of herb and grass species and provides a relatively diverse habitat. Crop fields, on the other hand, are generally monocultures and may lack vegetation during the nongrowing season. Overlapping but different suites of receptors would be expected to use these two habitat types. Because the GIRAS data do not distinguish between crop fields and pastures, the two habitat types were combined into one representative habitat (crop fields/pastures) to correspond with the land use classification.

22–Orchards, Groves, Vineyards, Nurseries, and Ornamental Horticultural Areas. Areas covered by this land use category generally consist of ornamental or non-native plant species interspersed with areas dominated by grasses and herbs. These areas would not be included in the Anderson land use classification for residential areas because they reflect entirely different human activities— that of horticultural operations versus homes. Considering receptor habitat characteristics, however, they are most similar to the residential habitat type.

24–Other Agricultural Land. Anderson land use code 24 covers a relatively wide variety of land uses associated with other agricultural categories, such as farmsteads, corrals, farm lanes, and horse training areas. In general, these areas are too small to be distinguished from the surrounding land use, and the definition of this category states that their small size and scattered occurrence “generally results in their inclusion with adjacent agricultural areas” (Anderson et al., 1976, p. 21). Therefore, areas classified as Anderson land use code 24 were delineated as part of the predominant adjacent habitat.

33–Mixed Rangeland. The mixed rangeland category covers sites that consist of a mixture of both shrub/scrub and grassland over at least one-third of their area. These areas were delineated as parts of the predominant proximate rangeland habitat. If none of the surrounding habitat was rangeland, then the mixed rangeland was randomly assigned to either code 31 or 32.

41 through 43–Forest Lands. The land use classification for forested areas includes separate categories for deciduous (41), evergreen (42), and mixed (43) forests; clearcut areas that have not been put into subsequent use are classified as forests. The representative habitats do not differentiate between deciduous or evergreen forests because the receptor groups are essentially the same for both. Therefore, all three forest land uses were delineated as forest habitat. Although clearcut areas provide a distinct habitat type that supports different receptor species than a

standing forest, these areas are included in Anderson land use codes 41 and 42. Lacking data to distinguish clearcuts from forests, clearcut areas were not addressed in the exposure assessment.

51 through 54–Water. GIRAS data were used to delineate lakes and ponds only when NWI data were not available.

61 and 62–Wetlands. GIRAS data were used to delineate wetlands only when NWI data were not available. When GIRAS data were used to delineate wetlands, it was assumed that the wetlands' flood regime was adequate to support fish. In general, GIRAS data do not recognize wetlands at the drier end of the flood regime continuum.

71–Dry Salt Flats. By definition, this land use category occurs only in the desert southwest and covers barren or nonvegetated areas. These areas were assigned to the shrub/scrub habitat, which was expected to be the dominant habitat in the desert southwest.

72–Beaches. Beaches are defined as a land use occurring along shorelines and presumably are associated with lakes and rivers. Therefore, these areas were included in the waterbody margin habitats. For example, a beach at a lake edge was delineated as a lake margin habitat. The waterbody margin habitats included terrestrial receptor groups that would be associated with river and stream corridors or pond and lake margins, including beaches. (Marine beaches were not included in the HWIR analysis.)

73–Sandy Areas Other than Beaches. This land use category covers a diverse range of ecosystems, including, for example, deserts, sandhills, and flood plains. For the HWIR analysis, it was assumed that a sand substrate indicates xeric, nutrient-poor conditions that can be expected to support shrub/scrub-type vegetation. Many prominent sand-based land features, such as southeastern coastal plain sandhills and desert dunes, are characterized by sparse scrub vegetation, thus indicating that shrub/scrub was a reasonable default habitat for this land use code.

74 and 75–Barren Lands. These land use categories are characterized by lack of vegetation, either as their natural state (bare exposed rock) or caused by mining or excavation activities (strip mines, quarries, and gravel pits). It was assumed that no significant habitat occurred in these areas and that no receptors were present.

76–Transitional Areas. Transitional areas are defined as those where some human activity has significantly altered the landscape, but the intended use is not yet evident. The remote imagery data were not sufficient for more specific classification. Examples include forests that have been cut, wetlands that have been drained, or areas that have been altered by filling. For the HWIR analysis, it was assumed that transitional areas do not support established food webs, and no receptors were attributed to these areas.

77–Mixed Barren Lands. The mixed barren land category includes combinations of categories 71 through 76. These areas were delineated as nonhabitat.

81 through 85–Tundra. The tundra category was not applicable to HWIR sites.

91 and 92–Perennial Snow or Ice. The perennial snow or ice category was not applicable to HWIR sites.

13.3.3 Delineation of Waterbody Margin Habitats

As described in Section 13.1, some terrestrial receptor species depend on aquatic habitats for some or all of their food. These exposure scenarios are assessed in the waterbody margin habitats. Stream corridor and pond and lake margin habitats were delineated adjacent to the waterbodies generated as part of the waterbody and watershed layout data processing. Data sources for delineation of streams include DEM data (USGS, 1990), RF3-Alpha data (U.S. EPA, 1994c), and GIRAS data (U.S. EPA, 1994b). Data sources for delineation of ponds and lakes include GIRAS and the National Wetland Inventory (NWI) (U.S. FWS, 1998b). Section 5.0 describes the collection and processing of these data and the delineation of waterbodies at each site. Once the streams, ponds, and lakes were delineated at each WMU site, their respective corridor and margin habitats were added. Several methodologies were considered to determine the size and shape of the corridor and margin habitats. There is no simple correlation between waterbody characteristics and wildlife distribution within corridors and margins, however. The vegetation, topography, and land use of the adjacent land as well as the size, depth, flow, and aquatic food web of the waterbody are but a few of the more prominent variables that affect wildlife use of waterbody margin habitats.

To develop a reasonable method requiring an appropriate level of effort for waterbody margin habitat delineation, a stepwise approach was adopted. Elevation contours were assumed to be the best indicators of stream corridors and pond and lake margins. Using DEM contour data, an attempt was made to determine a visual natural limit for the corridor or margin. Because waterbodies occur in the landscape along elevation contours, natural boundaries were frequently evident. If no contour-based boundaries were apparent, surrounding land use was used instead. For example, if GIRAS data indicated a forest buffer running parallel to a stream and a commercial or industrial area adjacent to the forest, the stream corridor would consist of the forest buffer. When neither contours nor land use indicated corridor or margin boundaries, a default minimal margin was delineated. Waterbody margin habitats at a single site were combined, or bridged, as were terrestrial habitat patches.

Delineation of waterbody margin habitats was based entirely on hand-delineation and required the most subjective decision-making in the habitat delineation process. Exposure and risk estimates for these habitats, therefore, include additional uncertainty as compared to the terrestrial and wetland habitats.

Figures 13-8, 13-9, and 13-10 illustrate the delineation of waterbody margin habitats. Figure 13-8 shows the land use data, and Figure 13-9 shows the elevation data for an example site. These data layers are the primary determinants of the waterbody margin habitats. Figure 13-10 shows the resultant habitat delineation for this site.

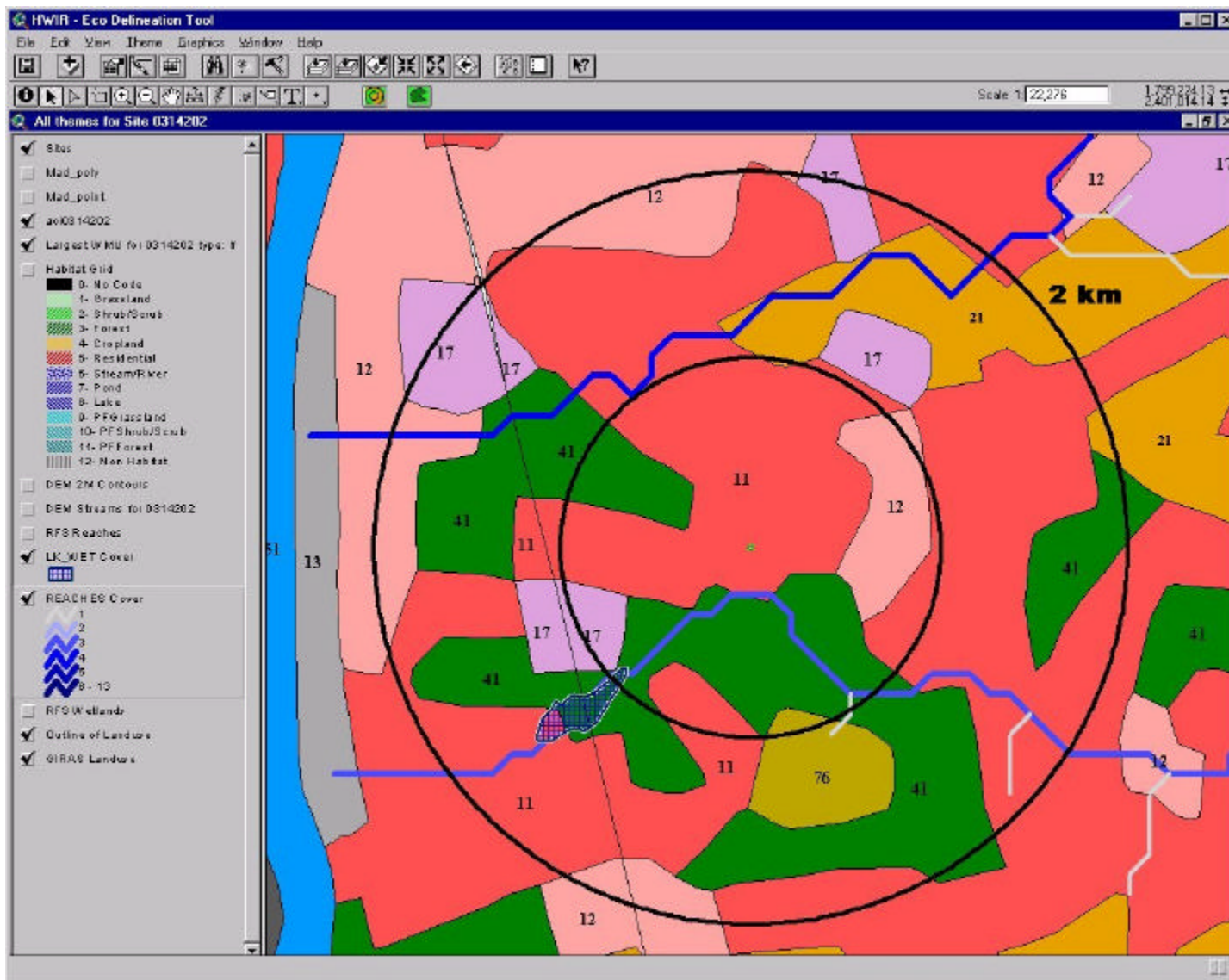


Figure 13-8. Example delineation of waterbody margin habitats–land use data.

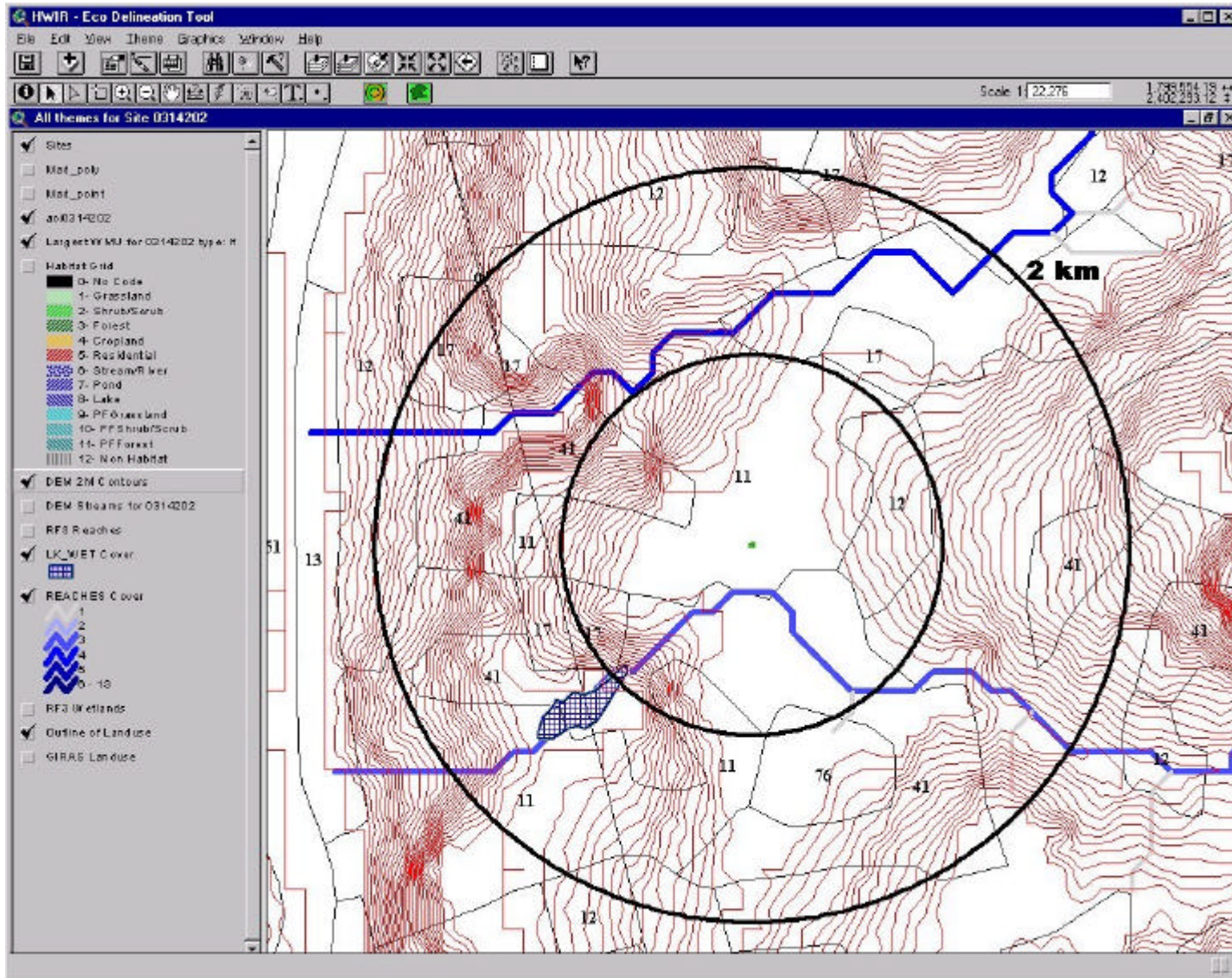


Figure 13-9. Example delineation of waterbody margin habitats–elevation data.

