

# Habitat Allocation to Maximize BiOdiversity

A technical description of the HAMBO model

R.A. Groeneveld  
D.P. Rudrum

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Wettelijke Onderzoekstaken Natuur & Milieu



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# **Habitat Allocation to Maximize BiOdiversity**

A technical description of the HAMBO  
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R.A. Groeneveld

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**Werkdocument 116**

Wettelijke Onderzoekstaken Natuur & Milieu

Wageningen, oktober 2008

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R.A. Groeneveld, D.P. Rudrum (2008). *Habitat Allocation to Maximize Biodiversity, A technical description of the HAMBO*. Wageningen, Wettelijke Onderzoekstaken Natuur & Milieu. 38 pp. 2 Fig. 3 Tab. 3 Ref. 4 Annexes

#### **Abstract**

To evaluate the cost-effectiveness of spatial allocations of nature conservation, it is necessary that a benchmark allocation can be known that achieves the maximum ecological value at given costs. This calls for an optimisation model that takes into consideration the main ecological considerations, such as habitat type and connectivity. This document presents the HAMBO model (Habitat Allocation to Maximise Biodiversity), which maximises the habitat quality of a nature reserve network for a number of species under a given financial budget. For each species the model takes into consideration the suitability of different ecosystems and the home range of the species. The document describes four ways to translate the spatial considerations in the ecological model LARCH to a linear optimisation model, and demonstrates the effects on conservation costs.

*Key words:* nature conservation, cost-effectiveness, biodiversity, habitat quality, ecosystem, HAMBO model, optimisation model

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The Working Documents series is published by the Statutory Research Tasks Unit for Nature & the Environment (WOT Natuur & Milieu), part of Wageningen UR. This document is available from the secretary's office, and can be downloaded from [www.wotnatuurenmilieu.wur.nl](http://www.wotnatuurenmilieu.wur.nl).

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## Samenvatting

Het model HAMBO (Habitat Allocation to Maximize BiODiversity) geeft inzicht in kosten-effectieve ontwikkelingsmogelijkheden voor ruimtelijke netwerken van natuurgebieden (habitats) gericht op het duurzaam behoud van biodiversiteit uitgedrukt in doelsoorten. Een kosteneffectief ruimtelijk netwerk kan twee dingen betekenen: i) het netwerk bereikt de ecologische doelstellingen met de laagste kosten, of ii) het netwerk bereikt met een gegeven budget de hoogste ecologische resultaten.

HAMBO kan voor verschillende typen van vraagstukken worden ingezet. Enerzijds kan HAMBO aangeven welke natuurgebieden optimaal zijn zonder rekening te houden met de onderlinge ruimtelijke relaties tussen natuurgebieden. Anderzijds kan het model worden ingezet voor optimalisatievraagstukken waarin wel rekening wordt gehouden met deze relaties.

Bij het tweede type vragen spelen naast de lokale factoren van een habitat ook de omvang en de kwaliteit van nabijgelegen habitats een rol om een duurzame populatie van een bepaalde doelsoort te vormen. Deze nabijgelegen habitats kunnen bijvoorbeeld dienen als voedselbron of als corridor naar andere, verder weg gelegen habitats. Geschikte habitats met een onderlinge afstand kleiner dan de actieradius van de betreffende soort vormen samen een habitatcluster. Is het habitatcluster voldoende groot dan is het een sleutelgebied, een gebied dat geschikt is voor de soort om zich voort te planten en dat groot genoeg is om een robuuste populatie te herbergen. Het model leunt op de methodologie van het LARCH model (Pouwels *et al.*, 2002). Voor het behoud van doelsoorten zijn meer sleutelgebieden nodig.

Met name de selectie van optimale gebieden waarbij rekening wordt gehouden met de ruimtelijke component is een relatief complex probleem. Vanwege de vele te modelleren interacties tussen de gebieden gaat dit werkdokument daarom alleen in op dit vraagstuk. In de analyses worden drie mogelijke modeltypen met elkaar vergeleken:

1. het 'complete cluster model' (CCM): neemt de bestaande structuur van de habitatclusters uit LARCH als gegeven aan;
2. het 'direct-vicinity model' (DVM): kan kleinere clusters construeren, maar alleen van geschikte locaties direct aansluitend (binnen de actieradius) op een centrale locatie;
3. het 'area-within-all cluster model' (AWA): gaat uit van de LARCH clusters en neemt aan dat daar uit willekeurige gebieden weggelaten kunnen worden zonder de ruimtelijke interactie te schaden. Met de afname in oppervlak wordt wel rekening gehouden.

De theoretische analyse van deze vergelijking geeft aan dat het CCM in staat is om alle doelsoorten te behouden, echter niet tegen de zo laagst mogelijke kosten. Het DVM kan, in het geval van een klein aantal te behouden doelsoorten, goedkopere habitatclusters identificeren dan het CCM. Echter, bij een groter aantal te behouden doelsoorten geeft het DVM een duurder oplossing. Het AWA kan onsamenhangende clusters construeren. Dit model is daarom niet geschikt voor het voorliggende probleem.

Bij een proefrun met HAMBO met 408 polygonen (natuurgebieden) en 215 doelsoorten komt naar voren dat het DVM geen oplossing bieden kan die alle 215 doelsoorten behoudt. Voor minder dan 50 doelsoorten heeft het DVM wel de meest kosteneffectieve oplossing. Tussen 50 en 130 doelsoorten is er weinig verschil tussen het DVM en het CCM. Voor meer dan 130 doelsoorten vindt het CCM de meest kosteneffectieve oplossing. Bij de meest kosteneffectieve oplossing waarmee het CCM alle 215 doelsoorten behoudt, liggen de kosten 15% lager dan wanneer alle polygonen mee zouden worden genomen.





# 1 Introduction

Policy makers pay increasing attention to the cost-effectiveness of spatial reserve networks. In this context, cost-effectiveness refers to whether a network achieves ecological objectives at minimum costs, or whether it achieves maximum ecological results under a fixed financial budget. This attention has led to the development of the HAMBO model (Habitat Allocation to Maximize BiOiversity), which aims at providing cost-effective solutions for developing spatial networks of nature reserves.

This report gives a description of the HAMBO model in order to provide a guide to the GAMS source code. Rather than a single model, HAMBO is a modelling framework consisting of several different equations, variables and parameters that can be combined to build different models of spatial network design. Regarding conserving species richness, HAMBO includes a number of different models that each approach the methodology currently included in the ecological model LARCH (Pouwels *et al.*, 2002). Depending on which models and restrictions are used, the problems solved are set cover problems or maximum cover problems if the sets associated with species conservation are given. Some models also incorporate procedures to calculate these sets during the run, adding to the complexity of the problem.

The report is organised as follows. Section 2 discusses the models in HAMBO and their mathematical structure. Section 3 describes the data used and the procedures necessary to import this data in HAMBO. Section 4 compares the performance of these models in a realistic example of reserve selection in The Netherlands. Section 5 concludes with a description of current and future developments regarding HAMBO.



## 2 HAMBO and its models

### 2.1 Introduction

HAMBO features two basic types of models:

1. models that do not include spatial relations between candidate locations;
2. models that include spatial relations between candidate locations.

The first type of model (spatially implicit models) focus exclusively on the area of habitat types, or the suitability of habitat types or candidate locations for target species. This type of models is further describes in section 2.2.

