

1 **16. The ConsNet Software Platform for Systematic Conservation Planning.**

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8 **16.1. Introduction.**

9 Central to systematic conservation planning is the use of software planning tools for decision support (Sarkar *et al.*  
10 2006; Margules and Sarkar 2007), the most important of which are being reviewed in this book. Contemporary  
11 planning practices require tools that are accessible over the Internet and integrated with Geographical Information  
12 Systems (GIS) such as ArcGIS<sup>®</sup>. Availability, as well as computational efficiency (speed), are important when these  
13 tools are used for real-time negotiations involving stakeholders. Integration with GIS, especially for visualization, is  
14 important if the tools serve as decision support systems for formulating plans under alternative scenarios of habitat  
15 change. The ConsNet Portal ([www.consnet.org](http://www.consnet.org)) is a web-based resource for conservation planning. It includes an  
16 online interactive course (the ConsNet Primer) and the ability to run two software packages (ResNet and  
17 MultCSync) over the web. These packages form part of the ConsNet Software Platform which consists of a suite of  
18 software packages for decision support during the identification of nominal conservation area networks (CANs).  
19 These packages enable the selection of conservation area networks, analysis of the performance of biodiversity  
20 surrogates, establishment of connectivity between selected areas, and multi-criteria analysis for incorporating socio-  
21 political criteria into network design. The ConsNet Software Platform was developed at the Biodiversity and  
22 Biocultural Conservation Laboratory (BBCL; <http://uts.cc.utexas.edu/~consbio/Cons/Labframeset.html>) at the  
23 University of Texas at Austin and is supported by it; BBCL is also responsible for maintaining the ConsNet Portal.  
24 Users' questions about the software are answered through the BBCL Software Google Group  
25 ([http://groups.google.com/group/bbcl\\_software](http://groups.google.com/group/bbcl_software)).  
26 Five software packages (ResNet, ResNet-GUI, Surrogacy, LQGraph, and MultCSync) can be downloaded free of  
27 charge from a dedicated web-site (<http://uts.cc.utexas.edu/~consbio/Cons/ResNet.html>) and run separately; as noted  
28 earlier, ResNet and MultCSync can also be run over the web. The development of all these packages has been

1 motivated by the objective of achieving computational efficiency in the analysis of large data sets. For instance,  
 2 ResNet has been successfully used to analyze a global marine dataset with 176 093 cells and 1038 fish, invertebrate,  
 3 and marine mammal species (Wood 2007). This chapter reviews these five packages and explains how they can be  
 4 used together. A subsidiary objective has been to enable and encourage the use of a variety of techniques for spatial  
 5 analysis and other multi-criteria analyses in conservation planning.

6

## 7 16.2. Basic Prioritization for Adequate Representation of Biodiversity Surrogates.

8 The objective of ResNet (and ResNet-GUI) is to prioritize areas, modeled as cells, to represent all biodiversity  
 9 surrogates (species, habitat types, etc.) up to an explicit target (number of occurrences of species, proportions of  
 10 species' ranges, habitat types, etc) in a nominal conservation area network. ResNet 1.2 is used to solve: (i) the  
 11 minimum area problem—representation of all biodiversity surrogates in as little selected area as possible; and (ii)  
 12 the maximum representation problem—represent as many surrogates as possible up to their targets in a budgeted  
 13 area. (Chapter 3 discusses the relation between these two problems and the set cover and maximal cover problems.)  
 14 ResNet is initiated by selecting an initial cell or set of cells and then uses a two-pass hierarchical heuristic algorithm  
 15 to select more cells iteratively (Garson *et al.* 2002; Sarkar *et al.* 2002). The first cell is selected either using the rarity  
 16 of surrogates within them or by the richness of these surrogates or by specifying an existing set of selected cells (for  
 17 instance, those representing existing protected areas). The user chooses between these three options.

18 In the heuristic algorithm that is then executed, during the first stage, cells are first selected on the basis of rarity  
 19 with ties broken by complementarity (Sarkar *et al.* 2002). Let  $\Sigma$  ( $\sigma_j \in \Sigma, j = 1, 2, \dots, n$ ) be a list of cells,  $\Lambda$   
 20 ( $\lambda_i \in \Lambda, i = 1, 2, \dots, m$ ) be a list of surrogates, and  $T$  ( $\tau_i \in T, i = 1, 2, \dots, m$ ) be a list of targets of expected  
 21 coverage for each surrogate, and  $e_{ij}$  ( $i = 1, 2, \dots, m; j = 1, 2, \dots, n$ ), be the probabilistic expectation of  $\lambda_i$  (the  $i$ -  
 22 th surrogate) at  $\sigma_j$  (the  $j$ -th cell). At any stage of the iteration, let  $\Gamma$  be the set of cells so far selected, and  $\Lambda'$  be  
 23 the set of surrogates that have already satisfied their targets. Then the rarity  $\rho_i$  ( $i = 1, 2, \dots, m$ ) of a surrogate is

24 defined by  $\rho_i = \frac{1}{\sum_{j=1}^n e_{ij}}$ , that is the rarity of a surrogate is the inverse of its total expected presence in the region.