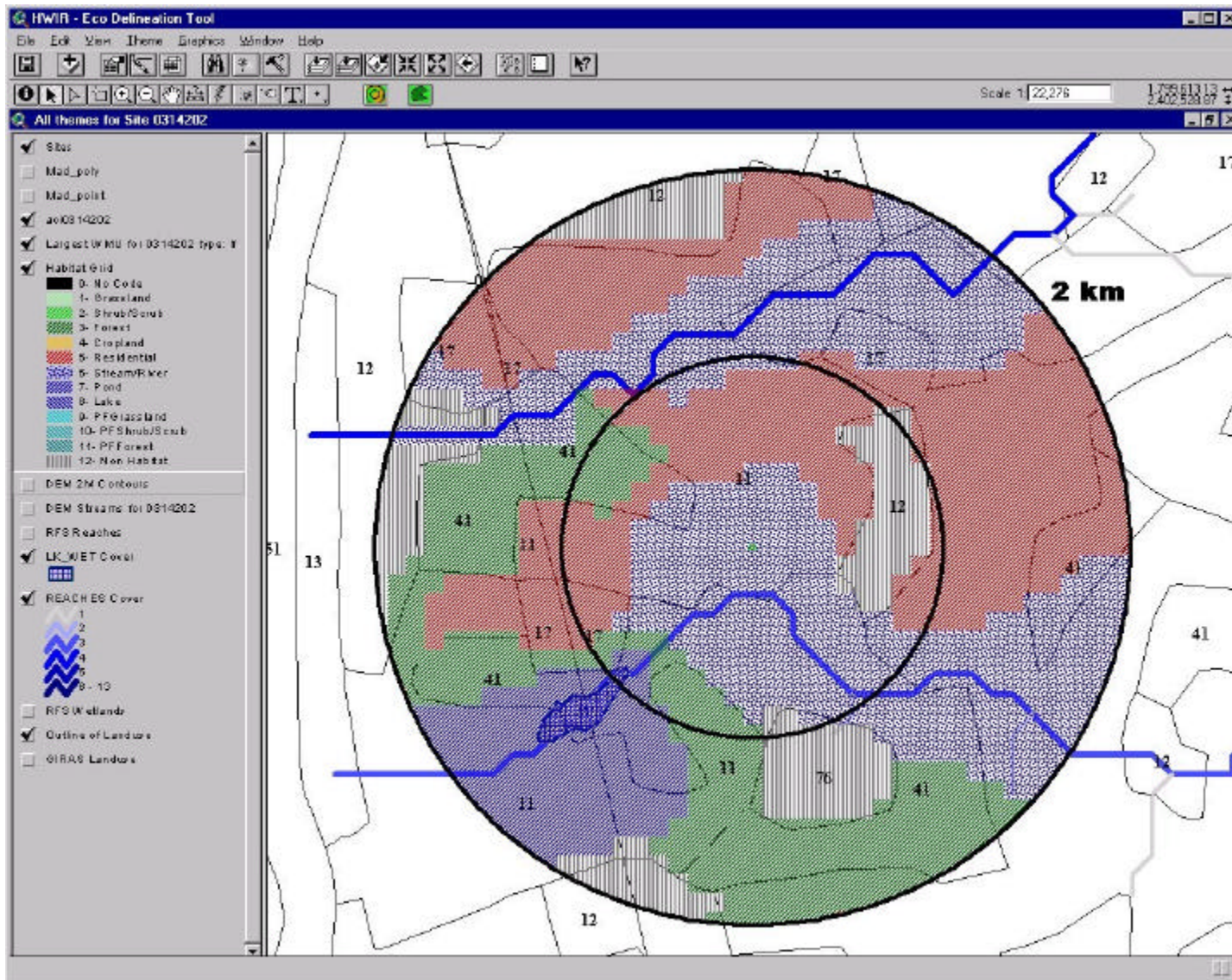


Figure 13-10. Example delineation of waterbody margin habitats.

13.3.4 Delineation of Wetland Habitats

NWI data provide the most complete and readily available digitized data on location and type of wetlands on a national scale (U.S. FWS, 1998b). NWI data, however, have not yet been digitized for the entire United States. Of the 201 WMU sites, 100 are in areas for which NWI data are digitized, but an alternate data source was needed for the remaining sites. Wetland data from GIRAS were used for areas where digitized NWI data were not available.

Wetland identification and classification in the NWI are based on photo interpretation of remote imagery at a 1:24,000 scale. Each wetland polygon identified is classified and coded according to the Cowardin et al. (1979) classification system, which indicates substrate type, dominant vegetation, and hydrologic regime, as well as additional details regarding soil and water chemistry where relevant. The GIRAS wetland data are on a 1:80,000 or smaller scale and only distinguish between wetlands dominated by woody vegetation and those not dominated by woody vegetation (Anderson et al., 1976). GIRAS data do not show wetlands smaller than 16 ha (39.5 acres). Consequently, there is significant variation in the level of detail in the wetland data for sites with and without NWI coverage. Because the NWI provides high-quality data that readily distinguish the different wetland habitat types, it was selected as the primary source for wetland data despite its coverage of only half the HWIR sites. GIRAS data were used to identify and delineate wetlands at the remaining sites.

13.3.4.1 Wetland Flood Regime. The HWIR representative habitats include three intermittently flooded and three permanently flooded wetland types (see Table 13-1). The primary criterion for this division is the wetlands' ability to support fish populations. When NWI data were available, this distinction was made based on water regime modifiers in the NWI code. Table 13-18 presents the NWI water regime codes that appear in the HWIR site wetlands and brief descriptions of the flood regime indicated by each code. Based on the descriptions in Cowardin et al. (1979), a decision was made about whether each water regime would be expected to support an aquatic food web that includes T3 or T4 fish. Wetland types with flood regimes that indicate the presence of sufficient flooding to support fish populations were delineated as permanently flooded wetlands. Those wetlands in which flooding is infrequent or of short duration were delineated as intermittently flooded wetlands. As discussed in Section 5.4 and Figure 5-4, wetlands were modeled as hydrologically connected or not connected to surrounding waterbody networks based on this same criterion and methodology.

When NWI data were not available, GIRAS data were used. GIRAS data, however, do not include information on the wetland flood regime. All GIRAS-identified wetlands were delineated as permanently flooded because GIRAS generally does not recognize wetland ecosystems at the drier end of the wetland flood regime continuum.

13.3.4.2 Treatment of Intermittently Flooded Wetlands. Table 13-19 indicates, based on the NWI water regime code, whether wetlands were considered intermittently or permanently flooded. Those wetlands designated as intermittently flooded were then further classified according to the representative wetland habitats as intermittently flooded grassland, shrub/scrub, or forest wetlands. These determinations also were made based on NWI codes. Table 13-20 shows a crosswalk of NWI codes with representative wetland habitat types.

Table 13-19. NWI Water Regime Modifiers Relevant to HWIR Analysis

Water Regime Modifier	Flood Regime	Wetland Habitat Type: Intermittent/Permanent
A–Temporarily flooded	Surface water present for brief periods during growing season	Intermittent
B–Saturated	Soil saturated to surface for extended periods during growing season	Intermittent
C–Seasonally flooded	Surface water present for extended periods, especially during early part of growing season; water table variable in absence of flooding	Intermittent Permanent if adjacent to stream order 3 or higher
D–Seasonally flooded/ well drained	Similar to C	Intermittent
E– Seasonally flooded/ saturated	Surface water present for extended periods, especially during early part of growing season; substrate remains saturated for most of growing season	Intermittent Permanent if adjacent to stream order 3 or higher
F–Semipermanently flooded	Surface water present throughout growing season; in absence of flooding, water table at or near surface	Permanent
G–Intermittently exposed	Surface water present throughout year except in times of extreme drought	Permanent
H–Permanently flooded	Surface water present throughout year in all years	
J–Intermittently flooded	Substrate usually exposed, but surface water present for variable periods without seasonal periodicity	Intermittent
K–Artificially flooded	This code is generally accompanied by a second code indicating the water regime	Permanent
N–Regularly flooded	Flooded by tides at least once daily; can be used for tidal freshwater systems	Permanent
R–Seasonal tidal	No definition given; can be used for tidal freshwater systems	Intermittent
S–Temporary tidal	No definition given; can be used for tidal freshwater systems.	Intermittent
T–Semipermanently tidal	No definition given; can be used for tidal freshwater systems	Permanent
U–Unknown	Water regime unknown	Intermittent
V–Permanent tidal	No definition given; can be used for tidal freshwater systems	Permanent

(continued)

Table 13-19. (continued)

Water Regime Modifier	Flood Regime	Wetland Habitat Type: Intermittent/Permanent
W—Intermittently flooded/ temporary	No definition given	Intermittent
Y—Saturated/semipermanently/ seasonal	No definition given	Intermittent
Z—Intermittently exposed/ permanent	No definition given	Permanent

Table 13-20. Crosswalk: National Wetland Inventory Codes and Wetland Habitats

NWI Code	Habitat
E—Estuarine	Not assessed
M—Marine	Not assessed
L1—Lacustrine, limnetic	Pond or lake ¹
L2 —Lacustrine, littoral OW, RB, UB, RS, EM AB water regime I ² AB water regime II ²	Pond or lake ¹ PFG IFG PFG
R—Riverine	River/stream
P—Palustrine RB,UB AB ML, EM water regime I ² ML, EM water regime II ² SS water regime I ² SS water regime II ² FO water regime I ² FO water regime II ²	Pond or lake ¹ PFG IFG PFG IFS IFF PFF PFS

¹ Use surface area to distinguish between lakes and ponds.

² Water regime I: codes A, B, C, D, E, J, R, S, U, W, or Y.

³ Water regime II: codes F, G, H, K, N, T, V, or Z.

Habitat codes:

IFG –intermittently flooded grassland
IFS–intermittently flooded shrub/scrub
IFF–intermittently flooded forest
PFG–permanently flooded grassland
PFS–permanently flooded shrub/scrub
PFF–permanently flooded forest

NWI class codes:

AB–aquatic bed
EM–emergent vegetation
FO–forested
ML–moss/lichen-dominated
OW–open water
RB–rock bottom
RS–rocky shore
SS–shrub/scrub
UB–unconsolidated bottom

For the HWIR analysis, the three intermittently flooded wetland habitats were identified and designated, but their boundaries were not delineated. Many intermittent wetlands occur as small scattered habitat patches and, even when combined with similar patches in an AOI, often do not constitute large enough areas for placement of home ranges. The placement of home ranges within the numerous small patches of intermittent wetland habitat was deemed more resource-intensive than warranted. However, these areas are known to provide important, albeit highly fragmented, habitat. Therefore, during site layout data processing, intermittent wetlands were identified as inclusions within surrounding upland habitats (e.g., grassland, forest), and their unique receptor species were included in the data passed to the ecological exposure module. In this manner, the receptors expected to occur in intermittent wetlands were included in the exposure assessment, although their habitat and home ranges were not delineated on a site-specific basis. The decision to assess exposure for these receptors without expending the resources to delineate each habitat and home range allows for their inclusion in the risk assessment at a reasonable level of effort.

An exception was made to this approach for certain intermittent wetlands adjacent to streams of order 3 and higher. Water regimes C and E (seasonally flooded and seasonally flooded/saturated) imply seasonal flooding for extended time periods; in wetlands adjacent to fishable stream reaches (stream order 3 and higher), water regimes C and E could potentially support an aquatic food web. Therefore, these intermittent wetlands, whether grassland-, shrub/scrub-, or forest-dominated, were delineated when they occurred adjacent to streams of order 3 or higher. These habitats were treated in a manner identical to the permanently flooded wetlands, as described in the following section.

13.3.4.3 Delineation of Permanently Flooded Wetlands. Permanently flooded wetlands were identified at each site based on the NWI codes, as shown in Tables 13-18 and 13-19. When NWI data were not available, GIRAS data were used. GIRAS data classify wetlands as forested or nonforested and do not include any information on the flood regime. Because most national data sets generally apply the term wetlands to tidal and other aquatic habitats and do not recognize noninundated areas as wetlands, the HWIR analysis assumes that wetlands identified in GIRAS data fall within the permanently flooded wetland habitats. The forested GIRAS wetlands were delineated as permanently flooded forested wetlands; the nonforested GIRAS wetlands were delineated as permanently flooded grasslands. Although some of the wetlands included in the GIRAS data are undoubtedly dominated by shrub/scrub vegetation, the data do not allow this distinction to be made. In the absence of better data, the intermittently flooded grassland habitat was considered the most appropriate alternative.