In the second type of models (spatially explicit models), the suitability of candidate location for a target species depends not only on local factors (environmental conditions), but also on the habitat area and quality in the vicinity of that location. The spatially explicit models can vary, depending on the definition of 'vicinity'. For instance, vicinity can include all locations within a given distance from the candidate location, or all locations in a predefined spatial cluster of locations. This type of models are further described in section 2.3.

A full list of equations (restrictions (R) and objectives (O)) are given in Appendix A. A full list of symbols is given in Appendix B. The model-equation matrix is given in Appendix C.

### 2.2 Spatially implicit models

Spatially implicit models in HAMBO include:

- a minimax habitat area model (2.2.1);
- a local site quality model (2.2.2).

#### 2.2.1 Minimax habitat area model

The minimax habitat area model maximizes the area of the habitat type of which the smallest fraction of the maximally possible area is realized, or minimizes costs such that each habitat type's fraction of its maximally possible area is greater than or equal to a predefined minimum. In other words, every habitat type  $h$  has a relative habitat area  $0 \leq R_h \leq 1$  that denotes how much of the maximally possible area of  $h$  is realized in the current solution:

$$R_h = \frac{\sum_{l \in \Lambda_h} \alpha_l F_{hl}}{\tau_h} \quad \forall h, \quad (\text{R1})$$

where

$R_h$	: the relative habitat area of habitat type $h$ ;	[fraction]
$\Lambda_h$	: the set of all sites $l$ where habitat $h$ can be realized;	$[\subseteq I]$
$\alpha_l$	: the area of site $l$ ;	[ha]
$F_{hl}$	: the fraction of site $l$ covered by habitat type $h$ ;	[fraction]
$\tau_h$	: the maximally possible area of habitat type $h$ ;	[ha]

Because  $F_{hl}$  is a fraction, the model needs to ensure that the sum of the fractions of all habitat types in site  $l$  is smaller than or equal to one:

$$\sum_{h \in \Lambda_l} F_{hl} \leq 1 \quad \forall l, \quad (\text{R2})$$

where

$\Lambda_l$  : the set of all habitat types  $h$  that can be realized in site  $l$  [subset of  $\mathcal{H}$ ]

Variable  $F_{hl}$  can be treated as either an integer or a continuous variable. The costs of the solution are:

$$K = \sum_l \sum_{h \in \Lambda_l} \kappa_{hl} F_{hl}, \quad (\text{O1})$$

where

$K$  : total costs; [€]

$\kappa_{hl}$  : the costs of realising habitat type  $h$  in site  $l$ . [€]

Lastly, the ecological objective is as follows:

$$M \leq R_h \quad \forall h, \quad (\text{R3})$$

where

$M$  : a minimum of the relative habitat areas. [fraction]

Maximising  $M$  is sufficient to meet the model's objectives.<sup>1</sup>

This model can be run to either maximise  $M$  with an upper bound on  $K$ , or to minimise  $K$  with a lower bound on  $M$ .

It is designated in GAMS as `AreaHabitatType`.

### 2.2.2 Local site equality

The local site quality model assumes the following: a target species is conserved if any site in the area exists that is (1) suitable for the species; and (2) that is conserved. Mathematically, this criterion is expressed as follows:

$$B_s \leq \sum_l \sum_{h \in \Lambda_l \text{ s.t. } \theta_{hs} > 0} F_{hl} \quad \forall s, \quad (\text{R4})$$

where

$B_s$  : species  $s$  is conserved (1) or not (0); [∈ (0,1)]

$\theta_{hs}$  : the suitability of site  $l$  for species  $s$ . [fraction]

<sup>1</sup> GAMS does not accept indices in its objective equations. Therefore, we need to introduce an additional variable  $A$ , that is equal to  $M$ :  $A = M$  (O2), with  $A$ : a minimum of the relative habitat areas [fraction].

The number of species conserved is calculated by

$$S = \sum_s B_s, \quad (03)$$

where

$S$  : the number of species conserved. [ $\in \mathbb{N}$ ]

The remaining equations of this model are:

(R2) to ensure that the sum of the fractions of all habitat types in a given site does not exceed unity; and

(O1) to calculate costs.

Because  $B_s$  can only be treated as an integer variable, the model can only be run as an MIP (Mixed integer problem) model. It can be run to either maximise  $S$  with an upper bound on  $K$ , or to minimise  $K$  with a lower bound on  $S$ .

The model is designated as `SpeciesDvNoArea` in GAMS.

## 2.3 Spatially explicit models

### 2.3.1 Introduction

Space becomes important when not the presence of a species, but the potential of that species to form a sustainable population, are traded off against the costs of conservation. An effective spatial habitat network allows target species to find food and mates, but also to migrate to and colonize new, uninhabited locations. A spatial reserve network may therefore include sites not only because they may be inhabited, but also because they may be sources of food, or because they may serve as stepping stones or corridors to other sites.

The LARCH model (Pouwels *et al.*, 2002) applies a straightforward method to estimate the spatial effectiveness of a habitat network. It describes each target species by the following properties:

1. its demand for habitat and space
2. its home range; and
3. the number of habitat keys needed to consider the species conserved.

The first property, demand for habitat, denotes the area of suitable habitat a species requires in its territory. The second property, the species' home range, expresses the expected dispersal range of the species. When two reserve sites are suitable for the species, and the distance between the sites is smaller than the species' home range, these reserve sites belong to the same habitat *cluster*, indicating that members of these species inhabiting either reserve site belong to the same population. Other reserve sites at similar or smaller distances from the principle two reserve sites also belong to this cluster, as do reserve sites at similar or smaller distances from those sites, and so on. A habitat cluster for species  $s$  is thus a cluster of sites /located such that the species can reach all sites without having to cross a distance larger than its home range. If the area of a cluster - weighing habitat area by the quality of the habitat for the species - is equal to or larger than the species' demand for habitat, the cluster is considered a habitat *key*, meaning that the cluster is large enough to sustain a population. The third property of the species, the number of habitat keys required, is thus the number of sufficiently large habitat clusters required to consider the species conserved.

However, by definition, linear programming models cannot fully include the LARCH method to evaluate whether a spatial habitat network is sufficient for a target species as they can only deal with direct relations, and not with indirect relations (e.g. A and B are connected if C is present is an indirect relation, depending on the status of C).

In order to be able to apply linear programming to reserve site selection, HAMBO features five different models for spatially explicit reserve site selection:

1. Direct-vicinity model with habitat types;
2. Direct-vicinity without habitat types;
3. Direct-vicinity model with habitat keys;
4. Area-within-cluster model
5. Complete-cluster model.

Each model is a second-best solution to the LARCH method. The following five sections give a short description of each of the models and show that each model has its own advantages and disadvantages compared to the other models.