25 At any iteration of the algorithm, the cell selected from all the available cells ( $\Sigma \setminus \Gamma$ ) is the one with the surrogate

1 with the highest value of  $\rho_j$  provided that  $\lambda_j$  has not already achieved its target,  $\tau_j$ , that is  $\lambda_j \notin \Lambda'$ . If there is a  
 2 tie, that is, more than one cell has a surrogate with the highest possible value of  $\rho_j$ , the tie is broken using  
 3 complementarity. Let  $\kappa_j$  ( $j = 1, 2, \dots, n$ ) be the complementarity value of a cell  $\sigma_j$ . Then  $\sigma_j = \sum_{\lambda_j \in \Lambda \setminus \Lambda'} e_{jj}$ , that  
 4 is it is the summed expectation in that cell of those surrogates that have not already achieved their targets.  
 5 Further ties may be optionally broken using adjacency (see § 16.4.1) and then at random (that is, using lexical  
 6 order). During the second pass cells that have become redundant are dropped from the solution, unless they come  
 7 from an existing set of selected cells (typically representing existing protected areas). Input from the user also  
 8 determines whether adjacency is used and whether the second pass is executed. A rarity-complementarity algorithm  
 9 is used because, with binary presence-absence data, this heuristic algorithm is known to produce more spatially  
 10 economical solutions compared to other such algorithms (Csuti *et al.* 1997; Sarkar *et al.* 2002, 2004). To solve the  
 11 minimum area problem, ResNet can be made to terminate when all representation targets are satisfied. To solve the  
 12 maximum representation problem, ResNet can be terminated when a maximum budgeted area or cost is exceeded.  
 13 ResNet-GUI 2.1 is a version of ResNet that can be run from within the ArcView® 3.2 GIS package.  
 14 ResNet requires two input text data files. Inside ResNet, the data from the first file is represented as a matrix in  
 15 which the rows correspond to the cells. The first column is a cell identifier, the second and third give the  $x$ - and  $y$ -  
 16 co-ordinate of the centroid of the cell (typically these are longitudes and latitudes or UTM co-ordinates), the next ten  
 17 are reserved for the cell identifiers of cells that may be adjacent to the current cell, the next two for the area and cost  
 18 of the current cell, and an indefinite number of further columns record the expected representation value of each  
 19 biodiversity surrogate in the current cell. If ResNet is run over the web through the ConsNet Portal, the expectations  
 20 can be any real number, for the version that can be downloaded, they are restricted to binary data (with “1”  
 21 signifying presence and “0” signifying absence). The second required input file consists of a list of surrogates  
 22 (identified by a number) and the required target of representation for each. (If these targets are larger than what can  
 23 be achieved with the data set, ResNet automatically decreases target levels to what is achievable.) Optional input  
 24 files can be used to specify which cells are already selected (for initialization as mentioned above) and which should  
 25 be excluded from the analysis. The basic output consists of a list of co-ordinates of the selected cells. A log file  
 26 keeps track of all input parameter options that were used; the user can also choose to record a “detailed” log file  
 27 which also tracks how each cell was selected. Log files also provide information on the quantitative representation

1 of surrogates in the selected cells.

2 Box 1 provides a characteristic example of the use of ResNet. Other important uses include a global prioritization of  
3 marine areas (Wood 2007), a series of prioritization exercises for sub-regions of México (Cirelli 2005; Dawson  
4 2005; Illoldi-Rangel *et al.* in press), an analysis of areas in the San Juan Islands National Wildlife Refuge in the San  
5 Juan Archipelago in Washington (Irvine 2005), and studies of the Iberian Peninsula (Abellán *et al.* 2005, 2007;  
6 Traba *et al.* 2007).

7 **[PLACE BOX 1 ABOUT HERE.]**

8

### 9 16.3. Testing and Developing Biodiversity Surrogate Sets.

10 The purpose of surrogacy analysis is to determine whether a set of “estimator” surrogates for biodiversity for which  
11 distribution data can reasonably be gathered (e. g., some well-known taxa or environmental layers) give the same  
12 results as those that would be obtained were the most appropriate or “true” components of biodiversity were used in  
13 planning analyses (Sarkar *et al.* 2005; Margules and Sarkar 2007). Surrogacy 1.1 automates procedures for testing  
14 the performance of estimator-surrogates which would potentially be used to represent desired biodiversity features  
15 (or “true surrogates”) in a planning protocol. It uses ResNet to select cells using estimator-surrogates and reports the  
16 extent to which true surrogates are represented.

17 Surrogacy 1.1 input files have the same format as ResNet input files. The user must provide separate files for the  
18 true and estimator surrogates. The graphical output consists of surrogacy graphs which are a generalization of  
19 species-accumulation curves. These graphs record the percentage of true surrogates that have achieved their targets  
20 as a function of the percentage of estimator surrogates that have achieved their targets or the total area of the  
21 selected cells. Surrogacy has been used to assess the performance of taxonomic surrogate sets in Latin America  
22 (Tognelli 2005, 2007) and environmental surrogate sets in Québec and Queensland (Sarkar *et al.* 2005).

23

### 24 16.4. Spatial Analysis.

25 Two types of spatial analysis are possible through the ConsNet Software Platform: a preference may be given to  
26 larger conservation areas (§ 16.4.1) and connectivity between areas may be established (§ 16.4.2).

27 16.4.1. **Size.** Larger contiguous conservation areas can optionally be constructed using ResNet by giving a  
28 preference to cells adjacent to already selected cells when breaking remaining ties after the use of rarity and

1 complementarity. Thus a preference for larger sizes of contiguous selected areas is expressed hierarchically (rather  
2 than through an explicit objective function). For binary data this method of finding larger conservation areas  
3 typically works well. However, it is ineffective if the data are probabilistic: ties after the use of rarity and  
4 complementarity are rare and this rule is not invoked very often.