Permanently flooded wetlands frequently occur in association with streams, rivers, lakes, and ponds. Thus, the potential arises for areas adjacent to waterbodies to include both wetlands and waterbody margin habitats. The most effective and straightforward approach to handle this situation appeared to be to default to the wetland habitat when wetlands and waterbody margin habitats overlapped. In fact, many wildlife receptors probably forage across both waterbody margin and wetland habitats, while other species show a preference for or tend to avoid the wetland habitat. Because this degree of variability in habitat usage is beyond the reach of the HWIR model, wetland habitats were delineated whenever they were indicated, including within a waterbody margin. Thus, wetlands occurring near waterbodies were not subsumed in the stream

corridor or lake and pond margin habitat. In general, waterbody margin habitats occur on HWIR sites more frequently than do wetland habitats, and a significant number of wetland habitats would have been eliminated from the assessment if waterbody margin habitats had been delineated to subsume co-occurring wetlands.

Examples of wetland habitat delineation are shown in Figures 13-11 and 13-12. Figure 13-11 shows NWI data for the example site, including the NWI codes indicating water regime. Figure 13-12 shows the resultant habitat delineation.

13.4 Placement of Receptor Home Ranges

The delineation of habitats allowed for the placement of receptor species at each site. A substantial amount of data processing takes place at this interval, including the assignment of receptor species based on habitat and region and the placement of the receptor species' home ranges at each site. These steps are described in the following subsections. The Arc marco language (AML) programs included in Appendices 13A and 13B place receptor species' home ranges within the delineated habitats.

The initial approaches proposed for home range placement required random placement of each receptor's home range within every habitat in which it occurs, at each of the 201 HWIR sites. In addition, home ranges must be placed so that predator and prey species' home ranges overlap to ensure that the predator has access to the prey. Any approach requiring individual placement of each receptor's home range area proved inordinately resource-intensive. Therefore, a binning approach was adopted to reduce the number of home range placement iterations. Each receptor's average home range size was assigned to one of four bins. Each bin comprises a range of home range sizes, as follows:

- # Bin 1—Home range = or <100,000 square meters (m²),
- # Bin 2—Home range >100,000 and = or <1 million m²,
- # Bin 3—Home range = or >1 million m² and = or <10 million m², and
- # Bin 4—Home range = or >10 million m².

Thus, all receptors with home ranges in Bin 1 were assumed to have a home range size of 100,000 m²; receptors in Bin 2, a home range size of 1 million m²; receptors in Bin 3, a home range size of 10 million m²; and receptors in Bin 4, a home range size of 1 billion m². Appendix 13C presents home range data divided into the four bins. Home ranges were assumed to be circular and placed within delineated habitats so that each bin was entirely contained within the next largest bin. This placement arrangement ensured that predator ranges overlapped with that of all potential prey.

Because receptor exposure dose, as calculated in the ecological exposure module, was adjusted based on the proportion of the home range that falls within the contaminated area (see Section 12.0 for further explanation), the binning approach potentially underestimates the exposure dose for receptors at the low end of each range. For example, the eastern newt has an average home range size of 91 m²; however, since it falls within Bin 1, its home range was assumed to be 100,000 m². Thus, the proportion of the eastern newt's diet taken from

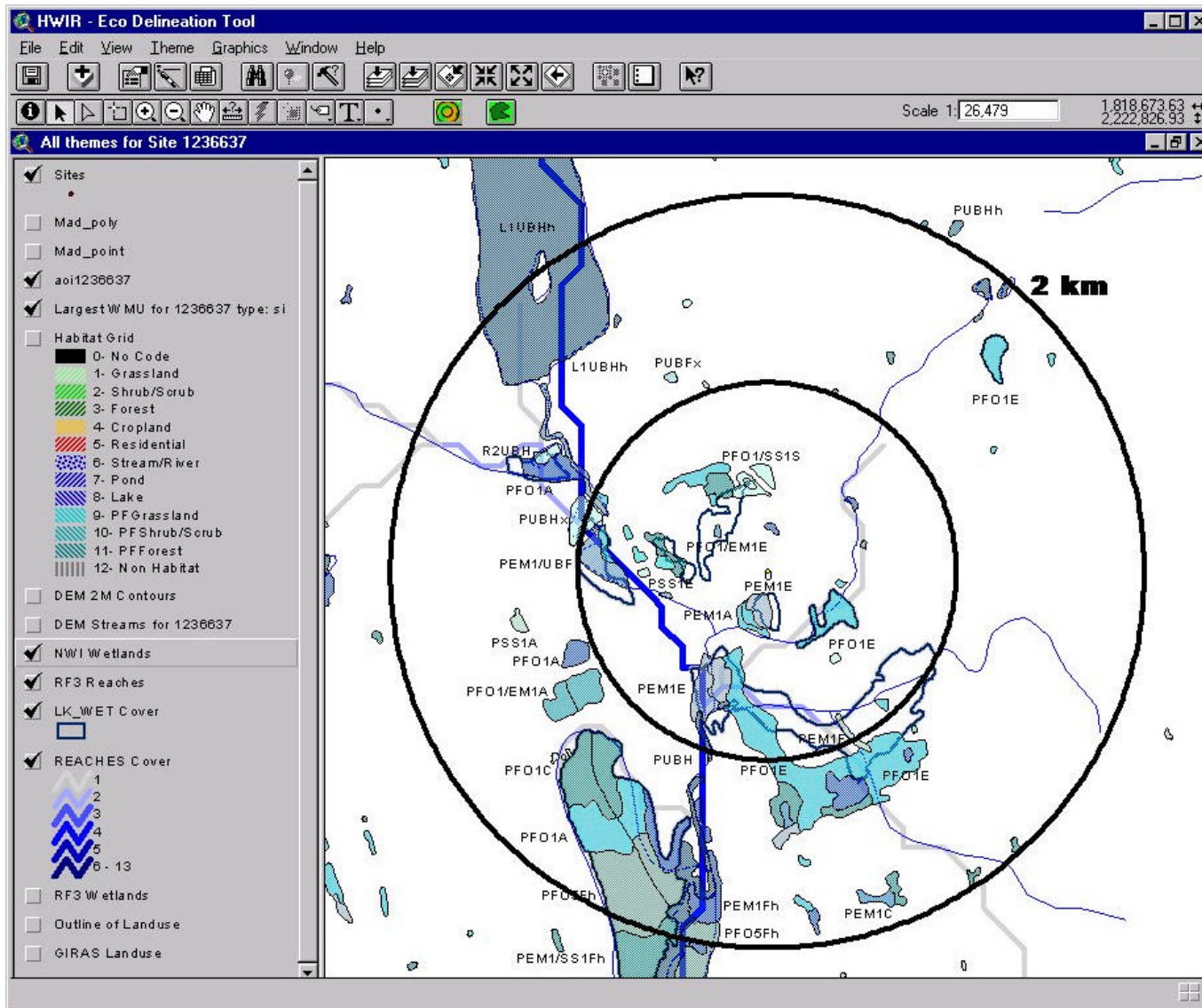


Figure 13-11. Example delineation of wetland habitats–NWI data.

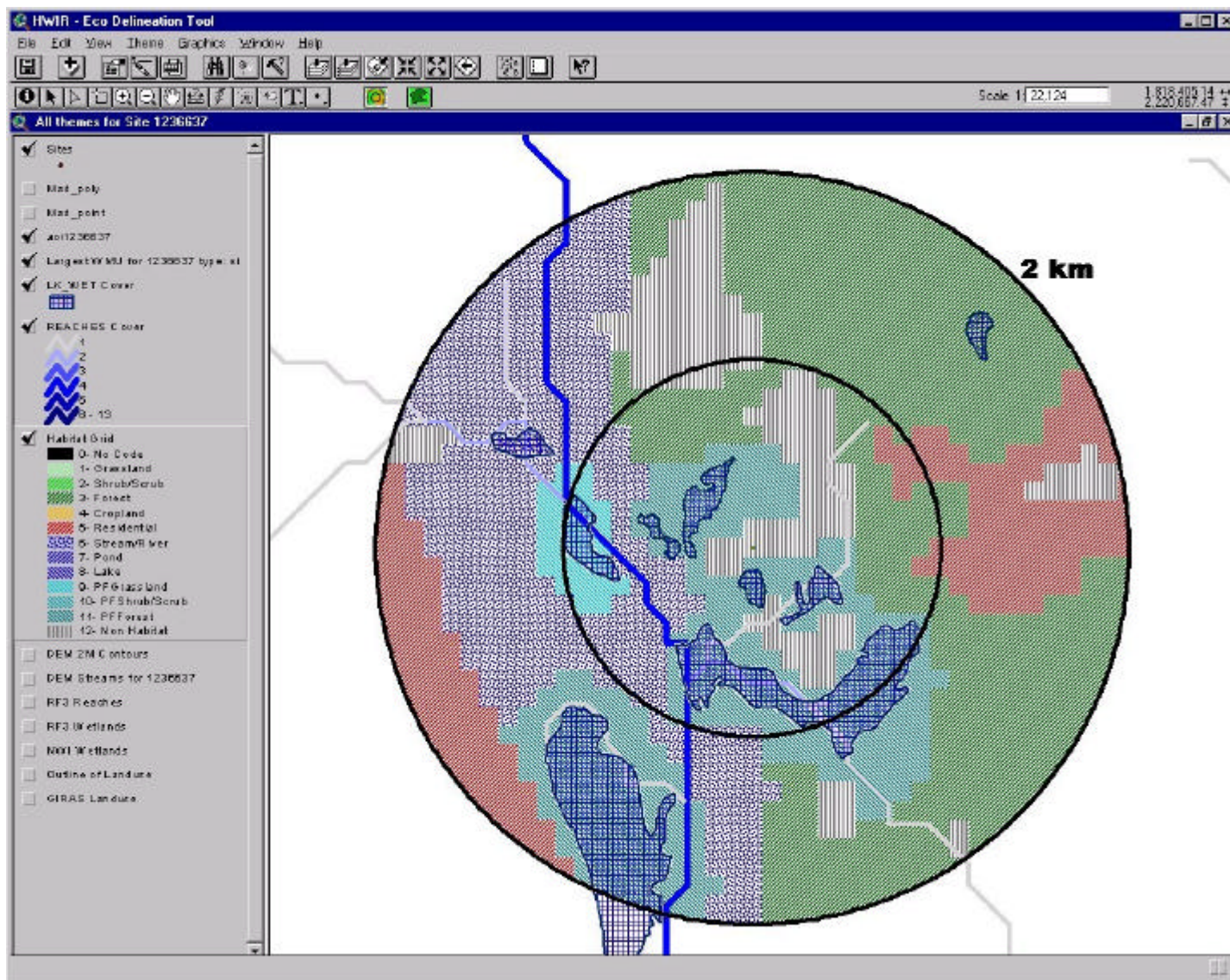


Figure 13-12. Example delineation of wetland habitats.

contaminated habitat will be calculated as the proportion of the 100,000 m² home range that falls within the contaminated area. Obviously, in certain cases, this will be a significantly smaller proportion of the diet than would be estimated if the true mean home range size (91m²) were used.

13.5 Automated Habitat Processing and Home Range Placement

Once habitats were delineated, the processing of the habitats and placement of the home ranges and receptors was fully automated. Processing for these steps took place with ARC/INFO on a SUN Microsystems 450 server. Automated programs written in Arc Macro Language (AML) were used. GIS files are referred to as "coverages" — the proprietary GIS file format used by the ARC/INFO GIS software. Coverages are self-contained GIS layers that hold graphic spatial information (points, lines, polygons) as well as attribute information. Figure 13-13 charts how habitats were delineated and processed. It also illustrates how ecological receptors are placed around each of the 201 HWIR sites and attributed with the information necessary to calculate exposure and risk in the HWIR risk model.

The primary AML programs used within the AML batch process are attached as Appendix 13A [process_habs_ranges.aml] and Appendix 13B [process_ranges.aml].