### 2.3.2 Direct-vicinity model with habitat types

The three direct-vicinity models feature a binary variable  $L_{ls}$  that denotes whether sufficient habitat is available for species  $s$  within site  $l$  and all other sites within  $s$ 's home range from  $l$ . In mathematical terms:

$$\mu_s L_{ls} \leq \sum_{m \in \Phi_{ls}} \sum_{h \in \Lambda_m} \alpha_m \theta_{hs} F_{hm} \quad \forall l, s, \quad (R5)$$

where

$L_{ls}$  : Species  $s$  is conserved in a cluster of locations centering around  $l$ , [ $\in (0,1)$ ]

$\mu_s$  : species  $s$ 's demand for space, i.e. the minimum area of suitable habitat required for a population of  $s$ ; [ha]

$\Phi_{ls}$  : the set of sites  $m$  that lie within  $s$ 's home range from site  $l$ . [ $\subseteq \mathcal{M}$ ]

To avoid solutions where  $s$  is conserved in sites that are not suitable for the species but have sufficient habitat in their direct vicinity,  $L_{ls}$  is also restricted by  $l$  having a suitable habitat type:

$$L_{ls} \leq \sum_{h \in \Lambda_l \text{ s.t. } \theta_{hs} > 0} F_{hl} \quad \forall l, s. \quad (R6)$$

A species is conserved if there is any site in the network with enough habitat area for the species:

$$B_s \leq \sum_l L_{ls} \quad \forall s. \quad (R7)$$

This model also features equation (R2) to restrict the number of habitat types per site to one, and equations (O1) and (O3) as objectives. It can be run to either maximise  $S$  with an upper bound on  $K$ , or to minimise  $K$  with a lower bound on  $S$ .

The model is designated in HAMBO as `SpecDvHabitType`.

### 2.3.3 Direct-vicinity model without habitat types

The direct-vicinity model described in the previous section judges the suitability of a site for a species by the suitability of the habitat located in that site. If the habitat types are treated as given, which means they are not endogenously included into the model, we can focus the optimization on whether or not sites are included in the network. Instead of equation (R5), this model includes the following:

$$\mu_s L_{ls} \leq \sum_{m \in \Phi_{ls}} \sum_{h \in \Psi_m} \alpha_m \theta_{hs} G_m \quad \forall l, s, \quad (R8)$$

where

$\Psi_m$  : the habitat type in site  $m$ , [⊆  $\mathcal{H}$ ]  
 $G_m$  : site  $m$  is included in the solution (1) or not (0). [∈ (0,1)]

To avoid conserving species in non-included sites, the model also has its own version of equation (R6):

$$L_{ls} \leq G_l \quad \forall l, s. \quad (R9)$$

Costs in this model depend on  $G_l$  instead of  $F_{ij}$ :

$$K = \sum_l \sigma_l G_l, \quad (O4)$$

where

$\sigma_l$  : the costs of including site  $l$  in the solution. [∈]

The model also features equation (R7) to relate overall species conservation  $B_s$  to  $L_{ls}$ , and (O3) to calculate the number of species in the solution. It can be run to either maximise  $S$  with an upper bound on  $K$ , or to minimise  $K$  with a lower bound on  $S$ .

The model is designated as `SpecDvVicinity1` in HAMBO.

### 2.3.4 Direct-vicinity model with habitat keys

The models in the previous sections implicitly assume that a species requires only one habitat key to be conserved. If more habitat keys have to be included, the model has to take into account the clusters as constructed by LARCH, as the previous models cannot distinguish between related and unrelated  $L_{ls}$  's. This is done in the direct-vicinity model with habitat keys by introducing an index  $c$  that denotes clusters. It maintains the objectives (O3) and (O4) to calculate the costs of conservation and the number of species conserved, and the restrictions (R8) and (R9) to relate  $L_{ls}$  to the habitat area in the vicinity of  $l$ . Instead of restriction (R7), the model includes two restrictions to relate overall species conservation  $B_s$  to the number of clusters where  $L_{ls} = 1$  for one or more sites. First, we introduce a variable  $C_{cs}$  that expresses whether cluster  $c$  meets all criteria for species  $s$ :

$$C_{cs} \leq \sum_{l \in \Gamma_{cs}} L_{ls} \quad \forall c, s, \quad (R10)$$

where

$\Gamma_{cs}$  : the set of all locations  $l$  included in cluster  $c$  of species  $s$ . [⊆  $\mathcal{I}$ ]  
 $C_{cs}$  : Species  $s$  is conserved in cluster  $c$ , 0=no, 1=yes; [∈ (0,1)]

It should be noted that the numbering of clusters is by no means related to the numbering of species or sites. For instance, a given site may belong to cluster 53 for species 1, to cluster 2 for species 2, and to cluster 835 for species 3. Second, we restrict species conservation by the number of clusters where  $C_{cs} = 1$ :

$$\gamma_s B_s \leq \sum_{c \in \Omega_s} C_{cs} \quad \forall s, \quad (\text{R11})$$

where

$\gamma_s$  : the minimum number of habitat keys required for species  $s$ ; [∈ N]  
 $\Omega_s$  : the set of all habitat clusters for species  $s$ . [⊂  $\mathcal{C}$ ]

This model is designated as `SpecDvVicinityX` in HAMBO. It can be run to either maximise  $S$  with an upper bound on  $K$ , or to minimise  $K$  with a lower bound on  $S$ .

### 2.3.5 Area-within-cluster model

Instead of looking at the direct vicinity of a site, we can also consider all sites in the same cluster and demand that a cluster meets the local criteria of a species if the area of suitable habitat within the cluster is larger than or equal to the species' demand for space:

$$\mu_s C_{cs} \leq \sum_{m \in \Gamma_{cs}} \sum_{h \in \Psi_m} \alpha_m \theta_{hs} G_m \quad \forall c, s. \quad (\text{R12})$$

The model also includes restriction (R11) to relate overall species conservation to  $C_{cs}$  and objectives (O3) and (O4) to calculate the costs of conservation and the number of species conserved.

This model is designated as `SpDivAreaInClus` in HAMBO, and it too can be run to either maximise  $S$  with an upper bound on  $K$ , or to minimise  $K$  with a lower bound on  $S$ .

### 2.3.6 Complete-cluster model

Instead of demanding sufficient habitat within a cluster, we can also demand that all sites suitable for the species have to be included in the solution. In other words, the cluster does not meet the species' criteria if any site  $l$  exists within the cluster that is not included in the solution:

$$C_{cs} \leq \prod_{l \in \Gamma_{cs}} G_l \quad \forall c, s.^2 \quad (\text{R13})$$

Except for this restriction, which replaces (R12), this model is similar to the model in the previous section: it includes restriction (R11) to relate overall species conservation to  $C_{cs}$  and objectives (O3) and (O4) to calculate the costs of conservation and the number of species conserved.

This model is designated as `SpDivCompltClus` in HAMBO.

---

<sup>2</sup> Mathematical representation of what the code does. LP modelling requires a more tedious method as variables cannot be multiplied with another.



## 3 Preparing and importing data

### 3.1 Introduction

Data needed for the model must be processed to a format that can be included in HAMBO. This paragraph describes the origin of the data (3.2), the preparation and processing of the data (3.3) and the way in which the processed data are imported into the model (3.4). Data preparation and processing includes 13 steps. The SQL code of these steps is given in Appendix D.

### 3.2 Data provided

The Data come from two sources:

1. LEI Wageningen UR for the economic data (3.2.1)
2. Alterra for the ecological data (3.2.2).

#### 3.2.1 Economic data

Costs of conservation are estimated conform the method described in De Koeijer *et al.* (2006). The dataset used in the model demonstrations in Section 4 is called *OKEAfweging* and is found in the file *OKE\_Afweging.mdb*. Table 1 lists the columns featured in this dataset.