5 16.4.2. **Connectivity.** Like ResNet, LQGraph divides the study region into cells that can be polygons of any shape.  
6 In LQGraph, each cell is either part of a conservation area or external to such areas. Conservation areas can include  
7 more than one cell. Quality scores between zero and one are assigned by the user to the external cells. Cells that are  
8 suitable as connectivity areas to link the conservation areas are assigned scores close to one. (The quality scores may  
9 refer to the irreplaceability of cells [Pressey *et al.* 1994], the selection frequency of different cells during area  
10 prioritization, be based on alignment with land cover types, etc.) LQGraph selects a subset of the external cells to  
11 serve as connectivity areas and can also find the set of cells that fragments a conservation area network most  
12 efficiently, which is called the “cut set.” The connectivity areas are optimal insofar as they represent the shortest  
13 path between conservation areas. Since the set of all such shortest paths may be too large to be put under a  
14 conservation plan, LQGraph can find a subset of the shortest paths, called the minimum spanning tree (MST). The  
15 MST constitutes the minimum number of paths required to link all conservation areas via high-quality cells. In  
16 addition, the user can request that all MSTs be found.

17 LQGraph models the study region using graphs, which are discrete mathematical structures consisting of sets of  
18 vertices and edges (Gross and Yellen 1998). (See Fuller and Sarkar [2005] for further illustration of graph-theoretic  
19 concepts and the stages of the LQGraph computations.) In the type of graph considered here, each edge connects  
20 exactly two vertices. In a directed graph, each edge has a head vertex at which the edge starts and a tail vertex at  
21 which the edge ends. In an undirected graph, each edge is incident to two vertices but the edge is not directed from  
22 its head to its tail. LQGraph first models the landscape as a “contiguity graph”, which is a directed graph, in which  
23 the vertices represent all cells and there is a directed edge between two vertices if the corresponding cells are  
24 adjacent to one another in geographical space (Fuller and Sarkar 2006). If the tail vertex of an edge of the contiguity  
25 graph represents a cell in a conservation area, then the edge weight is set equal to one. This ensures that the shortest  
26 path between conservation areas includes few cells in conservation areas. If the tail vertex of an edge represents a  
27 cell external to the conservation areas, the edge weight equals one minus the quality score of the tail vertex. The  
28 shortest path between the vertices that correspond to the centroids of the conservation areas is then found using

1 Dijkstra’s algorithm (Cormen *et al.* 2001). Due to the manner in which the edge weights are defined, each shortest  
2 path will correspond to high quality cells.

3 The shortest paths of the contiguity graph comprise the edges of the “landscape quality graph”, an undirected graph  
4 in which the vertices now represent conservation areas. The weight of each edge of the landscape quality graph  
5 equals the sum of the quality scores of the cells in the shortest path. An edge of the landscape quality graph  
6 constitutes the least cost path between a pair of conservation areas. However, the percent of the study region  
7 occupied by the least cost paths is typically so large that it would not be feasible to put all of the paths under a  
8 conservation plan (Fuller and Sarkar 2006). LQGraph prioritizes a subset of the least-cost paths by finding MSTs of  
9 the landscape quality algorithm using Prim’s algorithm (Siek *et al.* 2001). The algorithm is computationally  
10 efficient, with a running time that grows as a polynomial function of the number of vertices and edges of the  
11 landscape quality graph. An alternative approach based on graph theory for incorporating connectivity into the  
12 design of conservation areas is to search for a Steiner tree (Williams 1998). However, the running time of an  
13 algorithm to solve the Steiner tree problem optimally grows as a non-polynomial function of the size of the graph  
14 and near-optimal heuristics require a Manhattan geometry that may not be appropriate in most planning contexts  
15 (Kahng and Robbins 1995). LQGraph finds all MSTs via a generalization of Prim’s algorithm that accounts for ties  
16 in edge weight during the growth of incipient MSTs (Sedgewick 1983).

17 The input to LQGraph consists of a text file that identifies the conservation areas, the external areas, and the quality  
18 scores of the external areas (for details, see Fuller and Sarkar 2005). In addition, the user must provide a text file that  
19 lists the centroid cells of the conservation areas. LQGraph provides functions for constructing these input files from  
20 ResNet input and output files. Like ResNet, each run of LQGraph creates a text output file called a log file that  
21 summarizes the settings for and results of the run. Additional outputs that can be requested by the user include: (1) a  
22 file listing all of the cells in the shortest paths (called the “All Edges Output File”), (2) a MST output file, and (3) a  
23 cut sets output file. (1)-(3) are provided as txt files and raster files in GIS format. LQGraph can also generate EMF  
24 image files to display the cell quality scores, the MSTs, and the cut sets. Box 2 gives an example of the use of  
25 LQGraph.

26

27 **[PLACE BOX 2 ABOUT HERE.]**

28

1 16.5. **Multi-Criteria Analysis.**

2 Because biodiversity conservation is not the only possible valid social use of land- or seascapes, the sociopolitical  
3 consequences associated with the inclusion of an area must be considered during conservation area network design  
4 (Sarkar 2005). In addition to these sociopolitical criteria, network design must also consider spatial criteria such as  
5 the size of individual areas, their dispersion over the landscape, and their connectivity. The consideration of both  
6 sociopolitical and spatial criteria thus calls for the use of multi-criteria analysis (MCA) (Keeney and Raiffa 1993;  
7 Figuera *et al.* 2005).

8 There are two ways in which MCA can be used in conservation planning (Sarkar 2005; Moffett and Sarkar 2006). In  
9 an *iterative* stage protocol, all criteria are considered in the evaluation of each individual cell for potential inclusion  
10 in a conservation area network (Bojórquez-Tapia *et al.* 2004). In a *terminal* stage protocol, a number conservation  
11 area networks are first identified with each satisfying the specified biodiversity representation targets; the other  
12 criteria are then used to rank these nominal networks (Moffett and Sarkar 2006). Iterative stage protocols do not  
13 privilege biodiversity representation because they allow trade-offs between biodiversity representation and the other  
14 criteria. Terminal stage protocols privilege biodiversity representation over other criteria because biodiversity  
15 representation cannot be compromised through trade-offs. Mixed protocols may also be used which incorporate  
16 some criteria iteratively and others terminally (Margules and Sarkar 2007).