13.5.1 GIS Data Preparation/Preprocessing

Data preparation and preprocessing included the following steps:

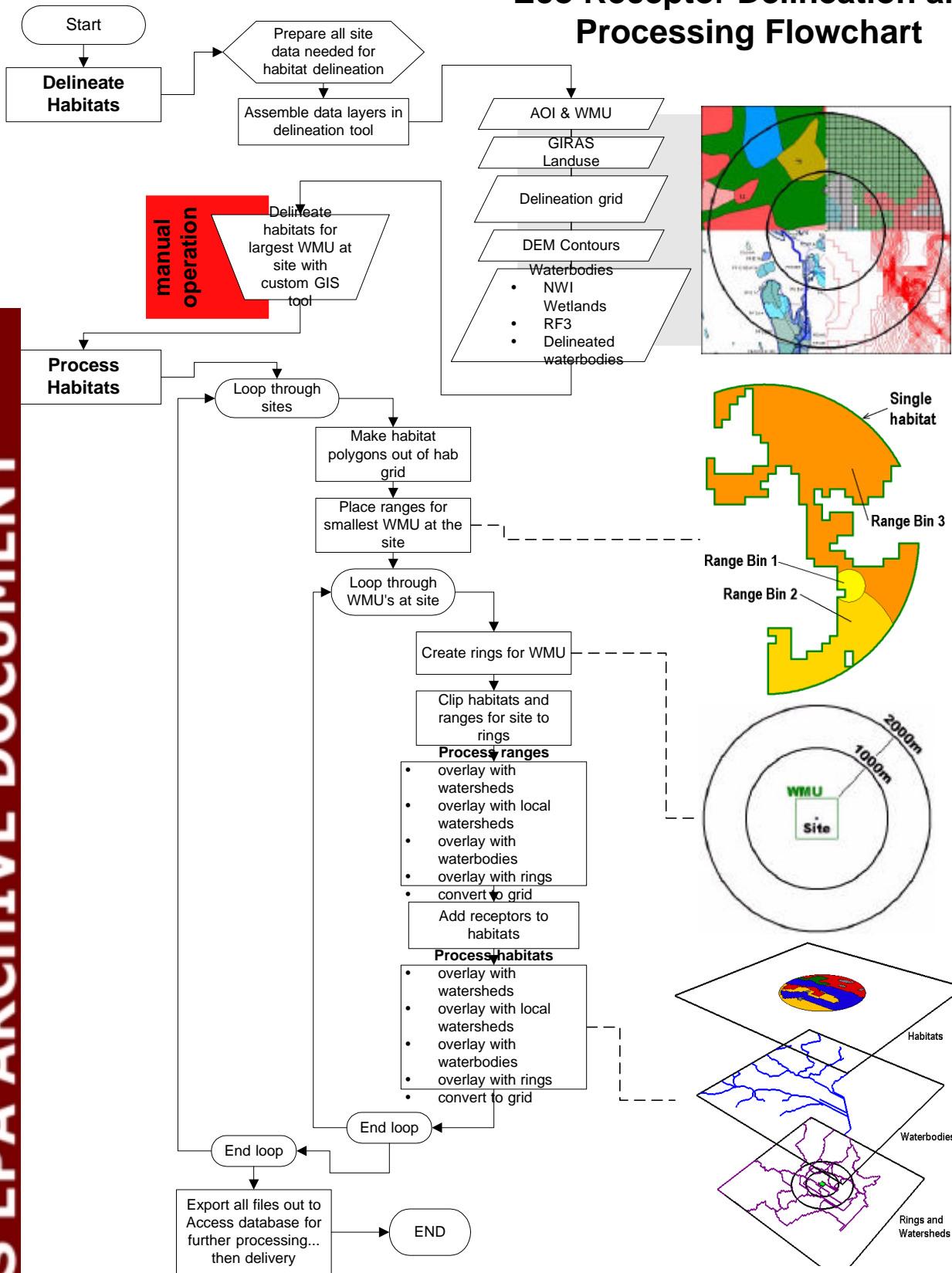
- # Importing finished habitat delineation grid from delineator's computers.
- # Creating AOI and WMU coverages for each site/WMU setting using automated AML programs.
- # Importing watershed and waterbody coverages (see Section 5.0; note that all watershed and waterbody processing must be complete before processing Eco data at a site).

13.5.2 Habitat Processing

This program was designed to process all or a subset of all 201 HWIR sites one site or WMU setting at a time. A master point coverage of all 201 HWIR sites was maintained and holds the location of the site as well as information about the WMU sizes and types at the site. Although there are multiple WMUs at a site, the program processes site-specific data first before looping through the WMUs at the site, as follows:

- # Select a site from the site coverage.
- # Convert the habitat delineation grid into habitat polygons

Eco Receptor Delineation and Processing Flowchart



US EPA ARCHIVE DOCUMENT

- # Place home ranges in habitats. Since habitats were delineated only for the largest WMU at a site, those habitats and the home ranges placed within them were clipped by the WMU specific rings for each WMU at a site.
- # Receptor home ranges were divided into 4 bins, as described above in Section 13.4:
 - Bin 4 = 1,000,000,000 square meters
 - Bin 3 = 10,000,000 square meters
 - Bin 2 = 1,000,000 square meters
 - Bin 1 = 100,000 square meters

Home ranges were placed by calculating a radius to produce a circle with an area matching that of each bin size. A random point was then selected inside of the delineated habitat where the bin was to be placed. A circle polygon was then generated around the random point with the calculated radius. The circle was then clipped by its bounding area (i.e., the delineated habitat boundaries). If the resultant clipped circle still approximately matched the bin area, then the range was placed and the program moved to the next range. If it did not match, then the radius of the circle was increased by 10-m increments until it reached the correct area. This incremental process was repeated until the program produced a polygon that approximately matched the bin area and was contained by the habitat.

Home ranges were placed largest to smallest with the following rules for the bounding areas:

- # Bin 3 must fall entirely within Bin 4
- # Bin 2 must start growing inside Bin 3 but can spill out, though it must stay within Bin 4
- # Bin 1 must start growing with the intersection of Bin 2 and Bin 3.

The following steps were repeated for every WMU at the site:

- # Create ring coverage for the site/WMU setting. Rings were created at 1,000 m and 2,000 m, starting from the diagonal corner of the square WMU and indexed as 1 and 2 respectively.
- # Clip the habitat and the range coverages with ring coverage.
- # Process the clipped home ranges:
 - Home range polygons were then processed with watersheds, local watersheds, and rings. The resultant files contained the home range index, the watershed, local watershed, or ring index and the area of their intersection. These indexes and areas were exported to the Microsoft

Access database program that calculated the home range /watershed fractions and home range /local watershed fractions (see Section 13.5.3).

- Home range polygons were then overlaid with the coverage of waterbodies at the site so that a nearest or impacting waterbody could be found. This was determined as the nearest second-order stream, pond, or lake to the home range.
 - Range polygons were converted to Universal Transverse Mercator (UTM) coordinates and overlaid with the master 100 by 100 m grid file to create the grid tables containing the home range x,y coordinates.
- # Add receptors to the habitat — By looping through the habitats at the site, the receptors were determined by using two lookup tables: receptors by habitat type and receptors by Bailey's section. If a receptor was listed for that habitat type and Bailey's section based on the lookup tables, that receptor was added to that habitat.
- # Process the clipped habitats:
- Habitat polygons were processed with watersheds, local watersheds, and rings. The resultant files contained the habitat index, the watershed, local watershed, or ring index and the area of their intersection. These indexes and areas were exported to the Microsoft Access database program that calculated the habitat /ring fractions (see Section 13.5.3).
 - Habitat polygons were then overlaid with the coverage of waterbodies at the site so that a nearest or impacting waterbody could be found. This was determined as the nearest second-order stream, pond, or lake.
 - Habitat polygons were converted to Universal Transverse Mercator (UTM) coordinates and overlaid with the master 100 by 100 m grid file to create the grid tables containing x,y habitat coordinates.

13.5.3 Database Processing

Following GIS processing, the resulting data tables were imported into Access databases, where Structured Query Language (SQL) and Visual Basic programs were used to prepare the final HWIR model-ready data set, according to HWIR 3MRA modeling system specifications. Database programs included the following processes:

- # Sending only the habitat or home range properties necessary for the models. GIS processed habitats and home ranges identically, but, since only home ranges required connectivity to the watersheds and local watersheds and only habitats required connectivity to the rings, HabRangeWSSubIndex and HabRangeLWSIndex were sent by home range and EcoRingHabIndex was sent by habitat. Similarly, only the coordinates for the home ranges were required by the

HWIR 3MRA modeling system.

- # Converting x,y home range coordinates from UTM to the site coordinate system (i.e., facility centroid = 0,0; see Section 2.0) and formatting the habitat data table in the grid database (grid.mdb) for the HWIR site layout processor (SLP).
- # Calculating all required fractions (*Frac variables in Table 13-1) using area data passed from GIS.
- # Formatting and indexing all variables according to input data table specifications for the site definition processor (SDP).

In addition to the general processing a few variables required more extensive processing.

- # The database processing for HabRangeNumLWSSubA, HabRangeLWSSubAIndex, and HabRangeLWSSubAFrac differentiated between WMU types assigning multiple subareas to the home ranges at land application units and waste piles sites only.¹ Landfills, surface impoundments and aerated tanks were not modeled using multiple subareas, so they had only one subarea consisting of the WMU itself. In addition, if the home range intersected the surface impoundment subarea, HabRangeNumSISrc was set to 1 for that home range.
- # In order to provide a home range for each receptor, the four home range bins (see Section 13.4) automatically generated by the GIS had to be split out by each receptor within the habitat. Table C13-1 in Appendix 13C was used in the database to connect each receptor to its appropriate bin. The bin number was combined with the receptor index (HabRangeRecIndex) to create a unique index for each variable dimensioned on HabNumRange.
- # The waterbody network and waterbody network reach connectivity for the habitats and home ranges, HabWBNIndex, HabNumWBNRch, HabWBNRchIndex, HabWBNRchFrac, HabRangeWBNIndex, HabRangeNumWBNRch, HabRangeWBNRchIndex, and HabRangeWBNRchFrac, needed to be determined on the database end, because the waterbody networks were created during database processing (see Section 5.0). The GIS-assigned reach connectivity was based on each reach at the site having a unique number. The database created waterbody networks, assigning each reach to a network and giving it a new identifier which included the waterbody network identifier and a new reach number. GIS-determined reach-habitat and reach-range connectivity were then converted to the new waterbody network identifiers using a lookup table of network identifier by GIS identifier.
- # The determination of fishable reaches was done by database processing as

¹ GIS processing always split local watersheds into multiple subareas independent of the WMU type.

described in Section 5.0. Home range connectivity to fishable reaches, HabRangeFishWBNIndex, HRangeNumFishWBNRch, and HRangeFishWBNRchInde, was determined in the database by using the reach number connected with each home range and a lookup table of fishable reaches (streams of order 3 or greater, lakes and wetlands) by reach number.

The resulting data were appended to the Site_Variable_Distribution_Data tables within the HWIR 3MRA input database. Grid files for home ranges were sent as a separate Access database (grid.mdb).

13.6 Quality Assurance/Quality Control

The habitat delineation procedures consist largely of subjective evaluation of each site and hand-delineation of habitat boundaries. These methods, therefore, pose challenges for quality control (QC) and quality assurance (QA). A totally automated habitat delineation procedure was considered but proved not to be feasible, given the enormous variety of numbers, sizes, and arrangement of habitat patches at the 201 sites. Because hand-delineation was determined to be the optimal approach, the following procedures were implemented:

- # Delineators—Only two designated senior ecologists performed all habitat delineations. Limiting the delineators to two individuals helped to limit the degree of variation in interpretation of spatial data. All electronic site maps were accessible to both delineators so that they could work closely together and consult each other regularly on the decision process for all sites.
- # Crosswalks—Both delineators adhered strictly to the crosswalks shown in tables 13-17, 13-18, and 13-19. Each site delineation began with application of the crosswalks; data interpretation and subjective decisions, such as placement of stream corridors and connection of habitat patches, followed.
- # Documentation of decisions— Both delineators kept records of any delineations that involved unique circumstances or conflicting issues. These notes were reviewed by both delineators on a weekly (or more frequent) basis. The purpose of the review was to maintain consistency in the decisions made for all sites.
- # Following delineation of the habitats at all sites, the delineators performed a QC on 75 percent each other's delineations. The QA check consisted of a complete redelineation of all habitats and resolution of any differences between the redelineation and the original delineation.
- # Before final data processing, automatic QC programs were used to query the GIS data tables to ensure that the number of home range bins did not exceed 4 for each habitat and that there were not grid cells in the range that were not also in the habitat containing the range.
- # After final data processing, automatic QC programs were used to check that all

values were within the minimum and maximum ranges set by the model dictionary files, that the number of indices were equal to the corresponding “Num” variable, that the number of habitats within each ring was not greater than the number of habitats for the entire site, and that there were no duplicate records in the data set. Extra indices and duplicate record sets were an indication of isolated grid cells, incomplete bridges, and other errors not visible to the delineators because of computer screen resolution in the delineation tool.