*Table 1: Columns in economic dataset 'OKEAfweging'*

Column	Description	Unit
Natuurdoel	Nature type code <sup>3</sup>	-
NDT_PATCH	ID number of polygon <sup>4</sup>	-
NDT_ID	ID number of nature target type of polygon	-
hectare	Area of polygon	ha
Totalekosten	Total costs of conserving polygon <sup>5</sup>	€
kostengeneriek	Costs of nationwide measures attributed to polygon <sup>6</sup>	€
specifiekekosten	Costs of polygon-specific environmental measures <sup>7</sup>	€
UitgavenEHS	Expenditures on polygon (as opposed to costs) <sup>8</sup>	€

Of these columns, HAMBO uses *NDT\_PATCH* to identify the polygons used; *hectare* to note the area of each polygon; and either *Totalekosten*, *kostengeneriek*, *specifiekekosten* or *UitgavenEHS* to note the costs of conserving each polygon.

<sup>3</sup> Dutch nature policy distinguishes *nature types* ('natuurdoelen') from *nature target types* ('natuurdoeltypes'). Nature target types are subdivisions of nature types. HAMBO currently uses nature target types.

<sup>4</sup> The ID numbers of polygons must be unique in this table to avoid, for instance, having one polygon ID with two different sizes.

<sup>5</sup> Thus including costs of nationwide as well as polygon-specific environmental measures.

<sup>6</sup> For instance, strengthening Dutch manure policy to reduce N deposition.

<sup>7</sup> For instance, increasing the local groundwater level.

<sup>8</sup> For instance, reduced agricultural production is a cost to society but not necessarily a government expenditure.

### 3.2.2 Ecological data

The relevant original ecological data are stored in five datasets: *spec\_normen1*, *ndtmulti\_18*, *soortgroepen*, *spec\_clusters*, *spec\_ndt\_belang*. All datasets are found in the file *rs\_ehs2006\_sc2018\_v2.mdb*.

#### ***spec\_normen1***

This dataset contains the target species and their relevant ecological characteristics. The considerations behind these characteristics are explained in more detail in Reijnen *et al.* (2007). Table 2 lists the columns in this dataset.

Table 2: Columns in 'spec\_normen1'

Column	Description	Unit
Doelsoort	Dutch name of target species	-
soortgroep	Species category of target species	-
key_opp	Minimum size of habitat key of species	ha
lokdist	Home range of species	m

#### ***ndtmulti\_18***

This dataset contains the polygons in the ecological data files and their ecological and geographic characteristics. Table 3 lists the columns in this dataset.

Table 3: Columns in 'ndtmulti\_18'

Column	Description	Unit
ID	ID number of polygon	-
GRIDCODE	Not used by HAMBO	-
MULTI_NAME	Code of nature target type	-
AREA	Area of polygon	m <sup>2</sup>

The polygon ID numbers do not match those in the economic dataset. Therefore, a separate table is necessary to link the economic and ecological data (see Section 3.1.2). The area of the polygons according to the two data files can be used to check this link.

#### ***soortgroepen***

This dataset lists per species category whether it is a vertebrate or invertebrate species. This information is relevant for the number of habitat keys needed by a species (Reijnen 2007).

#### ***spec\_clusters***

This dataset lists per target species (*soort*) its habitat clusters (*local\_id*) and the polygons belonging to each cluster (*polyid*)

#### ***spec\_ndt\_belang***

This dataset lists per combination of species (*naam*) and nature target type (*ndt*) the suitability of the nature target type for the species (*belang*).

### 3.2.3 Additional data

Before the economic and ecological data can be linked, three additional data sets are needed that are supplied separately or made by hand.

First, a data set is needed that provides the distance between selected pairs of polygons. Ideally, this data set contains the border-to-border distances between all possible polygon pairs. However, because such data sets typically contain  $n^2$  records, where  $n$  denotes the number of polygons, including all possible polygon pairs requires a huge amount of memory. Neither is it necessary to do so, because distances larger than the home range of the most mobile species in the data set (approx. 2 km) do not need to be considered anyway. Therefore, as a first step this data set contains only those polygon pairs where the distance does not exceed, say, 2.1 km. As a second step, several data sets are used containing different polygons to enable tests of the model with different data set sizes. In these tests the distance data set serves as a cut-out of the total set of polygons. The data set used for the calculations in Section 4 is the file *distmx500.dbf*.

Second, because the polygon IDs in the economic data set do not match those in the ecological data set, a table is needed that contains the IDs of one dataset with the corresponding IDs of the other. This data set is the file *idpatch.dbf*.

Lastly, a data set is needed to load the number of keys needed per species category according to Reijnen *et al.* (2007). This data set is easily made by hand, as it contains only two columns (vertebrates and invertebrates). The name of the data set is *VertKeys*.

### 3.3 Data preparation

Data preparation involves fifteen steps, of which thirteen are included in the database as queries. This paragraph only gives the name of the thirteen steps. The SQL code of the steps is given in Appendix D.

- Step 1: First selection of polygons
- Step 2: First selection of species
- Step 3: First selection of clusters
- Step 4: Select clusters of sufficient size
- Step 5: Second selection of polygons
- Step 6: Second selection of species
- Step 7: Selection of species characteristics
- Step 8: Select habitat types
- Step 9: Final selection of polygons
- Step 10: Select suitable polygons per species
- Step 11: Select polygon pairs
- Step 12: Link habitat types and species
- Step 13: Select clusters and polygons per species

### 3.4 Data import

HAMBO imports the data through the *mdb2gms* feature. After new data is available, the model needs to be run three times:

1. The first time to send the queries to Access and store the data as a GDX file. To perform this phase, the parameter *NewData* must be set at 'yes';
2. The second time to run precalculations and store the results in a second GDX file. To perform this phase, the parameter *NewData* must be set at 'no'.
3. The third time to run the model itself. This phase will be performed if phases 1 and 2 have been performed.



## 4 Results: comparing three spatially explicit models

### 4.1 Introduction

The spatially explicit models discussed in section 2.3 differ in important aspect from the method applied in LARCH. This paragraph provides more insight into their deviations from the LARCH method and their applicability to real situations. Three of the five discussed models are taken into account in the comparison to the original LARCH method: the direct-vicinity model with habitat keys, the area-within-cluster model and the complete-cluster model. The comparison has been performed through a theoretical analysis (4.2) and a test run with HAMBO with realistic data (4.3).

### 4.2 Theoretical analysis of a hypothetical configuration

#### 4.2.1 The hypothetical configuration

Suppose we wish to conserve three target species that reside in a hypothetical configuration of sites as depicted in Figure 1. The species have similar home range (depicted by the dotted lines), but they differ with regard to the minimum habitat cluster size: three sites for species 1, four sites for species 2 and five sites for species 3. As one can conclude from the costs of each site, total costs amount to € 6.800 if all sites are selected.