17 A number of MCA techniques can be used to support conservation planning (Moffett and Sarkar 2006). The  
18 MultCSync 1.0 software package (Moffett *et al.* 2005) implements three of these methods. The simplest of these is  
19 non-dominated set (NDS) computation, which identifies the set of Pareto-optimal alternatives (Keeney and Raiffa  
20 1993; see, also, Chapters 3 and 4). NDS computation assumes that each alternative has been ranked on the basis of  
21 each criterion. A Pareto-optimal alternative is one for which there is no other alternative that performs at least as  
22 well as it with respect to all criteria and better than it with respect to at least one criterion. NDS computation consists  
23 of finding all such alternatives—it only requires ordinal rankings of the alternatives and no ranking of the criteria. In  
24 addition to NDS computation, MultCSync also allows the use of the Analytic Hierarchy Process (AHP) and a  
25 version of multi-attribute value theory (MAVT). Each of these MCA techniques assigns a quantitative value to each  
26 alternative that represents the overall performance of the alternative according to the set of criteria (Belton 1986).  
27 These overall values are based upon an additive value function constructed from a set of quantitative weights  
28 assigned to the criteria through pairwise comparisons, along with the set of values assigned to the alternatives on the

1 basis of each criterion. Though the structure of these methods is thus quite similar, the methods differ in the ways in  
2 which the final values assigned to the alternatives are normalized (Dyer 1990). For this reason the methods may  
3 produce different results when applied to the same decision scenario. Though both the AHP and MAVT are  
4 available within MultCSync, the use of MAVT is recommended due to problems associated with the normalization  
5 procedure employed by the AHP (Moffett *et al.* 2006). Because the way in which MAVT is implemented in  
6 MultCSync uses the same (pairwise) elicitation procedure to calculate criterion weights that the AHP uses, it is  
7 called mAHP (“modified Analytic Hierarchy Project”) in the program.

8 In addition to these three MCA methods, the version of MultCSync that can be run over the web also includes the  
9 Regime method (Hinloopen *et al.* 1983). This outranking method provides a ranking of the alternatives based on a  
10 ranking of the criteria and a set of rankings of each of the alternatives on the basis of each of the individual criteria.  
11 Thus it requires only ordinal rankings for both the alternatives and the criteria and cardinal rankings for neither.  
12 When using MultCSync, different input files are needed depending upon the MCA method that is used. Each of the  
13 methods makes use of a common input file which consists of a matrix of  $m$  rows and  $n + 1$  columns, where  $m$  is  
14 equal to the number of alternatives and  $n$  is equal to the number of criteria. Each row provides information about one  
15 of the  $m$  different alternatives. In each row, the first column is an alternative identification number and the  
16 subsequent  $n$  columns provide the values of that alternative according to each of the  $n$  criteria. This input file is the  
17 only form of input needed for NDS computation. However, an additional input file is needed to use either the AHP  
18 or MAVT. This file consists of a matrix of  $n$  rows and  $n$  columns in which entry  $(i, j)$  represents the ratio by which  
19 criterion  $i$  is more important than criterion  $j$ .

20  
21 **[PLACE BOX 3 ABOUT HERE.]**

22  
23 The output files produced by MultCSync likewise depend upon the type of method that is used. For NDS  
24 computation a single output file is produced, which consists of a matrix identical in format to the input file, but with  
25 information provided only for the Pareto-optimal alternatives. If either the AHP or MAVT is selected, then two  
26 output files are produced. The first consists of a list of the alternatives in which each alternative has been assigned  
27 an overall value, with the alternatives ordered on the basis of their assigned values. The second provides information  
28 regarding the weights assigned to the criteria on the basis of the pairwise comparisons. Box 4 gives an example of

1 the use of MultCSync.

2  
3 **[PLACE BOX 4 ABOUT HERE.]**  
4

#### 5 **16.6. Applicability and Limitations of the ConsNet Framework.**

6 The basic software package of the ConsNet platform is ResNet and it is the one that has been used most often  
7 (Abellán *et al.* 2005, 2007; Irvine 2005; Pawar *et al.* 2007; Pérez-García *et al.* 2007; Traba *et al.* 2007; Wood 2007;  
8 Sarkar *et al.* 2007). In the simplest situation it is used to identify nominal conservation area networks. Surrogacy  
9 uses ResNet to prioritize areas but, since the ResNet code is incorporated within it, Surrogacy can be used  
10 independently. It has been used to assess the performance of various taxonomic surrogate sets on a continental scale  
11 for South America (Tognelli 2005, 2007). It has also been used to show that environmental surrogate sets perform  
12 reasonably well when the true surrogates are various taxa using large data sets from Québec and Queensland (Sarkar  
13 *et al.* 2005). LQGraph and MultCSync can use the output from ResNet but can also be used independently, for  
14 instance with the output of other area prioritization packages discussed in this book. The main advantage of all these  
15 packages is computational speed and the ability to handle large data sets. An additional advantage of ResNet and  
16 LQGraph is that they can provide the decision-maker with multiple alternative conservation actions. ResNet can find  
17 multiple conservation plans for the same target and budget levels either through the randomization of the rows of the  
18 input file (Box 2) or by defining (part of) a solution obtained in one ResNet run as the set of “Excluded Cells” in a  
19 subsequent ResNet run. As noted above, LQGraph can search for multiple minimum spanning trees. All MSTs are  
20 the same with respect to their connectivity-conferring properties, but the MSTs may differ with respect to other  
21 criteria that affect the successful implementation of the conservation plan, such as the cost or human population size  
22 of their constituent cells.