13.7 References

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Appendix 13A

Arc Macro Language Program for Processing Habitat and Receptor Data

```

/*
/* PROGRAM: process_habs_ranges.aml
/*
/* PURPOSE:
/*
/* INFO FILES NEEDED TO RUN:
/*     RECEPTOR_HABS.LUT
/*     RECEPTOR_BAILEYS.LUT
/*     RECEPTOR_HRANGE.LUT
/*     HAB_CODES.LUT
/*
/* FILES NEEDED TO RUN:
/*     /files10/hwir/p6720-06a/amllib/system/template
/*
/* ROUTINES: main
/*
/* CALLED BY:
/*
/* CALLS TO: process_ranges.aml
/*
/* GLOBAL VAR'S:
/*
/* INPUT FILES:
/*
/* OUTPUT FILES:
/*
/* NOTES:
/*
/* HISTORY: written by G. Conrad 12/20/98
/*
/* CONTACT: gtc@rti.org
/*
/* PROJECT: HWIR
/*

/*=====

&echo &on

&args site

&sv ws_org = [show workspace]

```

```

&severity &warning &ignore
&severity &error &routine errorhandler

&if %site% = 0136703 &then
&watch s0136703.watch

/* Check for arguments

&s data /files10/hwir/p6720-06a/data
&s sitecov /files10/hwir/p6720-06a/data/site_pts_al83
&s aoi_path /files10/hwir/p6720-06a/data/aoi /* path of aoi covers
&s wmu_path /files10/hwir/p6720-06a/data/sectors /* path of wmu covers
&s hab_path /files8/hwir/habitat_storage/h%site% /* path to the habitat coverages
&s eco_path /files8/hwir/eco
&s us_cov /data1/base/us_covers
&if [exists /files8/hwir/watershed_storage/s%site% -workspace] &then
  &s outpath /files8/hwir/watershed_storage/s%site%
&else &s outpath /files10/hwir/p6720-06a/data/watershed_storage/s%site%
&s storage /files10/hwir/p6720-06a/data/grids

&s start [date -full]

/* main loops that control program - site/wmu/ring loops
&sys touch progress.txt

cursor pop1 declare %sitecov% point ro id_num = [quote %site%]
cursor pop1 open
  &s site = %:pop1.id_num%
  &s x_cen = %:pop1.x-coord%
  &s y_cen = %:pop1.y-coord%

/* find the baileys section for the site
display 0
arplot
clearselect %sitecov% poly
resel %sitecov% points id_num = [quote %site%]
resel %data%/eco/baileys poly overlap %sitecov% point
&s baileys_id = [show select %data%/eco/baileys poly 1 item ecocode]
q

&call get_utm
&call make_habs

&call smallest_wmu
&call make_home_range

&s type_list = lau_aver surface_imp_aver waste_pile_aver landfill_aver
&do type &list %type_list%
  &if %type% = 'lau_aver' &then &s wmu_name = lau
  &if %type% = 'surface_imp_aver' &then &s wmu_name = si
  &if %type% = 'waste_pile_aver' &then &s wmu_name = wp
  &if %type% = 'landfill_aver' &then &s wmu_name = lf

  &if %type% = 'lau_aver' &then &s type_val = %:pop1.lau_aver%
  &if %type% = 'surface_imp_aver' &then &s type_val = %:pop1.surface_imp_aver%

```

```

&if %type% = 'waste_pile_aver' &then &s type_val = %:pop1.waste_pile_aver%
&if %type% = 'landfill_aver' &then &s type_val = %:pop1.landfill_aver%
&sys echo %type_val%

&if %type_val% > 0 &then
  &do
    &sys echo working on site: %site% for wmu: %wmu_name%

    &s area = %type_val%
    &call rings

    &call clip_it
    &call add_items

    &call process_ranges

    &call convert_to_grid
    &call add_receptors
    &call process_ws

    &call process_lws
    &call process_reach
    &call process_rings

    &call wrap_up

  &end
&end
cursor pop1 remove

&call clean_up

&s finish [date -full]
&sys echo Site %site% started %start% >> progress.txt
&sys echo Site %site% finished %finish% >> progress.txt
&wo %ws_org%

&watch &off
alert_me
&return /* main

/*=====
/*          END OF PROGRAM
/*=====

/* ROUTINE errorhandler*****
&routine errorhandler

&severity &error &ignore
&severity &warning &ignore
&mess &on
&wo %ws_org%
&s finish [date -full]
&sys echo Site %site% bombed at %finish% on line %AML$ERRORLINE% >> progress.txt
&sys echo last error - %AML$MESSAGE% >> progress.txt

```

```

cursor eco1 remove
cursor eco2 remove
cursor eco4 remove
cursor eco5 remove
cursor eco6 remove
cursor eco7 remove
cursor id1 remove
cursor pop1 remove
&sys echo Working on site %site%
&return &error An error has occurred in process_habs_ranges4.aml. \~
Last Error: %AML$MESSAGE%\~
Thread: %AML$ERRORTHREAD%\~
File: %AML$ERRORFILE%\~
Line: %AML$ERRORLINE%

/* *****
/* ROUTINE make_habs*****
&routine make_habs

&wo %hab_path%

/* make the hab cover
&if [exists h%site% -cover] &then kill h%site% all

dissolve grd%site% h%site% habcode poly

/* number habs 1 time
additem h%site%.pat h%site%.pat site_num 7 7 C
additem h%site%.pat h%site%.pat wmu 3 3 C
additem h%site%.pat h%site%.pat hindex 3 3 I

/* number habitats
&s i_cnt = 1

cursor id1 declare h%site%.pat info rw habcode <> 0 and habcode <> 12 and area > 41000
cursor id1 open
&do &while %:id1.AML$NEXT%
  &s :id1.site_num = %site%
  &s :id1.hindex = %i_cnt%
  &s i_cnt = %i_cnt% + 1
  cursor id1 next
&end
cursor id1 remove

&s num_habs = %i_cnt% - 1
&sys echo the number of habs is %num_habs%

&return

/* *****
/* ROUTINE smallest_wmu*****
&routine smallest_wmu

&s type_list = surface_imp_aver waste_pile_aver landfill_aver lau_aver

```



```

&s small = 99999999

&do type &list %type_list%

  &s type_val = [value :pop1.[value type]]

  &if %type_val% > 0 &then
    &do
      &if %type_val% < %small% &then
        &s small = %type_val%
      &end
    &end
  &end

&s area = %small%

/* create a rings coverage of smallest wmu at site to place ranges with
&call rings

&wo %hab_path%

&if [exists range_start -cover] &then
  kill range_start all
clip h%site% rng%site% range_start poly .01

&return

/* *****
/* ROUTINE clip_it*****
&routine clip_it

&wo %hab_path%

&if [exists hab%wmu_name% -cover] &then
  kill hab%wmu_name% all
&if [exists hab%wmu_name%_tmp -cover] &then
  kill hab%wmu_name%_tmp all

/* test for land application unit - erase wmu if not lau

/* &if [quote %wmu_name%] = 'lau' &then &do
/* &if [exists hab_tmp -cover] &then kill hab_tmp all
/* erase %hab_path%/h%site% %wmu_path%/wmu%site% %wmu_name% hab_tmp poly .1
/* kill %hab_path%/h%site% all
/* copy hab_tmp %hab_path%/h%site%
/* kill hab_tmp all
/* &end

clip h%site% rng%site% hab%wmu_name% poly .01

&return

/* ROUTINE add_items*****
&routine add_items

/*&if ^ [iteminfo %hab_path%/hab%wmu_name% -poly ECORINGHABINDEX -exists] &then &do

```

```
&wo %hab_path%
```

```
copy hab%wmu_name% hab%wmu_name%_tmp
```

```
joinitem hab%wmu_name%.pat /files8/hwir/eco/info!arc!template_hab.dat ~
hab%wmu_name%.pat $recno hindex
```

```
tables
```

```
sel hab%wmu_name%.pat
```

```
calc habarea = area
```

```
calc wmu = [quote %wmu_name%]
```

```
q
```

```
additem hab%wmu_name%_tmp.pat hab%wmu_name%_tmp.pat habarea 8 12 f 3
```

```
additem hab%wmu_name%_tmp.pat hab%wmu_name%_tmp.pat hindex 2 2 I
```

```
tables
```

```
sel hab%wmu_name%_tmp.pat
```

```
calc habarea = area
```

```
calc hindex = habcode
```

```
calc wmu = [quote %wmu_name%]
```

```
q
```

```
&wo %ws_org%
```

```
&return
```

```
/* ROUTINE add_receptors*****
```

```
&routine add_receptors
```

```
&wo %hab_path%
```

```
cursor eco4 declare hab%wmu_name% poly rw hindex > 0
```

```
cursor eco4 open
```

```
&do &while %:eco4.AML$NEXT%
```

```
&s hab = %:eco4.habcode%
```

```
&s :eco4.hindex = %:eco4.habcode%
```

```
&s max_range = 0
```

```
&do i = 1 &to 57
```

```
cursor eco1 declare %eco_path%/RECEPTOR_HABS2.LUT info ro species_id = %i%
```

```
cursor eco1 open
```

```
&s exist_hab = [value :eco1.hab[value hab]]
```

```
cursor eco1 remove
```

```
cursor eco2 declare %eco_path%/RECEPTOR_BAILEYS.LUT info ro species_id = %i%
```

```
cursor eco2 open
```

```
&s exist_bail = [value :eco2.b[value baileys_id]]
```

```
cursor eco2 remove
```

```
&if %exist_hab% = 1 and %exist_bail% = 1 &then &do
```

```
&s :eco4.receptor%i% = 1
```

```
&end
```

```
&end
```

```

cursor eco4 next
&end
cursor eco4 remove

&if [exists %outpath%/nwi_wet -cover] &then &do

cursor eco4 declare hab%wmu_name% poly rw hindex > 0
cursor eco4 open
&do &while %:eco4.AML$NEXT%
  &s hab = %:eco4.hindex%
  &s rec_lst
  &s :eco4.habindex = %:eco4.habcode%
  display 0
  arcplot
  clearselect hab%wmu_name% poly
  resel hab%wmu_name% poly hindex = %hab%
  resel %outpath%/nwi_wet poly overlap hab%wmu_name% poly
  resel %outpath%/nwi_wet poly area > 10000
  cursor eco6 declare %outpath%/nwi_wet poly ro
  cursor eco6 open
  &do &while %:eco6.AML$NEXT%
    &s wc = %:eco6.attribute%
    &s if_code = none
    &if [quote [substr %wc% 4 1]] in {'A' 'B' 'C' 'D' 'E' 'J' 'R' 'S' 'U' 'W' 'Y'} or [quote [substr %wc% 5 1]] in {'A'
'B' 'C' 'D' 'E' 'J' 'R' 'S' 'U' 'W' 'Y'} &then
      &if [quote [substr %wc% 1 4]] = 'L2AB' or [quote [substr %wc% 1 3]] in {'PFL' 'PML' 'PEM'} &then
        &s if_code = IFG

      &if [quote [substr %wc% 4 1]] in {'A' 'B' 'C' 'D' 'E' 'J' 'R' 'S' 'U' 'W' 'Y'} or [quote [substr %wc% 5 1]] in {'A'
'B' 'C' 'D' 'E' 'J' 'R' 'S' 'U' 'W' 'Y'} &then
        &if [substr %wc% 1 3] = 'PSS' &then
          &s if_code = IFSS

        &if [quote [substr %wc% 4 1]] in {'A' 'B' 'C' 'D' 'E' 'J' 'R' 'S' 'U' 'W' 'Y'} or [quote [substr %wc% 5 1]] in {'A'
'B' 'C' 'D' 'E' 'J' 'R' 'S' 'U' 'W' 'Y'} &then
          &if [substr %wc% 1 3] = 'PFO' &then
            &s if_code = IFFF

    &if ^ %if_code% = none &then &do
      clearsel %eco_path%/if_rec_hab2.lut info
      resel %eco_path%/if_rec_hab2.lut info wet_type = [quote %if_code%]
      resel %eco_path%/if_rec_hab2.lut info hidx = %hab%
      &sv rec_lst = %rec_lst% [listunique %eco_path%/if_rec_hab2.lut -info rindex]
    &end
  cursor eco6 next
&end
cursor eco6 remove
q

&if [token %rec_lst% -count] > 1 &then &do
  &do rec &list %rec_lst%
    &if ^ [null %rec%] &then
      &s :eco4.receptor%rec% = 1
    &end
  &end
&end

```

```

    cursor eco4 next
&end
cursor eco4 remove
&end

&wo %ws_org%
&return

/* ROUTINE make_home_range*****
&routine make_home_range

&wo %hab_path%

&do j = 1 &to %num_habs%
  &do k = 1 &to 4
    &if [exists mrange%j%_%k% -cover] &then kill mrange%j%_%k% all
    &if [exists range%j%_%k% -cover] &then kill range%j%_%k% all
  &end
&end

&do j = 1 &to %num_habs%

cursor eco4 declare h%site% poly ro hindex = %j%
cursor eco4 open

  &s hab = %:eco4.habcode%
  &s hab_area %:eco4.area%
  &s hix = %:eco4.hindex%

  &if [exists hab_clp -cover] &then kill hab_clp all
  copy h%site% hab_clp
  &if [exists range_clp -cover] &then kill range_clp all
  copy range_start range_clp

  ae
  ec hab_clp poly
  sel hindex = %hix%
  nsel
  delete
  save
  ec range_clp poly
  sel hindex = %hix%
  nsel
  delete
  save
  q

/* build hab_clp

&s group_list = 4 3 2 1

&do bucket &list %group_list%
  &if %bucket% = 4 &then &s u_bnd = 1000000000
  &if %bucket% = 3 &then &s u_bnd = 100000000
  &if %bucket% = 2 &then &s u_bnd = 1000000

```

```

&if %bucket% = 1 &then &s u_bnd = 100000

&sys echo working on range: %bucket% in habitat: %:eco4.hindex%

&if %hab_area% > %u_bnd% &then &do
  &call place_range
&end

&else &do
  &if [exists mrange%:eco4.hindex%_%bucket% -cover] &then kill mrange%:eco4.hindex%_%bucket% all
  copy hab_clp mrange%:eco4.hindex%_%bucket%
  copy range_clp mrange%:eco4.hindex%_%bucket%
  additem mrange%:eco4.hindex%_%bucket%.pat mrange%:eco4.hindex%_%bucket%.pat rindex 3 3 I #
hindex
  additem mrange%:eco4.hindex%_%bucket%.pat mrange%:eco4.hindex%_%bucket%.pat rangearea 8 12 F 3
hindex
  additem mrange%:eco4.hindex%_%bucket%.pat mrange%:eco4.hindex%_%bucket%.pat habindex 2 2 I
  additem mrange%:eco4.hindex%_%bucket%.pat mrange%:eco4.hindex%_%bucket%.pat habarefrac 8 12 F 4
  additem mrange%:eco4.hindex%_%bucket%.pat mrange%:eco4.hindex%_%bucket%.pat habrangefishwbni 2
2 I
  additem mrange%:eco4.hindex%_%bucket%.pat mrange%:eco4.hindex%_%bucket%.pat hrangefishwbnrch 2
2 I
  additem mrange%:eco4.hindex%_%bucket%.pat mrange%:eco4.hindex%_%bucket%.pat hrangenumfishwbni
2 2 I
  &end

&end
cursor eco4 remove
&end /* &do j

&wo %ws_org%
&return

/* ROUTINE process_ranges*****
&routine process_ranges

&wo %hab_path%

/* clean range data tables
&if [exists range_grid%wmu_name%.dat -info] &then &s d [delete range_grid%wmu_name%.dat -info]
&if [exists range_%wmu_name%_ws.dat -info] &then &s d [delete range_%wmu_name%_ws.dat -info]
&if [exists range_%wmu_name%_lws.dat -info] &then &s d [delete range_%wmu_name%_lws.dat -info]
&if [exists range_%wmu_name%_rng.dat -info] &then &s d [delete range_%wmu_name%_rng.dat -info]
&if [exists range_data%wmu_name%.dat -info] &then &s d [delete range_data%wmu_name%.dat -info]
&if [exists range_%wmu_name%_re.dat -info] &then &s d [delete range_%wmu_name%_re.dat -info]

&if [exists clip_hab -cover] &then kill clip_hab all
clip h%site% rng%site% clip_hab poly .1

&if [exists clip_hab.sum -info] &then &s [delete clip_hab.sum -info]
statistics clip_hab.pat clip_hab.sum hindex
sum area
end