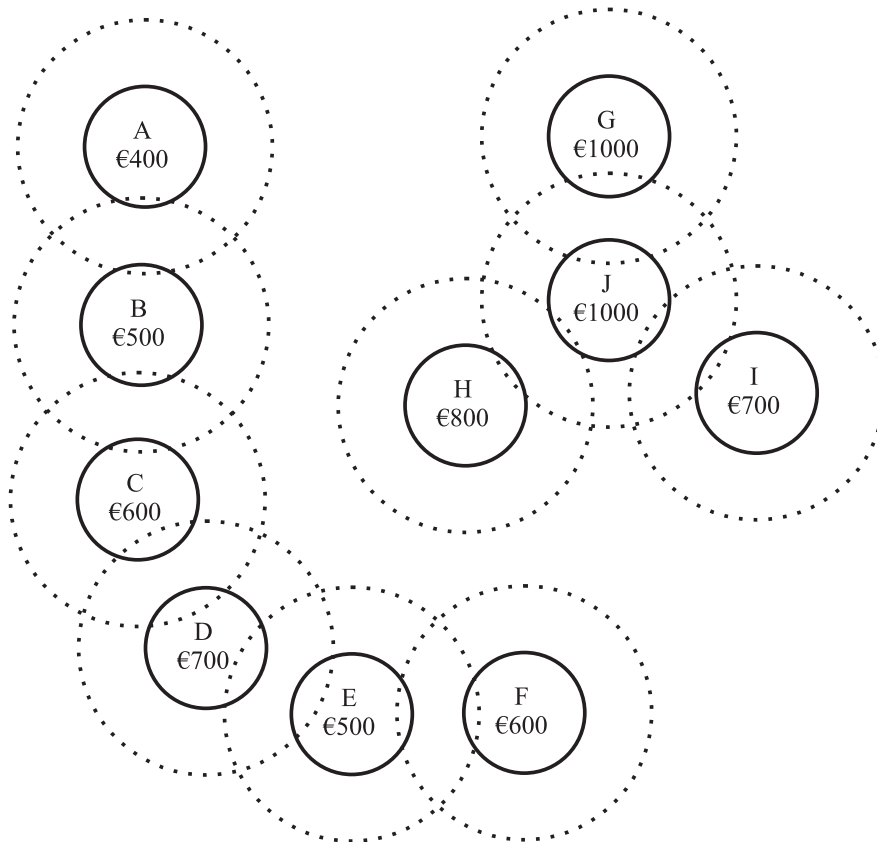


Figure 1: Hypothetical configuration of sites. (The dotted line denotes the home range of the target species).

The LARCH method (Pouwels *et al.* 2002) would identify two clusters, namely ABCDEF and GHIJ, where species 1 and 2 are conserved in both clusters and species 3 in ABCDEF only. In HAMBO, all spatially explicit models will take these clusters as input; their task is then to find configurations within either that conserve the demanded number of species at lower costs than € 3.300, the cost of cluster ABCDEF. Ideally the optimization would find the configuration with minimum cost.

Before discussing the three optimisation models, it is useful to identify the configurations that minimize costs under the constraint that one, two and three species are conserved respectively. Given conservation of at least one species, the obvious target species to be conserved is the one with the least severe requirements, namely species 1, which requires a cluster of at least three sites. The lowest-cost configuration of three sites is ABC at € 1.500. Conserving at least two species, is done at lowest cost in ABCD at € 2.200. Lastly, conserving all three species at minimum costs is done in ABCDE at € 2.700.

### 4.2.2 Complete Cluster Model

The complete-cluster model takes the composition of clusters as given and decides per species which clusters have to be conserved. Although, in reality, the clusters of a given species are likely to differ from those of other species, in this particular example all species have the same clusters, namely ABCDEF and GHIJ. Effectively, the complete-cluster model chooses between conserving cluster ABCDEF, GHIJ, or both<sup>9</sup>. Because ABCDEF conserves all three species at € 3.300, whereas GHIJ conserves only species 1 and 2 at € 3.500, the complete-cluster model will conserve ABCDEF whenever at least one species must be conserved or the budget is at least € 3.300. Therefore, the complete-cluster model is able to conserve all target species, albeit at higher costs than would have been optimal.

### 4.2.3 Direct-Vicinity Model

The direct-vicinity model can in principle construct smaller clusters within ABCDEF and GHIJ. However, because this model can only consider the direct vicinity of each site, a cluster identified by this model will include at least one site that lies within the species' home range from all other sites. Therefore, the model will be able to identify only clusters ABC, BCD, CDE, DEF, GHJ, GIJ, HIJ and GHIJ. If our target species' cluster size requirements are small, the model is able to identify lower-cost clusters than the complete-cluster model. For instance, species 1, which requires clusters of at least three sites, can be conserved in ABC at € 1.500, which is actually the lowest-cost solution we identified earlier. Species 2, however, can only be conserved in GHIJ at a cost of € 3.500. Sites A, B, C, D, E, and F cannot be grouped in a way that the direct-vicinity model can identify. Hence, for larger numbers of target species this model will identify solutions at even higher costs than the complete-cluster model. Moreover, species 3 cannot be conserved in any way because the largest cluster that the direct-vicinity model can identify consists of only four sites whereas species 3 requires at least five sites. Summarising, the direct-vicinity model outperforms the complete-cluster model for species with low cluster size requirements, but the model may not be able to conserve more demanding species, and will have in any way less degrees of freedom for those species.

---

<sup>9</sup> Therefore, the problem comes down to a standard non-spatial reserve site selection problem, although one should note that this will not be the case with more realistic settings where species' clusters overlap those of other species.

#### 4.2.4 Area-within-cluster model

The area-within-cluster model will identify for one, two and three species respectively the 'clusters' ABE at € 1.400, ABCE or ABEF at € 2.000 and ABCEF at € 2.600 respectively. Because none of these solutions constitute real, continuous clusters, however, we should dismiss each solution. Therefore, it is unlikely that the area-within-cluster model is suitable for the problems at hand.

### 4.3 Test run with HAMBO

All three models are run for a dataset of 408 polygons and 215 species. Because an error was made in area units (m<sup>2</sup> equal to ha) this many species could easily be conserved as they need ample area available in the 408 polygons. The result is of no use with regard to costs or for management of the area, but can still be used to assess the difference between the three optimization methods. The use of wrong criteria does not change the method.

For less than approximately 50 species, the direct vicinity model (DVM) is able to find lower-cost solutions than the complete-cluster model (CCM). Between approximately 50 and 130 species, there is not much difference between the two models, but for more than approximately 130 species, the CCM finds lower-cost solutions than the DVM. Furthermore, the DVM fails to conserve all target species. Lastly, the solution that conserves all 208 species at minimum costs according to the CCM costs only 15% of what the costs would have been if all polygons were included (Figure 2).

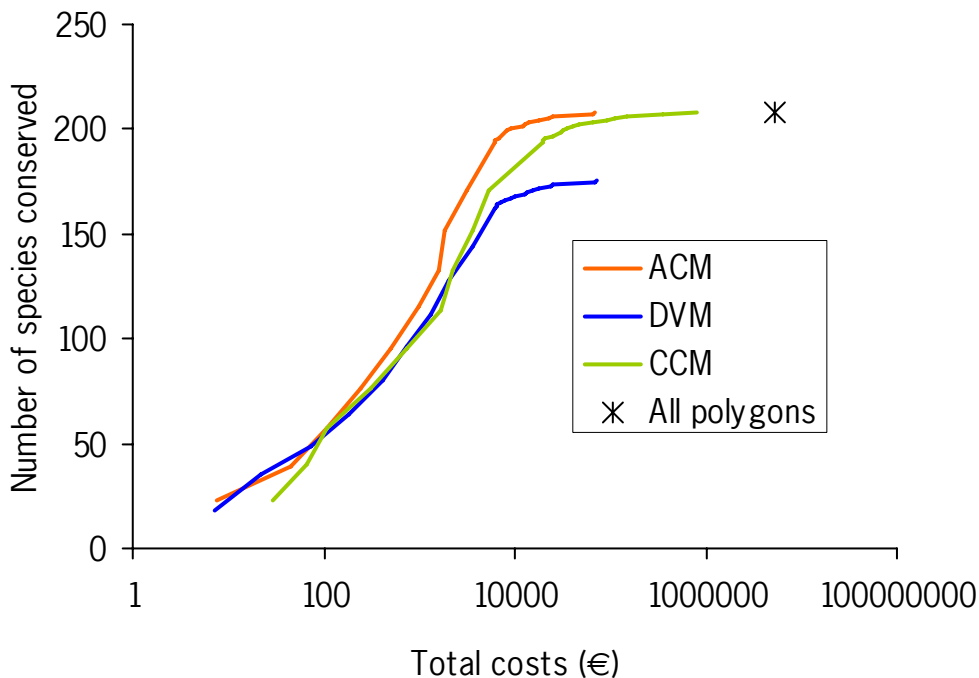


Figure 2: Relation between costs and number of species conserved of the Area-within-Cluster Model (ACM), the Direct-Vicinity Model (DVM) and the Complete-Cluster Model (CCM) (costs are presented on a logarithmic scale).