23 The main disadvantage is that the analysis of spatial configuration in ResNet remains limited. In addition,  
24 ResNet is not suited for planning problems in which a stochastic process determines which habitat cells are intact or  
25 available to serve as conservation areas. A limitation of the connectivity areas selected by LQGraph is that they may  
26 be too long and too narrow for the dispersal of many species or to be appropriate recommendations for habitat  
27 zoning. LQGraph also assumes that a single score can capture the suitability of a cell for all species in the planning  
28 exercise. However, a cell that is appropriate as a dispersal route for one species may be inappropriate for another

1 species. As noted above, like any terminal stage protocol, MultCSync presupposes that the decision maker's  
2 preferences are structured hierarchically such that the representation of biodiversity is more important than  
3 economic objectives. However, this preference structure is exhibited by some stakeholders in real-world  
4 conservation planning (Rekola *et al.* 2000) and is the basis for conservation legislation such as the Birds Directive in  
5 European Community law (Verschuuren 2004). Data size restrictions are important considerations for conservation  
6 practitioners when selecting a software planning tool. In ResNet, floating point precision appears to be a more  
7 important restriction than the number of cells, that is, the program runs appreciably more slowly as the precision of  
8 the data (the number of places after the decimal point) increases. ResNet has systematically analyzed a data set with  
9 176 093 cells (Wood 2007) and has been tested on 2 376 182 cells (J. Grand, personal communication). Ongoing  
10 work with ResNet involves up to 400 000 cells (Marcelo F. Tognelli, personal communication). The computational  
11 effort required to compute rarity and complementarity in ResNet increases if the occurrence data for the surrogates  
12 are probabilistic and the floating point precision of each probability is high. If the precision is high and the number  
13 of surrogates is large, ResNet may not be able to obtain a solution in a reasonable amount of time, though this  
14 limitation is yet to be experienced in practice. In LQGraph, the principal data size restriction pertains to memory  
15 rather than running time. If many cells have the same quality and the user requests that all MSTs be found, then the  
16 number of MSTs may be extremely large resulting in problems with storage of the incipient MSTs.

17

#### 18 16.7. **Future Plans.**

19 A new software package, ConsNet, is being developed at BBCL to solve the basic representation problem while  
20 incorporating the following spatial criteria: size, shape, connectivity, alignment (of selected areas with land cover  
21 types, e.g., ecotypes), and replication (the number of different contiguous clusters of selected areas in which a  
22 surrogate is represented). Replication is supposed to take care of representing independent populations of surrogates  
23 such as species. ConsNet will also incorporate uncertainty analysis in the form of information-gap decision theory  
24 using a linear envelope uncertainty model (Regan *et al.* 2005; Ben-Haim 2006; Moilanen *et al.* 2006).

25 ConsNet uses the tabu search metaheuristic algorithm (Glover and Laguna 1997) in trying to find near-optimal  
26 solutions incorporating all these criteria. One unexpected result from this work has been that, for all data sets  
27 analyzed so far (including that in Box 1), there are a very large number of solutions with very different spatial  
28 configurations all of which have the same (near-optimal) total area while meeting all representation targets. This

1 means that there may often be very little trade-off required to satisfy multiple spatial criteria in the design of  
2 conservation area networks.

3

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18

19

1 **Box 1. Herpetofauna Protection in the Eastern Himalayas** (Pawar *et al.* 2007).

The purpose of this analysis was to assess the performance of the existing protected areas of Northeast India with respect to the representation of herpetofaunal diversity and to identify new areas with which the existing set should be augmented to represent these biodiversity surrogates adequately in as little total area as possible. Maps of conservation area networks were created by selecting areas using ResNet. Algorithm runs were initiated either by rarity (choosing a cell with the rarest surrogate) or by including all the existing protected areas.

**Study Region:** The study region consisted of the part of the Eastern Himalayas within the political boundaries of India. The total area was about 218 663 km<sup>2</sup>. It intersects with both the Himalaya and Indo-Burma biodiversity hotspots (Mittermeier *et al.* 2004) and is thus of global significance for conservation. (Political boundaries were used because implementation in this region can only be reasonably envisioned at national levels. Prospects of collaboration between India and the military junta-led regime of Burma [the other entity in the region] are non-existent.)

**GIS Model:** For this analysis, the Eastern Himalayan biodiversity hotspot was divided into 285 461 cells with 80 species used as surrogates. Thus the average area of each cell was slightly less than 1 km<sup>2</sup>.

**Biodiversity Surrogates:** Amphibian and reptile species were used as biodiversity surrogates. Some data were available for 184 species (63 amphibian and 121 reptile species). The distributions of the species were modeled using the Maxent software package (Phillips *et al.* 2006) with these species records and environmental layers (from WorldClim [Hijmans *et al.* 2005] and SRTM data). Models could only be constructed for 131 species with  $\geq 4$  records. Most of the prioritization runs used only the distribution of 80 species for which statistically adequate niche models (AUC > 0.75;  $p < 0.05$  for at least one internal test) could be constructed. However, some runs used the 131 species with  $\geq 4$  records to see if these made any significant difference.

**Targets and Goals:** Priority areas for the representation of these species were identified at targets of 5-20 % at increments of 5 %. The performance of existing conservation areas was assessed by initializing runs with priority areas and comparing the results with those obtained when initialization was by rarity.

