

PROTECTED AREA SITE SELECTION BASED ON ABIOTIC DATA: HOW
RELIABLE IS IT?

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RELIABLE IS IT?

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ABSTRACT

PROTECTED AREA SITE SELECTION BASED ON ABIOTIC DATA: HOW RELIABLE IS IT?

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Protected area site selection is generally carried out using biodiversity data as surrogates. However, reliable and complete biodiversity data is rarely available due to limited resources, time and equipment. Instead of drawing on inadequate biodiversity data, an alternative is to use environmental diversity (ED) as a surrogate in conservation planning. However, there are few studies that use environmental diversity for site selection or that evaluates its efficiency; unfortunately, no such example exists for Turkey, where biodiversity is high but our knowledge about it is unsatisfactory.

Hence, this study was carried out to investigate the efficiency of environmental surrogates and the utility of different biological taxa in conservation planning. The objective was to find out the most efficient surrogates, either environmental or biological, for conservation planning, so that limited resources can be used more efficiently to establish an effective protected areas network.

The study was carried out in northeastern Turkey, within the Lesser Caucasus ecoregion. The taxonomic groups considered include large mammals, breeding birds, globally threatened reptiles and amphibians, butterflies, highly threatened plants, and ecological communities. The distribution data was taken from a previous study, while climate and topographical data were obtained from various sources and produced through spatio-statistical techniques. Complementarity-based site selection was carried out with Marxan software, where the planning unit

was the 100 sq.km. UTM grid square. Various statistical methods, including geographically weighted regression, principal components analysis, and p-median algorithm, were used to determine ED across the units. Performance of different approaches and different sets of surrogates were tested by comparing them to a random null model as well as representation success.

Results indicate that endemic or non-endemic highly threatened plant species, butterfly species and ecological communities represent biodiversity better than other taxa in the study area. As such, they can be used on their own as efficient biodiversity surrogates in conservation area planning. Another finding is that highly threatened plant species are required to be used in the site selection process if they need to be represented well; in other words, they are their own surrogates. It was demonstrated that while ED alone can be used as a surrogate to represent biodiversity of an area, they are not as good as biodiversity surrogates themselves.

It is also suggested that using species taxa with smaller distributional ranges or taxa that complement each other due to ecological differences as surrogates provide better results. On the other hand, ED might be a more suitable surrogate if resources are very limited or field work is impossible. In such cases, using ED in conjunction with one of the better biodiversity surrogates is probably the best solution.

Keywords: Biodiversity, environmental diversity, site selection, systematic conservation planning, surrogate taxa, Lesser Caucasus Ecoregion, Turkey

ÖZ

ABİYOTİK VERİLER İLE KORUNAN ALAN SEÇİMİ: NE KADAR GÜVENİLİRDİR?

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Korunan alan seçimi genellikle biyoçeşitlilik verisinin temsilci olarak kullanılmasıyla gerçekleştirilir. Fakat sınırlı kaynak, zaman ve ekipmandan dolayı, güvenilir ve tam bir biyolojik çeşitlilik verisi nadir olarak mevcuttur. Bu durumda bir alternatif olan çevresel çeşitlilik (ÇÇ), temsilci olarak koruma planlamasında kullanılır. Fakat çevresel çeşitliliği alan seçimi için kullanan ve verimliliğini değerlendiren az sayıda çalışma bulunmaktadır. Ne yazık ki, biyoçeşitliliğin yüksek fakat onun hakkındaki bilginin yetersiz olduğu Türkiye için böyle bir çalışmanın örneği bulunmamaktadır.

Bundan dolayı, bu çalışma çevresel temsilcilerin verimliliğini ve farklı biyolojik taksonların koruma planlamasındaki kullanışlılığını araştırmak üzere gerçekleştirilmiştir. Hedef koruma planlaması için daha verimli çevresel yada biyolojik temsilcilerin bulunmasıdır. Böylece kısıtlı kaynaklar etkili korunan alanlar ağı kurabilmek için daha verimli bir şekilde kullanılabilir.

Çalışma Türkiye'nin kuzeydoğusunda Aşağı Kafkaslar ekolojik bölgesinde gerçekleştirilmiştir. Dikkate alınan taksonomik gruplar endemik ve endemik olmayan yüksek derecede tehdit altında olan bitkiler, üreyen kuşlar, kelebekler, büyük memeliler, küresel ölçekte tehdit altında olan sürüngen ve çift yaşamlılar ve yaşam birliklerini kapsamaktadır. İklim ve topografya verileri farklı kaynaklardan toplanıp, mekansal istatistik yöntemleri ile üretilirken, dağılım verileri bir önceki çalışmadan temin edilmiştir. Tamamlayıcılık esasına dayanan alan seçimi 100 km²'lik UTM grid karelerinde Marxan alan seçim yazılımı ile belirlenmiştir. Coğrafi

ağırlıklı regresyon, temel bileşenler analizi ve p- medyan algoritması kullanılarak, çevresel çeşitlilik birimler boyunca belirlenmiştir. Farklı yaklaşımların ve farklı temsilci setlerinin performansı temsiliyet başarısı yanında rastgele null model ile de karşılaştırılarak test edilmiştir.