## 5 Conclusions and future plans

### *Conclusions*

Strictly speaking, this analysis suggests that the most suitable model to identify cost-effective clusters of sites depends on the spatial characteristics of the target species and the spatial configuration of sites. The model test runs, however, suggest that when all or many of the target species in the data set are to be conserved, the complete-cluster model is preferred over the direct-vicinity model. The Area-within-Cluster Model is not reliable because it may give non-compact configurations.

Besides the differences in outcome, there was also a difference in calculation time. Because the complete cluster model did not have to evaluate all possible location configurations the problem was far smaller with regard to memory use, and the calculations were completed faster.

### *Future plans*

It was decided that the complete cluster model was the only optimization method that had a chance of coping with the amount of data needed to optimize all of the Netherlands. Even then the problem has to be divided into smaller problems. If the need arises for more detailed analysis, the complete cluster model can be used in combination with a more detailed input of possible clusters and the addition of an extra restriction:

$$\sum_{l \in \Gamma_{cs}} C_{cs} \leq 1 \quad \forall l, s. \quad (\text{R14})$$

Currently procedures for dividing the problem are being developed.



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## Appendix A Full list of equations

### A.1 Restrictions

Number	GAMS name	Equation
(R1)	RestRelativeOpp	$R_h = \frac{\sum_{l \in \Lambda_h} \alpha_l F_{hl}}{\tau_h} \quad \forall h$
(R2)	RestFrNDTUnit	$\sum_{h \in \Lambda_l} F_{hl} \leq 1 \quad \forall l$
(R3)	RestMaxiMinOpp	$M \leq R_h \quad \forall h$
(R4)	RestSaveSpNoArea	$B_s \leq \sum_l \sum_{h \in \Lambda_l \text{ s.t. } \theta_{hs} > 0} F_{hl} \quad \forall s$
(R5)	RestVicNDTHab	$\mu_s L_{ls} \leq \sum_{m \in \Phi_{ls}} \sum_{h \in \Lambda_m} \alpha_m \theta_{hs} F_{hm} \quad \forall l, s$
(R6)	RestLocNDTHab	$L_{ls} \leq \sum_{h \in \Lambda_l \text{ s.t. } \theta_{hs} > 0} F_{hl} \quad \forall l, s$
(R7)	RestSaveSpArea	$B_s \leq \sum_l L_{ls} \quad \forall s$
(R8)	RestVicHab	$\mu_s L_{ls} \leq \sum_{m \in \Phi_{ls}} \sum_{h \in \Psi_m} \alpha_m \theta_{hs} G_m \quad \forall l, s$
(R9)	RestLocHab	$L_{ls} \leq G_l \quad \forall l, s$
(R10)	RestLocClus	$C_{cs} \leq \sum_{l \in \Gamma_{cs}} L_{ls} \quad \forall c, s$
(R11)	RestSaveSpClus	$\gamma_s B_s \leq \sum_{c \in \Omega_s} C_{cs} \quad \forall s$
(R12)	RestClusHab	$\mu_s C_{cs} \leq \sum_{m \in \Gamma_{cs}} \sum_{h \in \Psi_m} \alpha_m \theta_{hs} G_m \quad \forall c, s$
(R13)	RestClusTot	$C_{cs} \leq G_l \quad \forall c, l, s \in \Gamma$

### A.2 Objectives

Number	GAMS name	Equation
(01)	DoelTotKostenNDT	$K = \sum_l \sum_{h \in \Lambda_l} \kappa_{kl} F_{kl}$
(02)	DoelMaxiMinimOpp	$A = M$
(03)	Doel_AantSoorten	$S = \sum_s B_s$
(04)	DoelTotKosten	$K = \sum_l \sigma_l G_l$



## Appendix B Full list of symbols

### B.1 Indices

	GAMS name	Explanation
$c$	ClusterOfHabitat	Cluster
$h$	Natuur_Doel_Type	Habitat type
$l$	KandidaatLokatie	Site
$m$	KandidaatLokatie2	Alternate site
$s$	PlantOfDierSoort	Species

### B.2 Sets (mappings in GAMS)

Relations between elements, e.g. between habitat types  $h$  and sites  $l$  to indicate which habitat types are possible in a given site, are denoted as mappings in GAMS and as sets in this document. Indexed sets denote subsets depending on the index. For instance, the set  $\Lambda$  includes all possible combinations of  $h$  and  $l$ ;  $\Lambda_h$  includes all elements of  $l$  that can be combined with set  $h$ ; and  $\Lambda_l$  includes all elements of  $h$  that can be combined with set  $l$ .

#### Full sets

	GAMS name	
$\Gamma$	ClusterLocations	Set of combinations of sites $l$ , clusters $c$ and species $s$
$\Phi$	LocsWithinSpDist	Set of combinations of sites $l$ and alternate sites $m$ in the vicinity of sites $l$ /per species $s$
$\Lambda$	cbNatDoelLokatie	Set of habitat types $h$ possible in sites $l$
$\Omega$	ClustersVanSoort	Set of combinations of clusters $c$ and species $s$
$\Psi$	NatDoelInLokatie	Set of habitat types $h$ located in sites $l$

#### Subsets (GAMS names similar to full sets)

$\Gamma_{cs}$	Set of sites $l$ in cluster $c$ for species $s$
$\Phi_{ls}$	Set of sites $m$ in vicinity of site $l$ for species $s$
$\Lambda_l$	Set of habitat types $h$ possible in site $l$
$\Lambda_h$	Set of sites $l$ where habitat type $h$ is possible
$\Omega_s$	Set of clusters $c$ for species $s$
$\Psi_l$	Set of habitat types located in site $l$

### B.3 Parameters

	GAMS name		
$\alpha_l$	OppervlakLokatie	Area of site	ha
$\gamma_s$	MinNumberHabKeys	Minimum number of keys	number
$\kappa_{hl}$	KostenNatuurDoel	Costs of habitat in site	k€ ha <sup>-1</sup>
$\tau_h$	MaximaleOppervlk	Maximum area habitat type	ha
$\lambda_{ls}$	KwalteitSoortLok	Quality site for species	fraction
$\mu_s$	MinLocalAreaSpec	Demand for space of species	ha
$\sigma_{hs}$	KwalteitSoortNDT	Quality habitat type for species	fraction
$\sigma_l$	KostenKndLokatie	Costs of site	k€

#### B.4 Binary variables

	GAMS name		
$B_s$	vBehoud_DoelSoort	Global conservation of species	(0,1)
$C_{cs}$	vClustBehoudSoort	Conservation of species in cluster	(0,1)
$G_j$	vSelectie_Lokatie	Selection of site	(0,1)
$L_{js}$	vLokalBehoudSoort	Conservation of species in site	(0,1)

#### B.5 Custom variables

These variables can, depending on the model used, be used in different types, for instance either binary or continuous.