**Results:** Figure 16.1 shows the areas selected at representation targets of 10 % and 20 %, using 80 species as surrogates. Table 16.1 shows the amount of land selected. Note the low level of concordance between the existing protected areas and the conservation area networks selected without already including them. This result confirms a pattern seen throughout the world (Pressey 1994): traditional area prioritization for natural values is *ad hoc* from the

perspective of systematic conservation planning. (If all 131 species were used, the areas selected are marginally larger. With rarity initialization an additional 1 % of the land is required for the 5 % representation target and 3 % for the 20 % representation target.)

**Significance:** The practical importance of this analysis lies in that it was both the first assessment of the performance of existing protected areas in this region and the first priority area identification using systematic conservation methods. The importance of this analysis from the perspective of designing useful software is that it illustrates that ResNet can accommodate a relatively large data set which is typical of those encountered in sophisticated practical planning contexts. A typical run with 20 % representation targets and all 131 species (the most computationally complex case) took about 8 hours.

1

2 **[FIGURE 16.1 HERE.]**

3 **[TABLE 16.1 HERE.]**

1 **Box 2. Endemic Mammals of the Transvolcanic Belt (TVB), México** (Fuller *et al.* 2006).

The purpose of the analysis was to propose a plan for the transvolcanic belt (TVB) of México to assist ongoing conservation activities by two federal agencies in México, the Comisión Nacional para el Conocimiento y Uso de la Biodiversidad (CONABIO) and the Comisión Nacional de Áreas Naturales Protegidas (CONANP).

**Study Region:** The TVB tracks a mountain range in central México (latitude: 19-21° N; longitude: 97-105° W) that bisects the country between the Central Plateau and the Balsas Depression (Villaseñor *et al.* 2006). Rates of deforestation and other forms of habitat transformation in the TVB are high because of the region's human population of 40 million, which includes the México City metropolitan area with a population of 18.3 million.

**GIS Model:** A resolution of 0.01° × 0.01° was used for the analysis because, at this resolution, the cells were sufficiently small for them to be realistically put under a conservation plan (mean area: 1.163 km<sup>2</sup>) and the number of cells was sufficiently small that computations remained tractable. Using a remote-sensed land cover map (Mas *et al.* 2004), cells in the TVB were classified as having primary vegetation, secondary vegetation, or neither. Cells lacking such vegetation comprised 36% of the TVB. These cells were excluded from the analysis on the grounds that they cannot support mammal populations (see below for the choice of surrogates) without immigration from untransformed habitat. This left 67 752 cells for use in the planning exercise (total area: 78 796 km<sup>2</sup>).

**Biodiversity Surrogates:** México ranks second globally in mammal species richness (Fa and Morales 1993). The diversity of mammals in central México is particularly high due to the interdigitation of the geographical distributions of Nearctic and Neotropical species in the TVB region. Because of the importance of mammal conservation in this region, the biodiversity surrogates used in this planning exercise were all 99 non-volant mammal species of the TVB, which includes 24 species endemic to México, 14 endemic to the TVB, four species listed as endangered by the IUCN and four species listed as vulnerable. In addition, in the TVB, non-volant mammals are important as seed dispersers and their distributions are among the best documented of any taxonomic group.

**Targets and Goals:** In systematic conservation planning, targets denote the quantitative level of representation of the surrogates in a conservation area network (Margules and Sarkar 2007). GARP (Stockwell and Peters 1999) was used to model the geographical distributions of the 99 non-volant mammals based on occurrence points for each species and 10 explanatory variables (climatic and topographic parameters and vegetation type). The target of representation was set to 10 % of the geographical distribution of each species. This target, which has been used in

many planning exercises (Margules and Sarkar 2007), was selected in order to balance species' persistence, which is assumed to increase with increasing targets, and conflicts with competing land uses, which may also increase as the targets increase. Two conservation area networks were selected in order to satisfy the target of representation using ResNet. During the construction of the first network, the algorithm was required to select the 39 existing natural protected areas in the TVB (hereafter "NPA network"). For the second network (hereafter the "rarity network"), the algorithm ignored the existing NPAs. Instead, cells were selected based on species' rarity and ties were disambiguated using complementarity. Goals refer to the spatial properties of a conservation area network such as connectivity as well as to the network's social and economic properties (Margules and Sarkar 2007). Connectivity was incorporated into the design of the conservation area network using LQGraph. To build the contiguity graph, cell quality was defined as the frequency of selection in 2000 randomized replicates of the area prioritization procedure. Each replicate used a different randomization of the order of the cells in the ResNet input file. Since ResNet breaks ties in complementarity based on lexical order, this randomization of the input file may result in the selection of different cells in different replicates. The weight of each edge was one minus the quality of the tail vertex if the vertex was external to a conservation area or one otherwise. Dijkstra's algorithm was used to find the shortest path between each pair of vertices that represented the centroid cells of the conservation areas. These shortest paths formed the edges of the landscape quality graph. Separate landscape quality graphs were constructed for the NPA network and the rarity network. Social and economic criteria were addressed in the conservation plan by finding all MSTs of the landscape quality graphs. All of the MSTs were the same with respect to connectivity, but they differed with respect to human population size and land area. For both the NPA and the rarity network, the MST with the minimum human population and land area was identified.

**Results:** The existing protected areas occupied 7 % of the TVB. Aside from the existing NPAs, ResNet had to select 2085 km<sup>2</sup> of additional land in order to satisfy the target for the 99 mammal species. The rarity network required less land to meet the target (only 6 % of the TVB). Both networks were no more than 0.04 % larger than the optimal network found using CPLEX 9.1. The MSTs identified by LQGraph established connectivity among the conservation areas using 1 % of the TVB for the NPA network (Figure 16.2a) and 0.2 % of the TVB for the rarity network (Figure 16.2b).