Sonuçlar çalışma alanında endemik veya endemik olmayan yüksek derecede tehdit altında olan bitki türlerinin, kelebek türlerin ve ekolojik yaşam birliklerinin biyoçeşitliliği diğer taksonlara göre daha iyi temsil ettiğini göstermiştir. Bu sebeple, bu taksonlar korunan alan planlamasında verimli biyoçeşitlilik temsilcileri olarak kullanılabilirler. Diğer bir bulguda yüksek derece tehdit altında olan bitki türlerinin iyi temsil edilmelerine ihtiyaç duyuluyorsa alan seçim sürecinde mutlaka kullanılmaları gerekir. Diğer bir şekilde ifade etmek gerekirse bu taksonlar kendilerinin temsilcisidir. Çevresel çeşitliliğin kendi başına bir alanın biyoçeşitliliğini yansıtması için temsilci olarak kullanılabilmesine rağmen biyoçeşitlilik temsilcileri kadar iyi olmadığı gösterilmiştir.

Dar dağılışı gösteren tür taksonları ya da ekolojik farklılıklarından dolayı birbirinin tamamlayan taksonlar temsilci olarak kullanıldığında daha iyi sonuç verdiği önerilmiştir. Diğer taraftan, kaynakların çok sınırlı, arazi çalışmalarının olanaksız olduğu durumlarda çevresel çeşitlilik temsilci olarak daha uygun olabilir. Bu gibi durumlarda çevresel çeşitliliğin en iyi biyoçeşitlilik temsilcilerinden biri ile birlikte kullanılması muhtemelen en iyi çözüm olacaktır.

Anahtar Kelimeler: Biyoçeşitlilik, çevresel çeşitlilik, alan seçimi, sistematik koruma planlaması, temsilci taksonlar, Aşağı Kafkaslar bölgesi, Türkiye.

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TABLE OF CONTENT

ABSTRACT.....	IV
ÖZ	VI
ACKNOWLEDGEMENTS	VIII
TABLE OF CONTENT	IX
LIST OF TABLES.....	XII
LIST OF FIGURES	XIV

CHAPTER

1. INTRODUCTION	1
1.1 Biological Diversity	1
1.1.1 The Term Biodiversity	1
1.1.2 Definition of Biodiversity.....	2
1.1.3 Extent of Biodiversity on Earth	4
1.1.4 What is the Value of Earth's Biodiversity.....	7
1.1.4.1 Use Value	7
1.1.4.1.1 Direct Use Value	7
1.1.4.1.2 Indirect Use Value	8
1.1.4.2 Non-Use Value	10
1.1.4.2.1 Option Value.....	10
1.1.4.2.2 Existence Value.....	10
1.1.4.2.3 Bequest Value	10
1.1.4.2.4 Intrinsic Value.....	11
1.2 Biodiversity Loss on Earth	12
1.2.1 Extinction	12
1.2.2 Threats on Biodiversity	15
1.2.2.1 Habitat Destruction	16
1.2.2.2 Habitat Fragmentation	17
1.2.2.3 Habitat Degradation and Pollution	18
1.2.2.4 Overexploitation of Biodiversity.....	21
1.2.2.5 Introduction of Exotic Species.....	22
1.3 Conserving Biodiversity	23
1.3.1 Ex-situ Conservation.....	24

1.3.2	In-situ Conservation	25
1.3.2.1	Protected Area Concept of World (from past to present)	26
1.3.2.2	Current Conditions of Protected Areas in TURKEY: Status and Legislations.....	30
1.3.2.3	Deficiencies of Protected Area Systems	34
1.3.3	GIS in Biodiversity Conservation.....	35
1.3.3.1	Gap Analysis and Complementarity Approach.....	36
1.3.3.2	Systematic Conservation Planning.....	38
1.3.3.2.1	Surrogate Concept and Environmental Surrogates in Systematic Conservation Planning	39
1.3.3.2.2	How to Use Environmental Surrogates or Environmental Diversity (ED) in SCP.....	41
1.4	Objective of the Thesis.....	43
2.	MATERIALS AND METHODS	45
2.1	Study Area	45
2.1.1	Geographic Location.....	45
2.1.2	Biodiversity	46
2.2	Data and Working (Mapping) Units.....	47
2.2.1	Biodiversity Data.....	48
2.2.2	Environmental Diversity Data.....	52
2.2.2.1	Topography Data	52
2.2.2.2	Climate Data.....	53
2.2.2.3	Physical Data.....	59
2.3	Analysis.....	62
2.3.1	Biodiversity Analysis	62
2.3.1.1	Identifying Priority Biodiversity Protected Areas using Marxan Software.....	62
2.3.1.2	Detecting Priority Biodiversity Protected Areas for Different Taxa to Test Efficiency of Them as Surrogate	65
2.3.2	Environmental Diversity Analysis	67
2.3.2.1	Correlations and Variance Influence Factors (VIF).....	68
2.3.2.2	Geographically Weighted Regression (GWR)	68
2.3.2.3	Principle Component Analysis (PCA) & Dissimilarity Matrix	70
2.3.2.4	Performing ED model (P median Algorithm) to Detect Environmental Diversity (ED) areas.....	70