```

```

&do j = 1 &to %num_habs%
  &do bucket &list %group_list%

    &if [exists range%j%_%bucket% -cover] &then kill range%j%_%bucket% all
    clip mrange%j%_%bucket% rng%site% range%j%_%bucket% poly .1

    cursor eco4 declare clip_hab.sum info ro hindex = %j%
    cursor eco4 open
      &s chab_area = %:eco4.sum-area%
    cursor eco4 remove

    &if [exists range.sum -info] &then &s [delete range.sum -info]

    statistics range%j%_%bucket%.pat range.sum hindex
    sum area
    end

    cursor eco4 declare range.sum info ro hindex = %j%
    cursor eco4 open
      &s crng_area = %:eco4.sum-area%
    cursor eco4 remove

    &s habareafrac = %chab_area% / %crng_area%
    &if %habareafrac% < 0.1 &then &s habareafrac = 0.1
    &if %habareafrac% > 1 &then &s habareafrac = 1

    &r %eco_path%/process_ranges %site% %wmu_name% %j% %bucket% %habareafrac% %utmz% %hab%
  &end
&end

&return

/* ROUTINE process_ws*****
&routine process_ws

&wo %hab_path%
/* watershed

&if [exists hab_ws -cover] &then kill hab_ws all
&if [exists hab_%wmu_name%_ws.dat -info] &then &s d [delete hab_%wmu_name%_ws.dat -info]
&if [exists %outpath%/v2_%site% -cover] &then &do
  &if ^ [iteminfo %outpath%/v2_%site% -poly ws_area -exists] &then &do
    additem %outpath%/v2_%site%.pat %outpath%/v2_%site%.pat ws_area 4 12 f 3
  &end
  &wo %outpath%
  &data arc info
  ARC
  SEL [translate v2_%site%.pat]
  CALC WS_AREA = AREA
  Q STOP
&end
&wo %hab_path%

intersect hab%wmu_name%_tmp %outpath%/v2_%site% hab_ws

```

```

pullitems hab_ws.pat hab_%wmu_name%_ws.dat
site_num
wmu
hindex
habarea
wshd_num
ws_area
area
end
&end

```

```

tables
sel hab_%wmu_name%_ws.dat
resel hindex < 1
purge
y
q

```

```
&if [exists hab_ws -cover] &then kill hab_ws all
```

```

&wo %ws_org%
&return

```

```

/* ROUTINE process_lws*****
&routine process_lws

```

```
&wo %hab_path%
```

```
/* local watershed
```

```

display 0
arcplot
clearselect %wmu_path%/cir%site%wmu_name% poly
resel %outpath%/v2_%site% poly overlap %wmu_path%/cir%site%wmu_name% poly
&sv lwses = [listunique %outpath%/v2_%site% -poly wshd_num]
q

```

```

&if [exists hab_%wmu_name%_lws.dat -info] &then &s d [delete hab_%wmu_name%_lws.dat -info]
&if [exists hab_%wmu_name%_lws_tmp.dat -info] &then &s d [delete hab_%wmu_name%_lws_tmp.dat -info]

```

```
&do ws_num &list %lwses%
```

```
&if [exists hab_lws -cover] &then kill hab_lws all
```

```

&if [exists %outpath%/wmu_name%ws_num% -cover] &then &do
  &if ^ [iteminfo %outpath%/wmu_name%ws_num% -poly local_area -exists] &then
    additem %outpath%/info!arc!wmu_name%ws_num%.pat
%outpath%/info!arc!wmu_name%ws_num%.pat local_area 4 12 f 3 local_num
  &wo %outpath%
  &data arc info
  ARC
  SEL [translate %wmu_name%ws_num%.pat]
  CALC LOCAL_AREA = AREA
  Q STOP
&end

```

```

&wo %ws_org%
&if ^ [iteminfo %outpath%/ %wmu_name% %ws_num% -poly wshd_num -exists] &then &do
  additem %outpath%/info!arc!%wmu_name% %ws_num%.pat
%outpath%/info!arc!%wmu_name% %ws_num%.pat wshd_num 3 3 i
  &wo %outpath%
  &data arc info
  ARC
  SEL [translate %wmu_name% %ws_num%.pat]
  CALC WSHD_NUM = %ws_num%
  Q STOP
&end
&wo %ws_org%
&end

&wo %hab_path%

intersect hab%wmu_name%_tmp %outpath%/ %wmu_name% %ws_num% hab_lws
pullitems hab_lws.pat hab_%wmu_name%_lws_tmp.dat
site_num
wmu
hindex
habarea
wshd_num
local_num
local_area
area
end
&end

tables
sel hab_%wmu_name%_lws_tmp.dat
resel hindex < 1
purge
y
q

&if ^ [exists hab_%wmu_name%_lws.dat -info] &then
  copyinfo hab_%wmu_name%_lws_tmp.dat hab_%wmu_name%_lws.dat
&else &do
  &data arc info
  arc
  SEL [translate hab_%wmu_name%_lws_tmp.dat]
  MERGE INTO [translate hab_%wmu_name%_lws.dat] ON SITE_NUM UNSORTED
  Q STOP
  &end
&end

&end /*do

&if [exists hab_lws -cover] &then kill hab_lws all

&wo %ws_org%
&return

/* ROUTINE process_reach*****

```



```

&routine process_reach

&if [exists %outpath%/reaches -cover] &then &do

  &wo %hab_path%

  /* process imp_reach_idx

  &if [exists hab_re -cover] &then kill hab_re all
  &if [exists hab_lk -cover] &then kill hab_lk all
  &if [exists hab_%wmu_name%_re.dat -info] &then &s d [delete hab_%wmu_name%_re.dat -info]
  &if [exists hab_%wmu_name%_lk.dat -info] &then &s d [delete hab_%wmu_name%_lk.dat -info]
  &if [exists tmp_re_clp -cover] &then kill tmp_re_clp all

  &if ^ [iteminfo %outpath%/reaches -line value -exists] &then &pause

  clip %outpath%/reaches %aoi_path%/aoi%site% tmp_re_clp line

  identity tmp_re_clp hab%wmu_name%_tmp hab_re line

  pullitems hab_re.aat hab_%wmu_name%_re.dat
  site_num
  wmu
  hindex
  habarea
  habindex
  rch_num
  length
  value
  end

  &data arc info
  arc
  SEL [translate hab_%wmu_name%_re.dat]
  ALTER LENGTH,RCH_LENGTH,,,,,,,,,
  ALTER VALUE,STR_ORDER,,,,,,,,,
  Q STOP
  &end

  tables
  sel hab_%wmu_name%_re.dat
  resel hindex < 1
  purge
  y
  q

  additem hab_%wmu_name%_re.dat hab_%wmu_name%_re.dat lake_num 3 3 i
  additem hab_%wmu_name%_re.dat hab_%wmu_name%_re.dat area 8 18 F 5

  &if [exists %outpath%/lk_wet -cover] &then &do
    intersect %outpath%/lk_wet hab%wmu_name%_tmp hab_lk

  pullitems hab_lk.pat hab_%wmu_name%_lk.dat
  site_num
  wmu

```

```

hindex
habarea
habindex
lake_num
area
end

```

```

tables
sel hab_%wmu_name%_lk.dat
resel hindex < 1
purge
y
q

```

```

additem hab_%wmu_name%_lk.dat hab_%wmu_name%_lk.dat rch_num 3 3 I # habindex
additem hab_%wmu_name%_lk.dat hab_%wmu_name%_lk.dat rch_length 8 18 F 5 rch_num
additem hab_%wmu_name%_lk.dat hab_%wmu_name%_lk.dat str_order 4 5 B # rch_length

```

```

&data arc info
arc
SEL [translate hab_%wmu_name%_lk.dat]
MERGE INTO [translate hab_%wmu_name%_re.dat] ON SITE_NUM UNSORTED
Q STOP
&end

```

```
&end
```

```

&if [exists hab_lk -cover] &then kill hab_lk all
&if [exists hab_re -cover] &then kill hab_re all
&if [exists tmp_re_clp -cover] &then kill tmp_re_clp all

```

```

&wo %ws_org%
&end

```

```
&return
```

```

/* ROUTINE process_rings*****
&routine process_rings

```

```
&wo %hab_path%
```

```

&if [exists hab_rng -cover] &then kill hab_rng all
&if [exists hab_%wmu_name%_rng.dat -info] &then &s d [delete hab_%wmu_name%_rng.dat -info]

```

```

&if [exists rng%site% -cover] &then &do
intersect hab%wmu_name%_tmp rng%site% hab_rng
pullitems hab_rng.pat hab_%wmu_name%_rng.dat
site_num
wmu
hindex
habarea
ring_id
area
end

```

```

&end

tables
sel hab_%wmu_name%_rng.dat
resel hindex < 1
purge
y
q

&if [exists hab_rng -cover] &then kill hab_rng all

&wo %ws_org%

&return

/* ROUTINE check_for_lu*****
&routine check_for_lu

&if [iteminfo %hab_path%/h%site% -poly lucode -exists] &then &do

  &wo %hab_path%
  &data arc info
  ARC
  SEL H%site%.PAT
  ALTER LUCODE, CODE,,,,,,
  Q STOP
  &end

  &wo %ws_org%

&end

&return

/* ROUTINE convert_to_grid*****
&routine convert_to_grid

&wo %hab_path%

&if [exists hab_grid%wmu_name%.dat -info] &then &s d [delete hab_grid%wmu_name%.dat -info]

/* convert to utm coords

&if [exists hab_utm -cover] &then kill hab_utm all
&if [exists hab_temp -cover] &then kill hab_temp all

project cover hab%wmu_name%_tmp hab_utm /data1/base/prj_files/albers83-utm%utmz%_83.prj
build hab_utm

&data arc info
arc
SEL HAB_UTM.PAT
MOVEIT [quote %SITE%] TO SITE_NUM
MOVEIT [quote [translate %wmu_name%]] TO WMU
RESEL HABINDEX = 0

```

```

CALC HABINDEX = 12
RESEL AREA < 0
CALC HABINDEX = 0
Q STOP
&end

```

```

identity %storage%/grd%site% hab_utm hab_temp point .001 join
pullitems hab_temp.pat hab_grid%wmu_name%.dat
site_num
wmu
hindex
habindex
cell_add
x-coord
y-coord
end

```

```

&data arc info
ARC
  SEL [translate hab_grid%wmu_name%.dat]
  RESEL HINDEX = 0
  PURGE
  Y
  Q STOP
&end

```

```

&if [exists hab_utm -cover] &then kill hab_utm all
&if [exists hab_temp -cover] &then kill hab_temp all

```

```

&wo %ws_org%

```

```

&return

```

```

/* ROUTINE wrap_up*****
&routine wrap_up

```

```

&wo %hab_path%

```

```

&if [exists hab_data%wmu_name%.dat -info] &then &s d [delete hab_data%wmu_name%.dat -info]

```

```

copyinfo hab%wmu_name%.pat hab_data%wmu_name%.dat
dropitem hab_data%wmu_name%.dat hab_data%wmu_name%.dat
hab%wmu_name%#
hab%wmu_name%-id
habcode
end

```

```

tables
sel hab_data%wmu_name%.dat
resel hindex < 1
purge
y
q

```

```

&wo %ws_org%

```

```

&return

/* ROUTINE rings*****
&routine rings

&if [exists rng%site% -cover] &then
  kill rng%site% all
&if [exists rng%site%c -cover] &then
  kill rng%site%c all

&wo %hab_path%

&if [exists rng%site% -cover] &then
  kill rng%site% all
&if [exists rng%site%c -cover] &then
  kill rng%site%c all

/* get into arccedit
display 9
arccedit

/* find the side of the wmu based on area
&s hside = [sqrt %area%] / 2
&s corner = %hside% * [sqrt 2]

&s ring_list = 1000 2000

createcover rng%site% /files10/hwir/p6720-06a/amllib/system/template
ef arc

/* generate dce or circle
coord keyboard
arctype circle
add
  &do rings &list %ring_list%
  2,%x_cen%,%y_cen%
  2,%x_cen%, [calc %y_cen% + %corner% + %rings%]
  &end
  9

/* save the new coverage and quit ae
save
quit

/* clean the coverage
clean rng%site% rng%site%c 0 .1

/* create labels
createlabels rng%site%c 0
build rng%site%c

/* clean up
kill rng%site% all
rename rng%site%c rng%site%
additem rng%site%.pat rng%site%.pat ring_id 1 1 I