**Significance:** When cell selection was initialized with the existing NPAs, 3% more of the TVB was required to satisfy the target for the mammal species than when the cells were selected based solely on species' rarity and

complementarity. This is consistent with the findings of many previous planning exercises, which have documented a lack of spatial economy in existing protected areas throughout the world (Margules and Sarkar 2007). The connectivity areas selected using LQGraph are intended to facilitate dispersal among conservation areas for species with a metapopulation structure or to provide escape routes if a conservation area is destroyed. Whether species will actually use such connectivity areas is an open question (Williams *et al.* 2005). However, for nine of the ten species for which dispersal data were available, the maximum known dispersal distance was at least as large as the median length of the connectivity areas selected by LQGraph.

1

2 **[FIGURE 16.2 HERE.]**

3

1 **Box 3. Multi-Criteria Methods in MultCSync** (Moffett *et al.* 2005).

There are three methods of multi-criteria analysis implemented at present in the downloadable version of MultCSync:

**Non-Dominated Set (NDS)** (Sarkar and Garson 2004): These are the Pareto-optimal solutions or alternatives (potential conservation actions) that should be computed first in MultCSync. Any solution that is not in the NDS is worse than at least one of the NDS solutions by one criteria and no better by the other criteria. NDS computation only requires ordinal ranking of the solutions by the criteria and does not require the criteria to be independent of each other. Within the NDS there is no ranking of the solutions: each one is “as good” as any other. If the number of criteria is low, the NDS will often be small (that is, have very few alternatives) and no further multi-criteria analysis will be required.

**Analytic Hierarchy Process (AHP)** (Saaty 1980): This is a very popular method of aggregating criteria using a ratio scale (between 0 and 9) to compare alternatives (solutions or conservation plans). However, in spite of its popularity, its theoretical basis is controversial. The AHP also suffers from the problem of rank reversal: the ranks of two alternatives may be reversed when a new alternative is included in the analysis. For the procedure to be valid, the criteria must be difference-independent (Moffett *et al.* 2006).

**Multi-Attribute Value Theory (MAVT)** (Dyer and Sarin 1979): MAVT is multi-attribute utility theory without the complication of uncertainty. The implementation in MultCSync assumes that the value functions are linear which is probably justifiable in most situations in conservation planning. The elicitation procedure used to obtain users’ preferences is the same as for the AHP but a different normalization factor used to compute the final scores for alternatives (solutions or conservation plans) which also prevents rank reversal. For the procedure to be valid, the criteria must be difference-independent (Moffett *et al.* 2006). Because of the use of the AHP elicitation procedure, this version of MAVT is called mAHP within MultCSync. If the NDS is large and a further ranking of solutions is required, this is the recommended method for use in MultCSync (Moffett and Sarkar 2006).

1 **Box 4. Socio-economic Goals in Northern Namibia** (Moffett *et al.* 2006).

**Purpose:** A terminal stage protocol was used to incorporate multiple criteria into the design of conservation area networks for northern Namibia so as to evaluate potential networks on the basis of a set of sociopolitical criteria while simultaneously ensuring adequate representation of all biodiversity surrogates. The analysis was performed in response to requests for input from personnel of the Namibian Ministry of Lands, Resettlement and Rehabilitation (MLRR).

**Study Region:** The study region was northern Namibia, between Etosha National Park and the Angolan border to the north, a region roughly 83 400 km<sup>2</sup> in area. More than one-fourth of the region consisted of Etosha National Park which, at 22 700 km<sup>2</sup>, is one of the largest wildlife reserves in the world. The area north of Etosha is important because there is strong local interest in conservation, mainly because it may lead to ecotourism.

**GIS Model:** The region was divided into 120 different cells of varying shape. Besides the cell that represented Etosha National Park, the cells ranged in area from 0.02 to 1225.89 km<sup>2</sup>, with an average area of 517.95 km<sup>2</sup>. All analyses assumed that the Etosha National Park must remain a conservation area in any feasible plan for the region.

**Biodiversity Surrogates:** The 35 vegetation classes that occur in the study region were used as biodiversity surrogates. The expected value of each surrogate in each of the 120 cells was defined as the fraction of the area in which the surrogate was present.

**Targets and Goals:** ResNet was used to select networks of cells in which the total expectations of each surrogate satisfied a 10 % representation target. The unique networks were treated as alternatives and MCA methods were used to evaluate these alternatives on the basis of six different sociopolitical criteria: (1) area; (2) human population; (3) number of summer cattle; (4) number of winter cattle; (5) farming; and (6) number of wildlife. These criteria were chosen by MLRR personnel, who held that an optimal solution should minimize the values of criteria (1) through (5) while maximizing the value of criterion (6).

**Results:** ResNet was used to select networks of cells in which each biodiversity surrogate satisfied the 10 % representation target. A ResNet input file was created and 100 different input files were produced by randomly reordering the list of cells in the original input file. ResNet was then run 100 times using each of the input files; all runs were initialized with the cell representing Etosha National Park. As ties between cells were broken at random, different input files potentially resulted in the selection of different conservation area networks. Of the 100 networks selected, 94 were unique. These unique networks were treated as alternatives and MCA techniques were used to

evaluate the alternatives on the basis of the six sociopolitical criteria mentioned above.

The use of NDS computation within MultCSync resulted in the identification of 49 of the 94 networks as Pareto-optimal. The 49 Pareto-optimal alternatives were then evaluated using the AHP and MAVT. Pairwise comparisons of the criteria were provided by MLRR personnel and MultCSync was used to assign a weight to each criterion representing its importance. The results of these pairwise comparisons of the criteria are presented in Table 16.2. This table also presents the final criterion weights computed from these comparisons. As indicated in this table, criterion (6) received a weight more than twice as large as any other criterion and more than 9 times as large as the one assigned to criterion (1), the criterion finally assigned the smallest weight. These criterion weights were used to calculate final alternative rankings. Maps of two of the highest ranked alternatives, based on MAVT, are provided in Figure 16.3. As can be seen, there were relatively few differences between the top ranked alternatives. (AHP results were quite different.) A sensitivity analysis was performed to determine the degree to which the results of the analysis were dependent upon the particular weights assigned to the criteria. The sensitivity analysis indicated that the results were largely independent of the particular weights assigned to the criteria. Identical results were obtained using most sets of randomly generated criteria weights.