2.3.3 Simulated Random Null Model.....	72
2.4 Statistical Analysis and Measurements to Evaluate performance of both Biodiversity and Environmental Diversity Analyses	73
2.4.1 Identifying optimum number of random selections for simulated random null model.....	73
2.4.2 Measuring performance of each taxonomic group and taxonomic group combinations as surrogates.....	74
2.4.3 Comparing Complementarity based priority protected areas, environmental diversity areas and random null model	76
3. RESULTS AND DISCUSSION.....	79
3.1 Biodiversity Analysis.....	79
3.1.1 Priority Protected Areas of the Study Area Detected by Using Marxan Software	79
3.1.2 Efficiency of Each Taxonomic Group as Surrogate	84
3.1.3 Detecting Optimum Number of Random Selection for Null Model	104
3.2 Environmental Diversity Analysis.....	106
3.2.1 Detecting Collinear Environmental Variables	106
3.2.2 Determining Significant Environmental Variables for Each Taxon.....	107
3.2.3 Examining Variation Pattern of Environmental Surrogates and Calculating Dissimilarity matrix of These Surrogates.....	111
3.2.4 Efficacy of P Median Model for Representing Biodiversity of Lesser Caucasus Region.....	115
4. CONCLUSION	125
REFERENCES	128
APPENDICES	
Appendix-A: Species of Lesser Caucasus Region	153
Appendix-B: Meteorology Stations	165
Appendix-C: Protected Areas of Lesser Caucasus Region	168
Appendix-D: Results of Marxan.....	170
Appendix-E: Results of Marxan.....	179
Appendix-F: Correlation Table	188
CIRRICULUM VITAE	189

LIST OF TABLE

Table 1.1 Hierarchical Structure Of Biological Components	4
Table 1.2 Number Of Species Described In 1992 And Number Of Estimated Species For Various Taxonomic Groups. (Sources: Groombridge 1992, Redrawn By Heywood 1995).....	6
Table 1.3 Number Of Recorded Extinctions From 1600 (Source: Grombridge 1992)	14
Table 1.4 Number And % Of Protected Areas According To Years (Unep 2003, 2008)	28
Table 1.5 Iucn Protected Areas Management Categories And Definitions (Iucn; Cnppa And Wcmc 1994; Oecd 1996 Jeffries 1997; Primack 1998)	30
Table 1.6 Protected Area Status Governed By Either National Legislations Or International Conventions (Source; Moeaf/Gdonpanp, Ncc 2003-2005, Mocat)	32
Table 1.7 Twining Of Iucn Protected Area Management Categories With Protected Area Status Of Turkey (Source; Moeaf/Gdonpanp, Iucn 1994, Ncc 2003-2005, Mocat).....	33
Table 2.1 Distributions Of Plant Taxa According To Location, Systematic Classification And Endemism Status.....	46
Table 2.2 Distributions Of Biodiversity Data According To Number Of Records Of Taxonomic Groups.....	50
Table 2.3 Topographic Data Layers.	52
Table 2.4 Climate Data Layers.....	55
Table 2.5 Physical Data Layers.....	59
Table 2.6 All Environmental Variables Used For Analysis	61
Table 2.7 Table Showing Species And Record Distributions Of Each Taxonomic Group Combinations	67
Table 3.1 Table Showing Results Of 20 Solution Sets Of Marxan Software	80
Table 3.2 Table Showing Results Of Jaccard Coefficient For Taxonomic Group Combinations Including Only One Taxon As Surrogate.....	88
Table 3.3 Table Showing Results Of Jaccard Coefficient For Taxonomic Group Combinations Including Two And More Than Two Taxa As Surrogate	92
Table 3.4 Cross Taxon Congruence In Total Species Richness.....	101
Table 3.5 Cross Taxon Congruence In Complementarity	102
Table 3.6 Table Showing Vif's For Each Environmental Variables	106
Table 3.7 Table Showing Vif Values For Remaining Variables.....	107
Table 3.8 Table Demonstrates Significant Environmental Variables For Each Taxon.....	108
Table 3.9 Results Of Environmental Variable Exploration	110
Table 3.10 Table Demonstrates Results Of Pca For First Five Axes	112
Table 3.11 Table Shows Results Of Pca Loadings For First Five Axes	112

Table 3.12 Table Shows Results Of Jaccard Coefficient Between Complementarity Based Site Selection And P Median Model	117
Table 3.13 Table Shows Both Complementarity Scores And Their Percent Values For Complementarity Based Priority Biodiversity Areas, P Median Based Ed Areas And Random Selection	120

LIST OF FIGURE

Figure 1.1 Schematic Representation Of Three Fundamental Biodiversity Levels..	3
Figure 1.2 Estimates Of Described And Likely Totals Of Species For Selected Taxa (Heywood 1995)	5
Figure 1.3 A Total Of 1413000 Species Have Been Identified And Described By Scientists (Data From Wilson 1992).	6
Figure 1.4 Schematic Representation Of Values Of Biodiversity (Barbier 1993) ...	11
Figure 1.5 Birds Recently Extinct On Pacific Islands Relative To The Length Of Human Occupation (From Pimm Et Al. 1995b)	13
Figure 1.6 The Number Of Recorded Global Extinctions Of Animal Species Since 1600 (Smith Et Al. 1993)	14
Figure 1.7 Effects Of Human Population On Biodiversity (Vitousek Et Al. 1997a) .	15
Figure 1.8 Global Extent Of Protected Areas Measured By Number And Extent (Iucn 2008).	28
Figure 2.1 Geographic Position Of Study Area.	46
Figure 2.2 Map Showing Utm-37 Grid Cells And Border Coordinates	48
Figure 2.3 Maps Showing Distributions Of Numbers Of Species For Each Taxonomic Group According To Utm Grids.	51
Figure 2.4 Maps Showing Topographic Features Of The Study Area.	54
Figure 2.5 Maps Showing Different Climate Parameters Of The Study Area.	56
Figure 2.6 Maps Showing Physical Features Of The Study Area	60
Figure 2.7 Schematic Presentation Of All Biodiversity Analyses Together With Related Measurements And Statistics.	77
Figure 2.8 Schematic Presentation Of Environmental Diversity Analysis Together With Related Measurements And Statistics.	78
Figure 3.1 Map Showing Distributions And Locations Of Priority Protected Areas Network	81
Figure 3.2 Graph Showing Percent Representations Of Each Taxonomic Group..	83
Figure 3.3 Map Showing Overlap Between Existing P.A And Detected Priority P.A	84
Figure 3.4 Maps And Graphs Showing Distributions And Percent Representations Of Taxonomic Group Combinations Including One Taxon.	86
Figure 3.4 Maps And Graphs Showing Distributions And Percent Representations Of Taxonomic Group Combinations Including One Taxon.	87
Figure 3.5 Maps And Graphs Showing Distributions And Percent Representations Of Taxonomic Group Combinations Including Two And More Than Two Taxa.	90
Figure 3.5 Maps And Graphs Showing Distributions And Percent Representations Of Taxonomic Group Combinations Including Two And More Than Two Taxa.	91
Figure 3.6 Maps And Graphs Showing Distributions And Cumulative Representation Of Taxonomic Group Combinations Including One Taxon.	94