	GAMS name		
$F_{nl}$	vFractieNatDoelTp	Fraction of site under habitat type	(0,1)/-

#### B.6 Positive variables

	GAMS name		
$M$	vInstMaxiMinimOpp	Area of smallest-area habitat type	ha
$R_h$	vInstVarRelatvOpp	Relative area habitat type	-

#### B.7 Free variables

These variables are free because they can be used as objective variables. Except for costs, however, none of these have a real-world interpretation for a negative value, and in most cases the model structure is such that a negative value cannot occur.

	GAMS name		
$A$	vDoelVarRelatvOpp	Objective variable habitat area	ha
$K$	vTotaleKostenBehr	Total costs	k€
$S$	vAant_DoelSoorten	Number of species	-



## Appendix C Model-equation matrix

		AreaHabitatType	SpeciesDvNoArea	SpecDvHabitType	SpecDvVicinity1	SpecDvVicinityX	SpDivAreaInClus	SpDivCompltClus
	<b>Paragraph</b>	2.2.1	2.2.2	2.3.1	2.3.2	2.3.3	2.3.4	2.3.5
(R1)	RestRelatieveOpp	x						
(R2)	RestFrNDTUnit	x	x	x				
(R3)	RestMaxiMinOpp	x						
(R4)	RestSaveSpNoArea		x					
(R5)	RestVicNDTHab			x				
(R6)	RestLocNDTHab			x				
(R7)	RestSaveSpArea			x	x			
(R8)	RestVicHab				x	x		
(R9)	RestLocHab				x	x		
(R10)	RestLocClus					x		
(R11)	RestSaveSpClus					x	x	x
(R12)	RestClusHab						x	
(R13)	RestClusTot							x
(O1)	DoelTotKostenNDT	x	x	x				
(O2)	DoelMaxiMinimOpp	x						
(O3)	Doel_AantSoorten		x	x	x	x	x	x
(O4)	DoelTotKosten				x	x	x	x



## Appendix D Data preparation

Data preparation involves fifteen steps, of which thirteen are included in the database as queries.

### **Step 1: First selection of polygons**

In this step a first selection is made of the polygons, using the distance matrix *distmx500* and the polygon id translation file *idpatch*.

```
SELECT DISTINCT distmx500.PLY_ID1 AS Poly_id INTO polys500a
FROM (distmx500 INNER JOIN idpatch ON distmx500.PLY_ID1 =
idpatch.ID) INNER JOIN OKEafweging ON idpatch.PATCH_ID =
OKEafweging.NDT_PATCH;
```

### **Step 2: First selection of species**

Once the polygons to be analysed are selected, the next step is to make a first selection of the species in these polygons:

```
SELECT DISTINCT [Soorten in gebied].naam AS SoortNaam INTO
Spec500a
FROM [Soorten in gebied];
```

The table *[Soorten in gebied]* is a separate query that selects the polygons whose habitat type is suitable for the species:

```
SELECT polys500a.Poly_id, spec_ndt_belang.naam,
spec_ndt_belang.belang
FROM (polys500a INNER JOIN ndtmulti_18 ON
polys500a.Poly_id=ndtmulti_18.ID) INNER JOIN spec_ndt_belang ON
ndtmulti_18.MULTI_NAME=spec_ndt_belang.ndt
WHERE ((spec_ndt_belang.belang)>0);
```

### **Step 3: First selection of clusters**

Clusters are defined per polygon and per species. Therefore, once polygons and species are selected we can make the first selection of their clusters. This step selects the clusters of each species that have polygons in the area, and calculates per cluster the area of those polygons:

```
SELECT DISTINCT Spec_clusters.soort AS SoortNaam,
Spec_clusters.local_id AS Clus_id, Sum(ndtmulti_18.AREA) AS
ClusArea INTO Clus500a
FROM ((Polys500a INNER JOIN Spec_clusters ON Polys500a.Poly_id =
Spec_clusters.polyid) INNER JOIN Spec500a ON Spec_clusters.soort =
Spec500a.SoortNaam) INNER JOIN ndtmulti_18 ON Polys500a.Poly_id =
ndtmulti_18.ID
GROUP BY Spec_clusters.soort, Spec_clusters.local_id;
```

### **Step 4: Select clusters of sufficient size**

Because we select a sample of the entire ecological database, some clusters will not be included completely because some of their polygons lie outside the sample area. Therefore, some clusters may be too small to support the species they are defined for. This step therefore selects the clusters that are sufficiently large to support their species:

```
SELECT Clus500a.SoortNaam, Clus500a.Clus_id INTO Clus500b
FROM Clus500a INNER JOIN spec_normen1 ON Clus500a.SoortNaam =
spec_normen1.Doelsoort
WHERE ((Clus500a.ClusArea)>[spec_normen1].[key_opp])); *
```

### **Step 5: Second selection of polygons**

After Step 4, some polygons may be left in the database that do not belong to any sufficiently large cluster. Therefore, Step 5 selects the polygons present in *polys500a* that also belong to clusters present in *clus500b*:

```
SELECT DISTINCT Spec_clusters.polyid AS Poly_id INTO Polys500b
FROM Clus500b INNER JOIN (Polys500a INNER JOIN Spec_clusters ON
Polys500a.Poly_id = Spec_clusters.polyid) ON (Clus500b.Clus_id =
Spec_clusters.local_id) AND (Clus500b.SoortNaam =
Spec_clusters.soort);
```

### **Step 6: Second selection of species**

After Steps 4 and 5 it may turn out that some species cannot be conserved in the remaining polygons. The remaining species are selected in Step 6:

```
SELECT DISTINCT [Soorten in gebied 2].naam AS SoortNaam INTO
Spec500b
FROM [Soorten in gebied 2];
```

The table *[Soorten in gebied 2]* is a separate query that selects the polygons in the remaining dataset whose habitat type is suitable for the species:

```
SELECT polys500b.Poly_id, spec_ndt_belang.naam,
spec_ndt_belang.belang
FROM (polys500b INNER JOIN ndtmulti_18 ON
polys500b.Poly_id=ndtmulti_18.ID) INNER JOIN spec_ndt_belang ON
ndtmulti_18.MULTI_NAME=spec_ndt_belang.ndt
WHERE ((spec_ndt_belang.belang)>0));
```

### **Step 7: Selection of species characteristics**

The resulting table of Step 6 includes the final species set. Step 7 adds the characteristics of the species:

```
SELECT Spec500b.SoortNaam, spec_normen1.key_opp AS RuimteBeh,
spec_normen1.lokdist AS HomeRange, VertKeys.NumKeys INTO Spec500
FROM ((Spec500b INNER JOIN spec_normen1 ON Spec500b.SoortNaam =
spec_normen1.Doelsoort) INNER JOIN soortgroepen ON
spec_normen1.soortgroep = soortgroepen.SrtgroepId) INNER JOIN
VertKeys ON soortgroepen.E_Vert = VertKeys.Evert;
```

Because there are no species numbers in the input databases, an AutoNumber field is added to *Spec500* with the name *Spec\_id*.