```

```

&s counter = 0
ae
ec rng%site% poly

&do rings &list %ring_list%
&s counter = %counter% + 1
sel
%x_cen%,[calc %y_cen% + %corner% + %rings% - 50]
calc ring_id = %counter%
&end

save
quit

&wo %ws_org%

&return /* end of routine

/* ROUTINE get_utm*****
&routine get_utm

&s utm_zones /data1/base/us_covers/utm_zone_al83

display 0
arcplot
clearselect %utm_zones% poly
clearselect %sitecov% point
resel %sitecov% points id_num = [quote %site%]
resel %utm_zones% poly overlap %sitecov% point
&s utmz = [show select %utm_zones% poly 1 item utm_zone]
q

&return /* end of routine

*****
*****
*****
/* ROUTINE place_range*****
&routine place_range

&s hi %:eco4.hindex%
&s ri %bucket%
&s hx %x_cen%
&s hy %y_cen%
&s rarea %u_bnd%

&call make_points

/* &if %bucket% = 4 &then &s u_bnd = 1000000000
/* &if %bucket% = 3 &then &s u_bnd = 10000000
/* &if %bucket% = 2 &then &s u_bnd = 1000000
/* &if %bucket% = 1 &then &s u_bnd = 100000

/* make the range here
&if [exists range%hi%_%ri% -cover] &then kill range%hi%_%ri% all

```

```

&if [exists int_2_3 -cover] &then kill int_2_3 all

&if %bucket% = 2 &then
  &s sel_ply = range%hi%_3
&else
  &s sel_ply = range_clp

&if %bucket% = 1 &then &do
  intersect range%hi%_3 range%hi%_2 int_2_3
  &s sel_ply = int_2_3
&end

ap
clearsel tmp_pts point
resel tmp_pts point overlap %sel_ply% poly
resel tmp_pts point random 1
writesel habpt.sel
q
&if [exists hab_pt -cover] &then kill hab_pt all
reselect tmp_pts hab_pt point habpt.sel

/* figure radius from rarea (sq. meters)
&s r = %rarea% / 3.1415927
&s r = [sqrt %r%]
&ty %r%

&s right_size = .false.
&s tmp_r = %r%

&s trim = hab_clp
display 0
arcplot
clearselect hab_clp poly
resel hab_clp poly area > 0
&sys echo [show select hab_clp poly]
&s ply_num = [after [show select hab_clp poly] ,]
q
&if %ply_num% > 2 &then &do
  &if [exists holes -cover] &then kill holes all
  ae
  ec hab_clp poly
  sel area = 0
  put holes
  q
  build holes poly
&end

&s lp_cnt = 0

&do &until %right_size%
  &s lp_cnt = %lp_cnt% + 1
  &if [exists hab_pt_buf -cover] &then kill hab_pt_buf all
  &if [exists hab_pt_buf2 -cover] &then kill hab_pt_buf2 all
  &if [exists hab_pt_buf3 -cover] &then kill hab_pt_buf3 all
  buffer hab_pt hab_pt_buf # # %tmp_r% .1 point

```

```

build hab_pt_buf
clip hab_pt_buf %trim% hab_pt_buf2
&if %ply_num% > 2 &then &do
  rename hab_pt_buf2 hab_pt_buf3
  erase hab_pt_buf3 holes hab_pt_buf2 poly
&end
&s big = 0
&s cnt = 0
cursor hab2 declare hab_pt_buf2.pat info ro
cursor hab2 open
&do &while %:hab2.AML$NEXT%
  &s cnt = %cnt% + 1
  &s buf_area = %:hab2.area%
  &if %buf_area% > %big% &then
    &s big = %buf_area%
  cursor hab2 next
&end
cursor hab2 remove

&if [calc %big% + 1000] > %rarea% &then
  &s right_size = .true.
&if %rarea% = 100000 &then &do
  &if %lp_cnt% = 1 &then
    &s tmp_r = %tmp_r% + 25 /* tmp_r = ( %tmp_r% * %rarea% ) / %big%
  else
    &s tmp_r = %tmp_r% + 10
  &end
&else
  &s tmp_r = %tmp_r% + 100
&end

&s poly_list = [listunique hab_pt_buf2 -polygon hab_pt_buf2#]
&s num_poly = [token %poly_list% -count]

&if %num_poly% > 1 &then &do
  &s big = 0
  cursor hab2 declare hab_pt_buf2.pat info ro
  cursor hab2 open
  &do &while %:hab2.AML$NEXT%
    &s buf_area = %:hab2.area%
    &if %buf_area% > %big% &then
      &s big = %buf_area%
    cursor hab2 next
  &end
  cursor hab2 remove
  &s big = %big% - 100
  ae
  ec hab_pt_buf2 poly
  sel area < %big%
  delete
  save
  q
&end

copy hab_pt_buf2 mrange%hi%_%ri%

```



```
clip mrange%hi%_ri% rng%site% range%hi%_ri%
```

```
/* &if %hi% = 3 and %ri% = 2 &then &pause
```

```
additem mrange%hi%_ri%.pat mrange%hi%_ri%.pat site_num 7 7 C
additem mrange%hi%_ri%.pat mrange%hi%_ri%.pat wmu 3 3 C
additem mrange%hi%_ri%.pat mrange%hi%_ri%.pat hindex 3 3 I
additem mrange%hi%_ri%.pat mrange%hi%_ri%.pat rindex 3 3 I
additem mrange%hi%_ri%.pat mrange%hi%_ri%.pat rangearea 8 12 F 3
additem mrange%hi%_ri%.pat mrange%hi%_ri%.pat habindex 2 2 I
additem mrange%hi%_ri%.pat mrange%hi%_ri%.pat habareafrac 8 12 F 4
additem mrange%hi%_ri%.pat mrange%hi%_ri%.pat habrangefishwbni 2 2 I
additem mrange%hi%_ri%.pat mrange%hi%_ri%.pat hrangefishwbnrch 2 2 I
additem mrange%hi%_ri%.pat mrange%hi%_ri%.pat hrangenumfishwbn 2 2 I
```

```
&if [exists int_2_3 -cover] &then kill int_2_3 all
```

```
&return /* end of routine
```

```
/* ROUTINE make_points*****
&routine make_points
```

```
&if [exists tmp_pts -cover] &then kill tmp_pts all
```

```
ae
display 0
ec /files10/hwir/p6720-06a/data/supergrid/grd_at00 labels
coo key
sel all
put tmp_pts
ec tmp_pts labels
sel all
move
1,0,0
1,%hx%,%hy%
save
q
```

```
build tmp_pts point
```

```
&return /* end of routine
```

```
/* ROUTINE clean_up*****
&routine clean_up
```

```
&wo %hab_path%
```

```
&if [exists hab_clp -cover] &then kill hab_clp all
&if [exists range_clp -cover] &then kill range_clp all
&if [exists range_start -cover] &then kill range_start all
```

```
&wo %ws_org%
&return
```

```
/*=====metatdata=====
```

```

/* RECEPTOR_HABS.LUT
/*
/* COLUMN ITEM NAME      WIDTH OUTPUT TYPE N.DEC ALTERNATE NAME  INDEXED?
/*  1 SPECIES_ID        2  2  I  -  -
/*  3 HAB1              1  1  I  -  -
/*  4 HAB2              1  1  I  -  -
/*  5 HAB3              1  1  I  -  -
/*  6 HAB4              1  1  I  -  -
/*  7 HAB5              1  1  I  -  -
/*  8 HAB6              1  1  I  -  -
/*  9 HAB7              1  1  I  -  -
/* 10 HAB8              1  1  I  -  -
/* 11 HAB9              1  1  I  -  -
/* 12 HAB10             1  1  I  -  -
/* 13 HAB11             1  1  I  -  -
/* 14 HAB12             1  1  I  -  -
/*
/* RECEPTOR_BAILEYS.LUT
/*
/* COLUMN ITEM NAME      WIDTH OUTPUT TYPE N.DEC ALTERNATE NAME  INDEXED?
/*  1 SPECIES_ID        2  2  I  -  -
/*  3 B-212C            1  1  I  -  -
/*  4 B-212D            1  1  I  -  -
/*  5 B-212G            1  1  I  -  -
/*  6 B-212N            1  1  I  -  -
/*  7 B-221J            1  1  I  -  -
/*  8 B-222D            1  1  I  -  -
/*  9 B-222E            1  1  I  -  -
/*
/* RECEPTOR_HRANGE.LUT
/*
/* ITEM NAME      WIDTH OUTPUT TYPE N.DEC ALTERNATE NAME  INDEXED?
/* SPECIES_ID     10 10  I  -  -
/* SPECIES_NA     23 23  C  -  -
/* HRANGEMIN      12 12  I  -  -
/* HRANGEMID      11 11  I  -  -
/* HRANGEMAX      13 13  I  -  -
/*
/*
/* HAB_CODES.LUT
/*
/* COLUMN ITEM NAME      WIDTH OUTPUT TYPE N.DEC ALTERNATE NAME  INDEXED?
/*  1 HAB_CODE        11 11  I  -  -
/* 12 HAB_DESCR       14 14  C  -  -
/* 26 HAB_GRP_ID      14 14  I  -  -
/* 40 HAB_GROUP       12 12  C  -  -
/*

```

Appendix 13B

Arc Macro Language Program for Processing Home Range Data

```
/*
/* PROGRAM: process_ranges.aml
/*
/* PURPOSE: Process homeranges with grids, ws, lws, reaches, and rings
/*
/* INFO FILES NEEDED TO RUN:
/*
/* ROUTINES: main
/*
/* CALLED BY: process_habs_ranges.aml
/*
/* CALLS TO:
/*
/* GLOBAL VAR'S:
/*
/* INPUT FILES:
/*
/* OUTPUT FILES:
/*
/* NOTES:
/*
/* HISTORY: written by G. Conrad 12/20/98
/*
/* CONTACT: gtc@rti.org
/*
/* PROJECT: HWIR
/*

/*-----

/* &echo &on

&args site wmu_n hidx spec_id ha_frac utm habi

&sv ws_org = [show workspace]

&severity &warning &ignore
&severity &error &routine errorhandler

/* Check for arguments

&s data /files10/hwir/p6720-06a/data
```

```

&s sitecov /files10/hwir/p6720-06a/data/site_pts_al83
&s aoi_path /files10/hwir/p6720-06a/data/aoi /* path of aoi covers
&s wmu_path /files10/hwir/p6720-06a/data/sectors /* path of wmu covers
&s hab_path /files8/hwir/habitat_storage/h%site% /* path to the habitat coverages
&s eco_path /files8/hwir/eco
&s us_cov /data1/base/us_covers
&if [exists /files8/hwir/watershed_storage/s%site% -workspace] &then
  &s outpath /files8/hwir/watershed_storage/s%site%
&else &s outpath /files10/hwir/p6720-06a/data/watershed_storage/s%site%
&s storage /files10/hwir/p6720-06a/data/grids

&call add_items
&call convert_to_grid
&call process_ws
&call process_lws
&call process_reach
&call process_rings
&call wrap_up

/*&if [exists %hab_path%/range%hidx%_%spec_id% -cover] &then kill %hab_path%/range%hidx%_%spec_id%
all

&wo %ws_org%
/* alert_me
&return /* main

/*=====
/*          END OF PROGRAM
/*=====

/* ROUTINE errorhandler*****
&routine errorhandler

&severity &error &ignore
&severity &warning &ignore
&mess &on
&wo %ws_org%
cursor eco1 remove
cursor eco2 remove
cursor eco4 remove
cursor id1 remove
cursor pop1 remove
&sys echo Working on site %site%
&return &error An error has occurred in range_lookup.aml. \~
Last Error: %AML$MESSAGE%\~
Thread: %AML$ERRORTHREAD%\~
File: %AML$ERRORFILE%\~
Line: %AML$ERRORLINE%

/* ROUTINE add_items*****
&routine add_items

/*&if ^ [iteminfo %hab_path%/hab%wmu_n% -poly ECORINGHABINDEX -exists] &then &do

  &wo %hab_path%

```

```

/* number habitats

&if [iteminfo range%hidx%_%spec_id%.pat -info inside -exists] &then &do

cursor id1 declare range%hidx%_%spec_id%.pat info rw area > 0 and inside = 100
cursor id1 open
&do &while %:id1.AML$NEXT%
  &s :id1.hindex = %hidx%
  &s :id1.site_num = %site%
  &s :id1.wmu = %wmu_n%
  &s :id1.rindex = %spec_id%
  &s :id1.habareafrac = %ha_frac%
  &s :id1.habindex = %habi%
  cursor id1 next
&end
cursor id1 remove

&end
&else &do

cursor id1 declare range%hidx%_%spec_id%.pat info rw area > 0 and hindex <> 0
cursor id1 open
&do &while %:id1.AML$NEXT%
  &s :id1.hindex = %hidx%
  &s :id1.site_num = %site%
  &s :id1.wmu = %wmu_n%
  &s :id1.rindex = %spec_id%
  &s :id1.habareafrac = %ha_frac%
  &s :id1.habindex = %habi%
  cursor id1 next
&end
cursor id1 remove

&end

tables
sel range%hidx%_%spec_id%.pat
calc rangearea = area
q

&wo %ws_org%

&return

/* ROUTINE process_ws*****
&routine process_ws

&wo %hab_path%
/* watershed

&if [exists range_ws -cover] &then kill range_ws all
&if [exists %outpath%/v2_%site% -cover] &then &do
  &if ^ [iteminfo %outpath%/v2_%site% -poly ws_area -exists] &then &do
    additem %outpath%/v2_%site%.pat %outpath%/v2_%site%.pat ws_area 4 12 f 3
  &end