Figure 3.6 Maps And Graphs Showing Distributions And Cumulative Representation Of Taxonomic Group Combinations Including One Taxon.....	95
Figure 3.7 Maps And Graphs Showing Distributions And Cumulative Representation Of Taxonomic Group Combinations Including More Than One Taxon.....	96
Figure 3.7 Maps And Graphs Showing Distributions And Cumulative Representation Of Taxonomic Group Combinations Including More Than One Taxon.....	97
Figure 3.8 Graph Showing Cumulative Representation Of All Taxa In Combination	99
Figure 3.9 Graph Showing Efficiency Of Each Random Selection.....	105
Figure 3.10 Graph Showing Average Cumulative Representation Of Null Model	105
Figure 3.11 Maps Showing Geographic Distributions Of Pca Axes Scores Of Environmental Surrogates.....	114
Figure 3.12 Map Showing Distributions And Locations Of Environmental Diversity (Ed) Areas.....	115
Figure 3.13 Maps Showing Distributions And Locations Of Both P Median Based Environmental Diversity (Ed) Areas And Complementarity Based Priority Biodiversity Protected Areas	116
Figure 3.14 Graph Showing Percent Representations Of Each Approach.....	118
Figure 3.15 Graph Showing Cumulative Representations Of Each Approach	119
Figure 3.16 Graph Showing Environmental Variation Scores Of Pca-1&2 For Priority Biodiversity Areas, Ed Areas And Random Selection.....	122
Figure 3.16 Graph Showing Environmental Variation Scores Of Pca-1&2 For Priority Biodiversity Areas, Ed Areas And Random Selection.....	122
Figure 4.1 Schematic Presentation Of Conclusion Of The Thesis	127

CHAPTER 1

INTRODUCTION

1.1 Biological Diversity

1.1.1 The Term Biodiversity

The diversity of life on Earth has not been only the central point of natural science and also one of the major interest of human population from past to recent times. Both in ancient and modern societies, scientists try to classify species in order to understand variety and nature of life (Oksanen and Pietarinen 2004). For instance, the Greek philosopher Aristotle tried to figure out relationships and varieties of species by classifying them with modern folk classifications (Jeffries 1997). As, it seems apparent that the richness of life has been already the main concern of human society and science because firstly they want to know with whom they share the planet, and secondly they depend on biological resources for their survival. Although the concern of humanity is not new about the diversity of life, to become the term biodiversity in use and common takes time.

Previously, the term was used as “natural diversity”. This term was introduced by the Nature Conservancy in 1975 with publication of “The Preservation of Natural Diversity”. The original term, biological diversity was first used by Schwarz et al. and States et al. in the late 1970s (1976; 1978). Secondly, a wildlife scientist and conservationist Raymond F. Dasmann was utilized the term in the early-1980s but after their usage, the term “biological diversity” came into common only in science and environmental policy. And use of the term by Lovejoy, Norse and Mcmanus in

1980 with the publication of two papers, “biological diversity” term launched in the field of Conservation Biology and introduced to the Conservation Biology Scientific Community (Jeffries 1997). Afterwards, this term was contracted by W.G. Rosen in 1985 as biodiversity. And this contraction form of the term was first used in the National Forum on Biological Diversity organized by the National Research Council (NRC) which was to be held in Washington, D.C. in September 1986 (Wilson 1988; UNDP 1995; Oksanen and Pietarinen 2004). And then, use of the term “biodiversity” increased very rapidly. The number of scientific publications on biodiversity issue has grown exponentially since late 1980s and currently exceeds 3000 per year (Oksanen and Pietarinen 2004). Subsequently, the term has quickly gained popularity outside from scientific world and today has been widely used by the political world, the media and at least to some extent the general public (Levegue and Mounolou 2004).

1.1.2 Definition of Biodiversity

Many formal definitions of biodiversity have been proposed by scientists (Gaston and Spicer 1998). Delong (1996) reviewed these definitions and determined the number as eighty-five. The most commonly used definition of these refers the biodiversity in broad sense as the richness, variety and variability of living organisms (Groombridge 1992; Heywood and Baste 1995; Pearce and Moran 1995; Savage 1995; Jeffries 1997). This definition can also be abstracted as all life on Earth. Although less inclusive definitions restrict the meaning of biodiversity, this broad definition includes both the number of biological component (richness) and the differences (variety and variability).