**Significance:** The protocol used in this analysis allowed for the inclusion of sociopolitical criteria in conservation area network design while assuring the adequate representation of biodiversity. This biodiversity constraint resulted in the selection of a set of similar alternatives, the ranking of which thus proved to be robust to changes in the criteria weights. In addition, the differences between results produced using MAVT and the AHP indicated the importance of selecting a proper MCA method.

1

2 **[TABLE 16.2 HERE.]**

3 **[FIGURE 16.3 HERE.]**

1 **Table 16.1**

2 **The Effect of Target Level and Algorithm Initialization on the Required Size of Conservation Area Networks**

3 **in Northeast India.**

Initialization of cell selection based upon:	Target of representation (%)	Area selected (km <sup>2</sup> )	Percent of the study region	Change from existing protected areas (%)	Intersection between existing protected areas and CAN selected by ResNet (%)
Species' rarity	5	8812	4.02	-1.14	3.82
	10	18 033	8.25	+3.08	7.85
	15	27 465	12.56	+7.39	12.35
	20	37 237	17.03	+11.86	19.96
Existing protected areas	5	12 208	5.58	+0.41	100
	10	19 753	9.03	+3.86	100
	15	28 898	13.22	+8.04	100
	20	38 351	17.54	+12.37	100

1 **Table 16.2**

2 **Calculation of Criteria Weights.** The calculation of weights for each of the six criteria used to evaluate  
 3 conservation area networks in northern Namibia is illustrated in this table. The order of the rows and columns are  
 4 based on: (1) area; (2) human population; (3) number of summer cattle; (4) number of winter cattle; (5) farming;  
 5 and (6) number of wildlife. The values in the matrix were obtained by comparing the importance of each pair of  
 6 criteria on a ratio scale of 1 / 9 to 9. The comparisons were made by MFRR personnel familiar with the ranges over  
 7 which the criteria varied. Entry  $(i, j)$  represents the ratio by which the  $i$ -th criterion is thought to be more important  
 8 than the  $j$ -th criterion. For instance, criterion 1 (area) was evaluated to be one fifth as important as criterion 2 (the  
 9 human population) after considering the range of values of these criteria, and so  $(1, 2) = 1 / 5$ . The adjoining vector  
 10 is the eigenvector with the highest eigenvalue of the matrix. The eigenvector components were normalized so as to  
 11 sum to 1. The weight of the  $i$ -th criterion is then given by the  $i$ -th entry of this eigenvector.

12

13

$$\begin{pmatrix} 1 & 1/5 & 1 & 1/3 & 1/4 & 1/8 \\ 5 & 1 & 1 & 1 & 4 & 1/2 \\ 1 & 1 & 1 & 1 & 1/3 & 1/7 \\ 3 & 1 & 1 & 1 & 1 & 1/3 \\ 4 & 1/4 & 3 & 1 & 1 & 1/2 \\ 8 & 2 & 7 & 3 & 2 & 1 \end{pmatrix} \Rightarrow \begin{pmatrix} 0.047927 \\ 0.196843 \\ 0.080739 \\ 0.134108 \\ 0.143483 \\ 0.396900 \end{pmatrix} \Rightarrow \begin{matrix} \omega_1 = 0.047927 \\ \omega_2 = 0.196843 \\ \omega_3 = 0.080739 \\ \omega_4 = 0.134108 \\ \omega_5 = 0.143483 \\ \omega_6 = 0.396900 \end{matrix}$$

1 **Figure Captions**

2 **Figure 16.1:** Conservation area network evaluation (initialization by rarity) and area prioritization (initialization by  
3 the existing conservation area network) for Northeast India obtained by ResNet analyses. In the left column, the  
4 initial rule for the selection of cells was based on species' rarity and ties in rarity were broken by appeal to  
5 complementarity. In the right column, the selection of cells was initialized with the existing protected areas. In both  
6 columns, cells were selected to represent the potential distributions of the 80 species for which statistically adequate  
7 niche models could be constructed. Panels on the same row are conservation area networks that satisfy the same  
8 target of representation.

9 **Figure 16.2:** Results of the connectivity establishment procedure for the TVB. In (a) the MSTs shown in black  
10 connect the conservation areas selected to augment the TVB's existing protected areas via external cells with  
11 primary or secondary vegetation. In (b) the MSTs link conservation areas selected by ResNet without incorporating  
12 the existing protected areas. The NPA network had 48 MSTs and the rarity network had 32. Of all the MSTs  
13 identified by LQGraph, the MSTs shown here have the minimum human population and land area. The median  
14 length of the connectivity areas in (a) and (b) is 4.24 km.

15 **Figure 16.3:** The maps are of the area in Namibia in which the study was performed. The image inset in map (a)  
16 indicates the position of the study area relative to the rest of Namibia. In each map, the grey cell represents Etosha  
17 National Park. The black cells represent cells chosen for inclusion in a conservation area network, while the white  
18 cells represent cells that were not chosen. The two maps represent different networks. Map (a) represents the  
19 alternative ranked first according to MAVT, while map (b) represents the alternative ranked within the top five that  
20 differed the most from the alternative ranked first. Both alternatives contain 13 cells of which 11 are shared.