```

```
&wo %outpath%
```

```
&data arc info
```

```
ARC
```

```
  SEL [translate v2_%site%.pat]
```

```
  CALC WS_AREA = AREA
```

```
  Q STOP
```

```
&end
```

```
&wo %hab_path%
```

```
intersect range%hidx%_%spec_id% %outpath%/v2_%site% range_ws
```

```
pullitems range_ws.pat range_ws.dat
```

```
site_num
```

```
wmu
```

```
hindex
```

```
rindex
```

```
rangearea
```

```
wshd_num
```

```
ws_area
```

```
area
```

```
end
```

```
&end
```

```
&if ^ [exists range_%wmu_n%_ws.dat -info] &then &do
```

```
  &data arc info
```

```
  ARC
```

```
  SEL [translate range_ws.dat]
```

```
  RESEL HINDEX = 0
```

```
  PURGE
```

```
  Y
```

```
  Q STOP
```

```
  &end
```

```
  copyinfo range_ws.dat range_%wmu_n%_ws.dat
```

```
  &end
```

```
&else &do
```

```
&data arc info
```

```
ARC
```

```
  SEL [translate range_ws.dat]
```

```
  RESEL HINDEX > 0
```

```
  MERGE INTO [translate range_%wmu_n%_ws.dat] ON SITE_NUM
```

```
  Q STOP
```

```
  &end
```

```
&end
```

```
&if [exists range_ws -cover] &then kill range_ws all
```

```
&wo %ws_org%
```

```
&return
```

```
/* ROUTINE process_lws*****
```

```
&routine process_lws
```

```
&wo %hab_path%
```

```
/* local watershed
```

```

display 0
arcplot
clearselect %wmu_path%/cir%site%%wmu_n% poly
resel %outpath%/v2_%site% poly overlap %wmu_path%/cir%site%%wmu_n% poly
&sv lwses = [listunique %outpath%/v2_%site% -poly wshd_num]
q

&do ws_num &list %lwses%

&if [exists range_lws -cover] &then kill range_lws all

&if [exists %outpath%/wmu_n%ws_num% -cover] &then &do
  &if ^ [iteminfo %outpath%/wmu_n%ws_num% -poly local_area -exists] &then
    additem %outpath%/info!arc!wmu_n%ws_num%.pat %outpath%/info!arc!wmu_n%ws_num%.pat
local_area 4 12 f 3 local_num
  &wo %outpath%
  &data arc info
  ARC
  SEL [translate %wmu_n%ws_num%.pat]
  CALC LOCAL_AREA = AREA
  Q STOP
  &end
  &wo %ws_org%
  &if ^ [iteminfo %outpath%/wmu_n%ws_num% -poly wshd_num -exists] &then &do
    additem %outpath%/info!arc!wmu_n%ws_num%.pat %outpath%/info!arc!wmu_n%ws_num%.pat
wshd_num 3 3 i
  &wo %outpath%
  &data arc info
  ARC
  SEL [translate %wmu_n%ws_num%.pat]
  CALC WSHD_NUM = %ws_num%
  Q STOP
  &end
  &wo %ws_org%
&end

&wo %hab_path%
intersect range%hidx%_%spec_id% %outpath%/wmu_n%ws_num% range_lws
pullitems range_lws.pat range_lws.dat
site_num
wmu
hindex
rindex
rangearea
wshd_num
local_num
local_area
area
end
&end

&if ^ [exists range_%wmu_n%_lws.dat -info] &then &do
  &data arc info

```

```

    ARC
    SEL [translate range_lws.dat]
    RESEL HINDEX = 0
    PURGE
    Y
    Q STOP
&end
copyinfo range_lws.dat range_%wmu_n%_lws.dat
&end
&else &do
&data arc info
    ARC
    SEL [translate range_lws.dat]
    RESEL HINDEX > 0
    MERGE INTO [translate range_%wmu_n%_lws.dat] ON SITE_NUM
    Q STOP
    &end
&end

&if [exists range_lws -cover] &then kill range_lws all

&end

&wo %ws_org%
&return

/* ROUTINE process_reach*****
&routine process_reach

&if [exists %outpath%/reaches -cover] &then &do

    &wo %hab_path%

    &if [exists range_re -cover] &then kill range_re all
    &if [exists range_lk -cover] &then kill range_lk all

    /* &if ^ [iteminfo %outpath%/reaches -line value -exists] &then &pause

    identity %outpath%/reaches range%hidx%_%spec_id% range_re line

    pullitems range_re.aat range_re.dat
    site_num
    wmu
    hindex
    rindex
    rangearea
    rch_num
    length
    value
    end

    &data arc info
    arc
    SEL [translate range_re.dat]
    ALTER LENGTH,RCH_LENGTH,,,,,,,,,

```



```
ALTER VALUE,STR_ORDER,,,,,,,,,
RESEL HINDEX < 1
PURGE
Y
Q STOP
&end
```

```
additem range_re.dat range_re.dat lake_num 3 3 i
additem range_re.dat range_re.dat area 8 18 F 5
```

```
&if [exists %outpath%/lk_wet -cover] &then &do
  intersect %outpath%/lk_wet range%hidx%_%spec_id% range_lk
```

```
pullitems range_lk.pat range_lk.dat
site_num
wmu
hindex
rindex
rangearea
lake_num
area
end
```

```
tables
sel range_lk.dat
resel hindex < 1
purge
y
q
```

```
additem range_lk.dat range_lk.dat rch_num 3 3 I # rangearea
additem range_lk.dat range_lk.dat rch_length 8 18 F 5 rch_num
additem range_lk.dat range_lk.dat str_order 4 5 B # rch_length
```

```
&data arc info
arc
SEL [translate range_lk.dat]
MERGE INTO [translate range_re.dat] ON SITE_NUM UNSORTED
Q STOP
&end
```

```
&end
```

```
&if ^ [exists range_%wmu_n%_re.dat -info] &then
  copyinfo range_re.dat range_%wmu_n%_re.dat
&else &do
&data arc info
  ARC
  SEL [translate range_re.dat]
  MERGE INTO [translate range_%wmu_n%_re.dat] ON SITE_NUM
  Q STOP
  &end
&end
```

```
&if [exists range_lk -cover] &then kill range_lk all
```

```

&if [exists range_re -cover] &then kill range_re all

&wo %ws_org%
&end

&return

/* ROUTINE process_rings*****
&routine process_rings

&wo %hab_path%

&if [exists range_rng -cover] &then kill range_rng all

&if [exists rng%site% -cover] &then &do
  intersect range%hidx%_%spec_id% rng%site% range_rng
  pullitems range_rng.pat range_rng.dat
  site_num
  wmu
  hindex
  rindex
  rangearea
  ring_id
  area
  end
&end

&if ^ [exists range_%wmu_n%_rng.dat -info] &then &do
  &data arc info
  ARC
  SEL [translate range_rng.dat]
  RESEL HINDEX = 0
  PURGE
  Y
  Q STOP
  &end
  copyinfo range_rng.dat range_%wmu_n%_rng.dat
  &end
&else &do
&data arc info
  ARC
  SEL [translate range_rng.dat]
  RESEL HINDEX > 0
  MERGE INTO [translate range_%wmu_n%_rng.dat] ON SITE_NUM
  Q STOP
  &end
&end

&if [exists range_rng -cover] &then kill range_rng all

&wo %ws_org%

&return

/* ROUTINE convert_to_grid*****

```

```

&routine convert_to_grid

&wo %hab_path%

/* convert to utm coords

&if [exists range_utm -cover] &then kill range_utm all
&if [exists range_temp -cover] &then kill range_temp all

project cover range%hidx%_%spec_id% range_utm /data1/base/prj_files/albers83-utm%utm%_83.prj
build range_utm

identity %storage%/grd%site% range_utm range_temp point .001 join
pullitems range_temp.pat range_temp.dat
site_num
wmu
hindex
rindex
cell_add
x-coord
y-coord
end

&if ^ [exists range_grid%wmu_n%.dat -info] &then &do
  &data arc info
  ARC
  SEL [translate range_temp.dat]
  RESEL HINDEX = 0
  PURGE
  Y
  Q STOP
&end
copyinfo range_temp.dat range_grid%wmu_n%.dat
&end
&else &do
&data arc info
ARC
SEL [translate range_temp.dat]
RESEL HINDEX > 0
MERGE INTO [translate range_grid%wmu_n%.dat] ON SITE_NUM
Q STOP
&end
&end

&if [exists range_utm -cover] &then kill range_utm all
&if [exists range_temp -cover] &then kill range_temp all

&wo %ws_org%

&return

/* ROUTINE wrap_up*****
&routine wrap_up

&wo %hab_path%

```

```
pullitems range%hidx%_%spec_id%.pat range%hidx%_%spec_id%.dat
area
perimeter
site_num
wmu
hindex
rindex
rangearea
habindex
habareafrac
habrangefishwbni
hrangefishwbnrch
hrangenumfishwbn
end
```

```
&if ^ [exists range_data%wmu_n%.dat -info] &then &do
  &data arc info
  ARC
  SEL [translate range%hidx%_%spec_id%.dat]
  RESEL HINDEX = 0
  PURGE
  Y
  Q STOP
&end
copyinfo range%hidx%_%spec_id%.dat range_data%wmu_n%.dat
&end
&else &do
&data arc info
ARC
  SEL [translate range%hidx%_%spec_id%.dat]
  RESEL HINDEX > 0
  MERGE INTO [translate range_data%wmu_n%.dat] ON SITE_NUM
  Q STOP
&end
&end

&wo %ws_org%
&return
```

Appendix 13C

Table C13-1. Receptor Home Ranges and Bins

Receptor Index	Receptor Species	Home Range (min) m ²	Home Range (max) m ²	Home Range (midpt) m ²
Bin 1 :h =/ <100,000 m²				
19	Eastern newt	28	153	91
20	Flatwood salamander	100	100	100
21	Gopher frog ¹	7	200	104
24	Green frog	7	200	104
10	Bullfrog	1	400	201
35	Meadow vole	2	830	416
44	Prairie vole	73	980	527
16	Deer mouse	140	1,280	710
38	Muskrat	480	1,700	1,090
28	Least weasel	8,000	8,000	8,000
34	Marsh wren	156	2,600	1,378
54	Spotted sandpiper	2,500	2,500	2,500
30	Little brown bat	2,549	2,549	2,549
3	American robin	1,100	8,400	4,750
50	Short-tailed shrew	300	18,000	9,150
22	Great Basin pocket mouse	500	24,000	12,250
40	Northern water snake ²	18,000	30,000	24,000
53	Southern hognose snake ²	18,000	30,000	24,000
46	Racer	18,000	30,000	24,000
17	Eastern box turtle	4,600	52,000	28,300
43	Pine vole	310	68,800	34,555
18	Eastern cottontail rabbit	8,000	78,000	43,000
42	Painted turtle ³	2,400	83,800	43,100
52	Snapping turtle	2,400	83,800	43,100
7	Belted kingfisher ⁴	6,000	84,000	45,000
25	Green heron ⁴	6,000	84,000	45,000
31	Loggerhead shrike ⁴	6,000	84,000	45,000
23	Great blue heron	6,000	84,000	45,000
56	Western meadowlark	12,000	130,000	71,000

(continued)

Table C13-1. (continued)

Receptor Index	Receptor Species	Home Range (min) m ²	Home Range (max) m ²	Home Range (midpt) m ²
Bin 2: h >100,000 and <1 million m²				
39	Northern bobwhite	36,000	186,000	111,000
51	Short-tailed weasel	20,000	250,000	135,000
6	Beaver	164,084	164,084	164,084
9	Black-tailed jackrabbit	162,000	202,000	182,000
13	Cerulean warbler ⁵	20,000	600,000	310,000
55	Tree swallow	20,000	600,000	310,000
32	Long-tailed weasel	50,000	1,210,000	630,000
4	American woodcock	3,000	1,712,000	857,500
29	Lesser scaup	890,000	890,000	890,000
Bin 3: h = or >1 million and <10 million m²				
11	Burrowing owl	400	4,810,000	2,405,200
2	American kestrel	97,000	5,000,000	2,548,500
57	White-tailed deer	590,000	8,040,000	4,315,000
33	Mallard duck	380,000	14,400,000	7,390,000
27	Kit fox	2,600,000	13,700,000	8,150,000
14	Cooper's hawk	180,000	18,000,000	9,090,000
Bin : hr >10 million m²				
37	Mule deer	1,286,800	21,227,200	11,257,000
48	Red-tailed hawk	600,000	24,650,000	12,625,000
47	Red fox	570,000	34,200,000	17,385,000
26	Herring gull ⁶	18,300,000	18,800,000	18,550,000
41	Osprey ⁶	18,300,000	18,800,000	18,550,000
5	Bald eagle	18,300,000	18,800,000	18,550,000
1	Alligator snapping turtle	180,000	38,480,000	19,330,000
45	Raccoon	53,000	49,460,000	24,756,500
36	Mink	78,000	78,540,000	39,309,000
15	Coyote	14,300,000	68,000,000	41,150,000
8	Black bear	79	177,000,000	88,500,040
12	Canada goose	1,800,000	1,029,220,000	515,510,000
49	River otter	2,950,000	19,113,450,000	9,558,200,000

¹ No data available. Home range data for the green frog used.² No data available. Home range data for the racer used.³ No data available. Home range data for the snapping turtle used.⁴ No data available. Home range data for the great blue heron used.⁵ No data available. Home range data for the tree swallow used.⁶ No data available. Home range data for the bald eagle used.