There has also a great variation among definitions with respect to the biological components that are included in the biodiversity concept. Generally, early definitions were least inclusive and characterize biodiversity as species richness (Schwarz et al. 1976; Lovejoy 1980). However, species is only the one hierarchical level of biodiversity and then more recent definitions include other levels of biological hierarchy as well (Oksanen and Pietarinen 2004). Of these, the most important one is that contained in the Convention on Biological Diversity (CBD). This convention was signed by more than 150 nations in 1992. As this definition; “Biodiversity means the variability among living organisms from all sources including, inter alia (among other things), terrestrial, marine and other aquatic

ecosystems and the ecological complexes of which they are part; this include diversity within species, between species and of ecosystems ” (CBD, Article 2 1992, Glowka et al. 1994).

As not only the definition included in CBD but also in many other definitions, hierarchical structure of biodiversity has been described at three fundamental levels; genes (within species diversity), species and ecosystems (McNeely, 1990, Angermeier and Karr 1994; Heywood and Baste 1995; Jeffries 1997, Figure 1.1). However, these three levels reveal that they have their own hierarchical levels as well (Heywood and Baste 1995, Table 1.1).

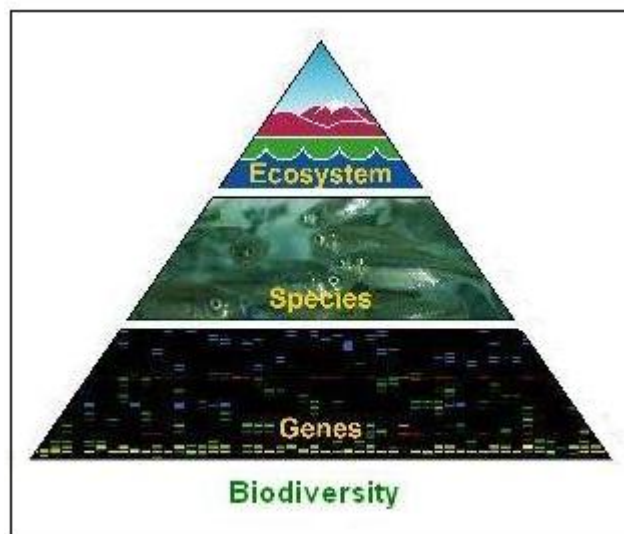


Figure 1.1 Schematic representation of three fundamental biodiversity levels

The levels are nested within each main hierarchy; for instance populations comprise individuals, which comprise genes and so on. Understanding the definition of biodiversity together with its hierarchical levels is important for the implication of biodiversity assessment and conservation because definition of biodiversity concept reveals the structure and relationships among biodiversity components. And this may influence the selection of more applicable and effective conservation strategies for biodiversity (Angermeier and Karr 1994, Prance 1996).

Table 1.1 Hierarchical Structure of Biological Components

Fundamental Levels Of Biodiversity		
Genetic Diversity	Taxonomic (Species) Diversity	Ecosystem Diversity
Populations	Kingdoms	Biosphere
Individuals	Phyla	Biomes
Genome	Classes	Bioregions
Chromosomes	Orders	Landscapes
Genes	Families	Ecosystems
Nucleotides	Genera	Communities
	Species	Habitats
	Subspecies	Niche
	Populations	Populations
	Individuals	

1.1.3 Extent of Biodiversity on Earth

Actually, the extent of biodiversity is hidden in its definitions. As the most widely used definitions of biodiversity indicate that biodiversity is the richness, variety and variability of genes, species and ecosystems. Then, Quantifying the variety and richness of life on Earth is the key point to determine the extent of biodiversity. However, since it doesn't seem possible, the quantitative assessment of biodiversity roughly means as the number of species on Earth (Gaston and Spicer 1998).

There are several methods that have been used to estimate species diversity. But detection of present day diversity of species usually depends on using known species and estimates of likely numbers (Jeffries 1997). And reliability of these estimates varies greatly with number of known taxa. Estimates about how many different species live on Earth are range between 7 and 100 million (Harper and Hawksworth 1996, Table 1.2). These huge shifts between estimates are due to the lack of knowledge for some groups. Certain groups such as birds, mammals and temperate flowering plants are relatively well known and there is only small amount of undefined species for them, however for some groups such as nematodes, insects, spiders, mites and fungi, there are still huge number of species mostly in tropical areas and in the temperate zone that have not been discovered and described yet (Heywood 1995, Figure 1.2).

The number of species that have been identified is around 1.5 million of species in total (Figure 1.3). And 13.000 new species are described and added on this number per year (Gaston 1996c, Pimm, Alves, Chivian and Bernstein 2008). The sources for newly discovered species are mainly situated in the tropics, in coral reefs and in deep sea beds but also found anywhere in the world. There are also some regions in the Earth that are difficult to access and realms of small species like soil fauna, marine and parasites (Gaston 1996a). Because of these challenging parts, the number of new discovered species cannot be increased greatly. Therefore, it is clear that the extent of biodiversity is very far from complete and there is still considerable long time to detect its extent with all aspects (Figure 1.2). However, the quantitative assessment of biodiversity is crucial and is required for human society because of management and conservation purposes and also to evaluate the impact of human on biodiversity systems (Oksanen and Pietarinen 2004).