### **Step 8: Select habitat types**

Step 8 selects all habitat types suitable for the final species set:

```
SELECT DISTINCT spec_ndt_belang.ndt INTO NDT500
```

---

\* This is the equation where  $m^2$  (Clus500a.ClusArea) and  $ha$  ([spec\_normen1].[key\_opp]) are wrongly compared. See section 4.3.

```
FROM spec_ndt_belang INNER JOIN Spec500 ON
spec_ndt_belang.naam=Spec500.SoortNaam
WHERE ((spec_ndt_belang.belang)>0));
```

Because there are no habitat type numbers in the input databases, an AutoNumber field is added to *NDT500* with the name *NDT\_id*.

### **Step 9: Final selection of polygons**

Step 9 selects the polygons whose habitat types are suitable for any species in the final species set:

```
SELECT Polys500b.Poly_id, ndtmulti_18.AREA AS Area, NDT500.NDT_id,
[Kosten Per Poly_id].Totalekosten INTO Polys500
FROM ((Polys500b INNER JOIN ndtmulti_18 ON
Polys500b.Poly_id=ndtmulti_18.ID) INNER JOIN NDT500 ON
ndtmulti_18.MULTI_NAME=NDT500.ndt) INNER JOIN [Kosten Per Poly_id]
ON Polys500b.Poly_id=[Kosten Per Poly_id].Poly_id;
```

The resulting table contains the final polygons set. The table *[Kosten Per Poly\_id]* is a separate query that calculates the conservation costs of each polygon. These costs, however, are calculated using a different numbering and even aggregation of polygons. In other words, not only do the same polygons have different id numbers in the ecological database than in the economic database, in some cases costs are calculated for groups of polygons that are included separately in the ecological database. In the latter cases, costs are distributed evenly over the polygons:

```
SELECT idpatch.ID AS Poly_id,
OKEafweging!Totalekosten*[Oppervlakte polygonen ecol data tov
polygonen econ data]!RelOpp AS TotaleKosten
FROM (idpatch INNER JOIN OKEafweging ON idpatch.PATCH_ID =
OKEafweging.NDT_PATCH) INNER JOIN [Oppervlakte polygonen ecol data
tov polygonen econ data] ON idpatch.ID = [Oppervlakte polygonen
ecol data tov polygonen econ data].ID
GROUP BY idpatch.ID, OKEafweging!Totalekosten*[Oppervlakte
polygonen ecol data tov polygonen econ data]!RelOpp;
```

The table *[Oppervlakte polygonen ecol data tov polygonen econ data]* is a separate query that calculates per polygon in the sample database how much of the corresponding polygon in the economic database it represents:

```
SELECT ndtmulti_18.ID, ndtmulti_18.AREA, [Oppervlakte polygonen
economische dataset].SumOfAREA, [ndtmulti_18]![AREA]/[Oppervlakte
polygonen economische dataset]![SumOfAREA] AS RelOpp
FROM ndtmulti_18 INNER JOIN (idpatch INNER JOIN [Oppervlakte
polygonen economische dataset] ON idpatch.PATCH_ID = [Oppervlakte
polygonen economische dataset].PATCH_ID) ON ndtmulti_18.ID =
idpatch.ID;
```

Suppose that, say, polygon 25 in the economic database has size 10 ha and it consists of two polygons that are listed separately in the ecological database under the numbers 14 with 4 ha and 83 with 6 ha. In that case, this query lists polygons 14 and 83 with the values 0.4 and 0.6, respectively. The table *[Oppervlakte polygonen economische dataset]* is another query that calculates the total surface area of the polygons in the economic dataset:

```
SELECT idpatch.PATCH_ID, Sum(ndtmulti_18.AREA) AS SumOfAREA
```

```
FROM ndtmulti_18 INNER JOIN idpatch ON ndtmulti_18.ID = idpatch.ID
GROUP BY idpatch.PATCH_ID;
```

Although the economic dataset also lists the area of each polygon, the areas mentioned differ from those in the ecological database. Therefore, the total area is recalculated with the data available in the ecological database.

### ***Step 10: Select suitable polygons per species***

Step 10 selects per species the polygons whose habitat type is suitable for the species:

```
SELECT DISTINCT Spec500.Spec_id, Polys500.Poly_id INTO SpecPoly500
FROM (Polys500 INNER JOIN SpecNDBelang ON Polys500.NDT_id =
SpecNDBelang.NDT_id) INNER JOIN Spec500 ON SpecNDBelang.Spec_id
= Spec500.Spec_id
WHERE ((SpecNDBelang.belang)>0));
```

The difference between this step and Step 9 is that Step 10 results in a mapping of species and polygons with the corresponding suitability of each polygon, whereas Step 9 results in a set of polygons.

### ***Step 11: Select polygon pairs***

Step 11 constructs a table that lists per species the pairs of polygons the distance between which is shorter than the home range of the species:

```
SELECT DISTINCT Spec500.Spec_id, SpecPoly500.Poly_id,
distmx500.PLY_ID2 AS Poly_id2 INTO SpecPolyPoly500
FROM ((SpecPoly500 INNER JOIN distmx500 ON SpecPoly500.Poly_id =
distmx500.PLY_ID1) INNER JOIN Spec500 ON SpecPoly500.Spec_id =
Spec500.Spec_id) INNER JOIN SpecPoly500 AS SpecPoly500_1 ON
(distmx500.PLY_ID2 = SpecPoly500_1.Poly_id) AND
(SpecPoly500.Spec_id = SpecPoly500_1.Spec_id)
WHERE ((distmx500.DIST)<[Spec500.HomeRange]));
```

### ***Step 12: Link habitat types and species***

This step maps species to habitat types and gives the quality of each habitat type:

```
SELECT DISTINCT [Spec500.Spec_id]*1 AS Spec_id, [NDT500.NDT_id]*1
AS NDT_id, spec_ndt_belang.belang INTO SpecNDBelang
FROM Spec500 INNER JOIN (NDT500 INNER JOIN spec_ndt_belang ON
NDT500.ndt = spec_ndt_belang.ndt) ON Spec500.SoortNaam =
spec_ndt_belang.naam;
```

### ***Step 13: Select clusters and polygons per species***

Lastly, Step 13 selects per species which of its clusters are present in the sample area and of which polygons they consist:

```
SELECT DISTINCT [Spec500.Spec_id]*1 AS Spec_id,
[Clus500b.Clus_id]*1 AS Clus_id, Polys500.Poly_id INTO
SpecClusPoly
FROM ((Spec500 INNER JOIN Clus500b ON Spec500.SoortNaam =
Clus500b.SoortNaam) INNER JOIN Spec_clusters ON (Clus500b.Clus_id
= Spec_clusters.local_id) AND (Spec500.SoortNaam =
Spec_clusters.soort)) INNER JOIN Polys500 ON Spec_clusters.polyid
= Polys500.Poly_id;
```

# Wot-onderzoek

## Verschenen documenten in de reeks Werkdocumenten van de Wettelijke Onderzoekstaken Natuur & Milieu vanaf 2006

Werkdocumenten zijn verkrijgbaar bij het secretariaat van Unit Wettelijke Onderzoekstaken Natuur & Milieu, te Wageningen. T 0317 – 48 54 71; F 0317 – 41 90 00; E [info.wnm@wur.nl](mailto:info.wnm@wur.nl)  
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