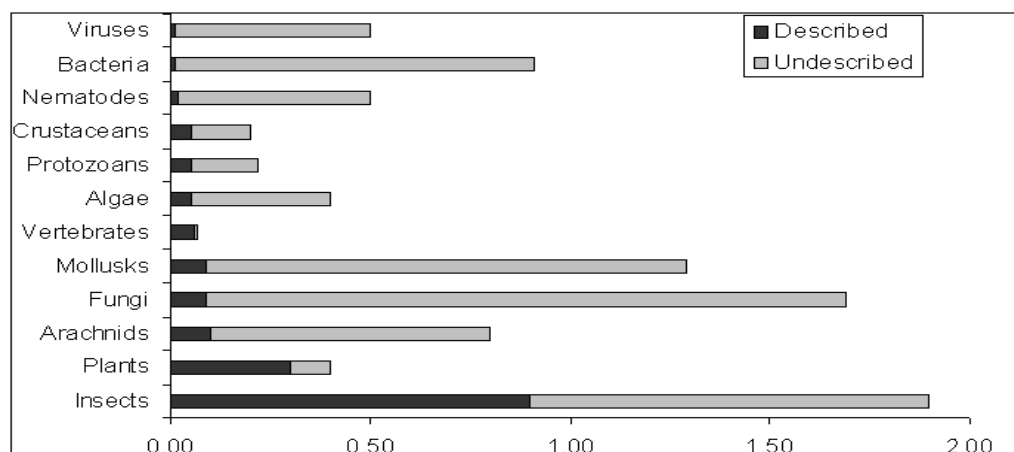


Figure 1.2 Estimates of described and likely totals of species for selected taxa (Heywood 1995)

Table 1.2 Number of Species Described in 1992 and number of estimated species for various taxonomic groups. (Sources: Groombridge 1992, redrawn by Heywood 1995).

Taxon	Number of Species Described in 1992	Number of Species Total (estimate)
Coleoptera	550,000.00	3,500,000.00
Lepidoptera	120,000.00	510,000.00
Hymenoptera	100,000.00	250,000.00
Diptera	90,000.00	165,000.00
Other Insects	120,000.00	600,000.00
Arachnids	75,000.00	900,000.00
Crustaceans	50,000.00	110,000.00
Other Arthropods	30,000.00	75,000.00
Other Invertebrates	80,000.00	230,000.00
Molluscs	30,000.00	240,000.00
Nematodes	20,000.00	500,000.00
Vertebrates	50,000.00	80,000.00
Plants	250,000.00	500,000.00
Algae	50,000.00	250,000.00
Fungi	75,000.00	1,100,000.00
Protozoans	50,000.00	250,000.00
Bacteria	5,000.00	400,000.00
Viruses	5,000.00	50,000.00
Totals:	1,750,000.00	9,710,000.00

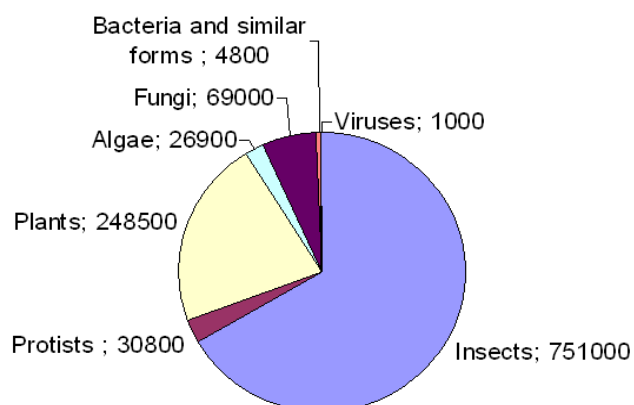


Figure 1.3 A total of 1413000 species have been identified and described by scientists (Data from Wilson 1992).

1.1.4 What is the Value of Earth's Biodiversity

Earth's biodiversity at all level provide conditions and drive processes that sustain the planet and that means our health, livelihoods and survival as a species.

All benefits and services provided by biodiversity for human being are assessed as their value. Since evaluating and assigning value for biodiversity is too difficult; there have been a variety of proposed approaches. Although, none of them have been accepted as universally, one recommended by McNeely (1988), McNeely et al. (1990), and Barrier et al. (1994) is thought as the most useful approach and as this approach; value of biodiversity can be classified into two broad groups: **use values** and **non-use values**. Use values are **direct use value** (consumptive use and productive use values) that are used for products consumed by people and **indirect use value** that are used for benefits and services provided by biodiversity and includes water quality, pollution control, ecosystem productivity, soil protection, recreation, education, scientific research and regulation of climate. **Non-use values** include **existence value**, **option value**, **bequest value** and **intrinsic value** (Figure 1.4, Schematic representation).

1.1.4.1 Use Value

Biological communities provide great variety of resources for human being and people consume these directly or indirectly both in local and global scale. These sources that can be consumed by human population are classified as use value and divided as direct and indirect use values.

1.1.4.1.1 Direct Use Value

It deals with consuming and harvesting products by people and determined by calculating the import and export statistics. And it can be divided as **consumptive** and **productive use value** (Perrings 1995).

Consumptive use value; Some goods like game and fuel wood are consumed only locally. And do not appear in the national and international market place.

Productive use value: These are products that are harvested and obtained from wild and sold both in the national and international market place (Primack 1998).

1.1.4.1.2 Indirect Use Value

Biodiversity provides a great variety of services. Although these do not have any consumptive value for human, they can provide many benefits in terms of health and survival. These include;

Maintenance of Water and Soil quality: Biological diversity is crucial to protect water and soil quality. Plants can slow down rain and reduce its impact on soil. Plant roots and soil organisms increase water holding capacity and can help absorption of water by soil. This prevent flood after heavy rain (Pimental, Wilson and McCullum 1997).

Erosion and flood can make water undrinkable. But biological communities keep away harmful substances from water. This provides protection for human and water organisms (Pimental et al. 1995).

Climate Regulation: Plant communities are vital to organize climate in local, regional and global scale. They regulate oxygen and carbon dioxide cycle and recycle water between earth and atmosphere. By managing these required cycles in both terrestrial and aquatic environments, plants contribute health and survival of not only humans, but also all other living things (Nobre et al. 1991, Clark 1992).

Pest Control: Around 99 per cent of potential crop pests are controlled by a variety of other organisms, including insects, birds and fungi. These natural pesticides are in many ways superior to their artificial equivalents, since pests can often develop resistance to chemical controls (UNDP).

Waste Treatment and Nutrient Retention: Billion tons of toxic materials and organic waste from farms, human settlements and industries released into environments, especially aquatic environments. Earth's decomposer organisms are capable of breaking down organic materials and biological communities have abilities to immobilize toxic materials (Odum 1997). But if people damage and degrade ecosystems, services mentioned above collapse and to handle pollution, expensive

waste control plans must be operated to assume these ecosystem services (Costanza et al. 1997).

Pollination and crop production: Many flowering plants rely on various animal species such as bees, butterflies, bats, birds to reproduce through the transportation of pollen. More than one-third of people's food crops depend on this process of natural pollination. Moreover, many fruit-eating animal species have evolved to serve seed dispersion of several useful wild plant species (Pimental 1997). Degradation of these relationships among species may have detrimental effect on all other biodiversity features.

Recreation and Ecotourism: While some recreational activities such as bird-watching, hiking and photography provide non-consumptive enjoyment through nature, some have monetary values like commercial hunting, fur trapping, zoos and animal parks and involve consumption of nature (Duffus and Dearden 1990). These serve both as recreational activities and as economic profit activities. And many countries have income from such kind of consumptive recreation activities. For example; In the United States, almost 100 million people engage in some form of nondestructive nature recreation each year, spending \$4 billion on fees, travel, lodging, food and equipment (Costanza et al. 1997).

Moreover, ecotourism is another nature related industry and continue to grow dramatically. It is new profession for people and has a potential to provide protection of biodiversity, particularly when it is integrated into management plans (Whelan 1991; Wells and Brandon 1992, 1993; Southgate and Clark 1993).

Educational and Scientific Value: Educational and scientific value of biodiversity is enormous. Several books, movies and programs are produced for education purposes. Also, many professional scientists and amateurs deal with ecological observations and studies. These increase human knowledge, enhance education and enrich the human experience (Hair and Pomerantz 1987).

1.1.4.2 Non-Use Value

It is related with biodiversity resources that are not directly or indirectly exploited by people. They don't have any market price. Nevertheless, they are assigned with a value due to their religious, philosophical, moral, cultural or even economic importance. Essentially, these values are the amounts that are willing to pay to conserve, willing to accept for not exploiting or willing to forgo to keep biodiversity. These non-use values include option value, existence value, bequest value and intrinsic value.

1.1.4.2.1 Option Value

Species have potentials to provide benefits for human being in future. It is especially crucial for healthy agencies and pharmacy industries since many unknown and untapped species can be solution for human diseases. Also species may be genetic resource and food supply for future generations (Weisbrod 1964, Morowitz 1991). And if these species are lost irretrievably, consequences can be very serious for people.

1.1.4.2.2 Existence Value

Almost all of the biodiversity values are expressed for well being of humans. However, biodiversity have its own value as human population have. And this value means that all plant and animal species have right to exist in their healthy and natural environment. Many people recognize this and care about wildlife and plants and concerned with their protection (Wilson 1984). These attempts of interest groups and volunteer people ensure continuum of unique species, communities and landscapes.

1.1.4.2.3 Bequest Value

It is closely related, but distinct from the option value. Bequest value is the value of biodiversity that should be passing intact or as near as possible to future

generations (Krutilla 1987). This means that our future generations have right at least as us to provide benefits from all biodiversity features. This notion is embodied in the final section of Convention on Biological Diversity (1992) as conserving and sustainably uses biological diversity for the benefit of present and future generations.

1.1.4.2.4 Intrinsic Value

All of the biodiversity features have value in its own right and they should not simply be viewed as usefulness for human. People have responsibility towards all living things and obligations for future generations. These provide a strong basis for conserving biodiversity as Convention on Biological Diversity express (Ehrlich and Wilson 1991).

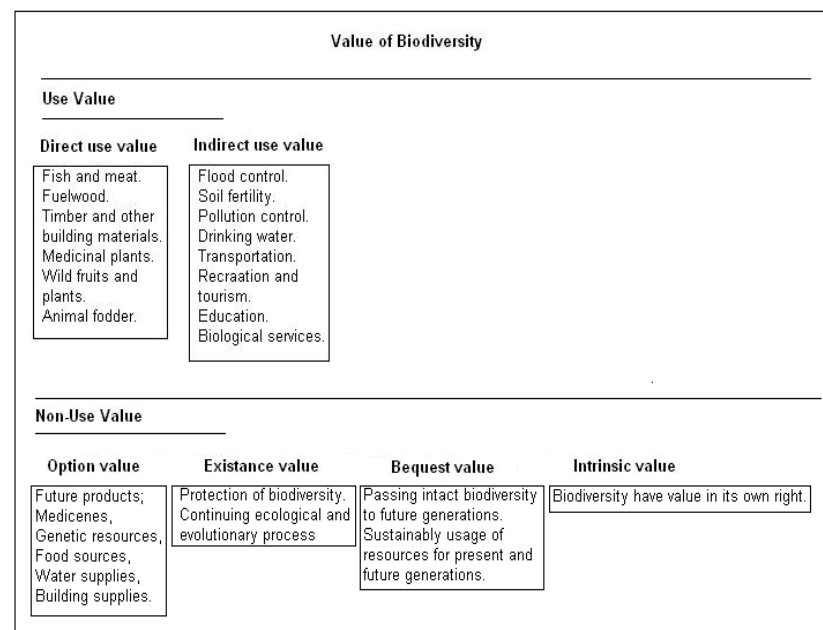


Figure 1.4 Schematic representation of values of biodiversity (Barbier 1993)

1.2 Biodiversity Loss on Earth

Although, humankind is an essential part of life on Earth, they have had negative and irreversible impact on biodiversity. Actually over all geological time, the trend has been towards an increase in biodiversity. However, after late quaternary period, there has been an explicit loss in biodiversity due to the direct and indirect consequences of human activities (Gaston and Spicer 1998). This decrease not only includes reducing biodiversity but also simplifying biological heterogeneity from genes to ecosystems.

Biodiversity loss may be assessed in two major phase. These are extinction and threats on biodiversity including habitat destruction, fragmentation, overexploitation, pollution and introduced species

1.2.1 Extinction

The most widely discussed impact of human activities on biodiversity is species extinction. Although extinction is a natural process and has been occurring since life first originated in the Earth and the diversity of life has been characterized by speciation and extinctions, current rate of species extinction attract too much attention than any time in the past because of its extraordinary rate (Sepkoski and Raup 1986; Wilson 1987; Raup 1992).

Actually, impact of human population on biodiversity have lasted for a long time, probably for almost 100,000- 200,000 years since modern human have existed. However, unusual species extinction coincided explicitly with human arrival in Australia (30,000-50,000 years ago), North and South America (11,000-12,000 years ago), Madagascar (1400 years ago) and New Zealand (1000 years ago). After these arrivals, much of the megafauna disappeared due to either hunting or disrupting ecosystems (Martin 1984, 2001; MacPhee 1999; Miller et al. 1999; Flannery 2001; R. G. Roberts et al. 2001; Grayson 2001; Brook and Bowman 2002).

Generally, effects of early human activities on biodiversity have emerged on continents and islands. And can be best demonstrated by the large number of avian extinctions. These extinctions were result from colonization of tropical pacific

islands between 30,000 years BP and 1000 years BP. The combined effects of colonization were exploitation, deforestation and introduction of alien species led to the almost half of the native bird species driven to extinction. Estimates of total bird species losses from Pacific islands are at least 2000 species, 20% of all known bird species (Milberg and Tyrberg 1993; Pimm et al. 1995b; Steadman 1995; Figure 1.5).

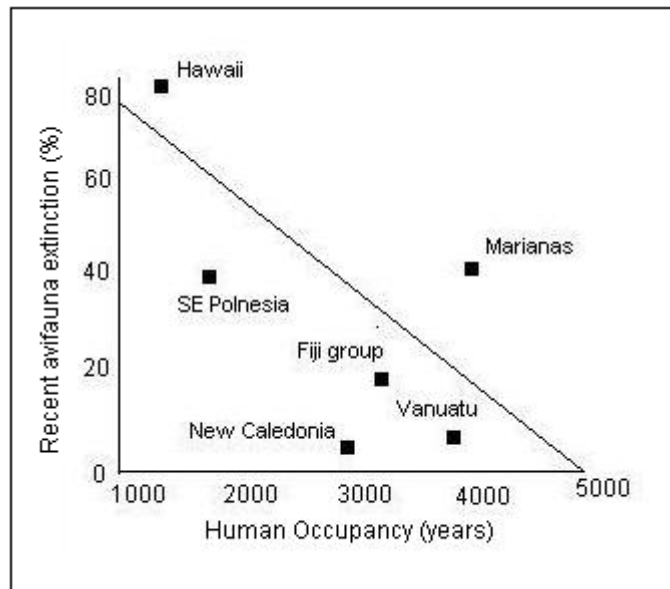


Figure 1.5 Birds recently extinct on Pacific islands relative to the length of human occupation (from Pimm et al. 1995b)

Extinctions have been recorded since 1600 and there have been approximately 1000 recorded extinctions for certain groups from that time. These records indicate, for example, that about 85 species of mammals and 113 species of birds have become extinct since the year 1600, representing 2.1% of known mammals and 1.3% of known birds (Table 1.3). Almost half of these extinctions took place in the last century (Reid and Miller 1991) and there has been also a significant rise in the rate of extinction for known groups of animals for the past 400 years (Figure 1.7). While these numbers may not seem dramatic initially, the trend of these extinction rates is on the rise, with the majority of extinctions occurring in the last 150 years. The extinction rate for birds and mammals was about one species every decade during the period from 1600 to 1700, but it rose to one species every year during the period from 1850 to 1950, and four species per year between 1986 and 1990 (Smith et al. 1993, Heywood 1995).

Although, all of these give an idea about species extinctions, they can not exactly reflect the reality since there are still many groups of undefined living species and species assumed extinct. However, as these indicate; the inevitable fact is that there is an accelerating increase in the rate of species extinction and it is a serious threat for both present and future human generations.

Table 1.3 Number of recorded extinctions from 1600 (source: Grombridge 1992)

Recorded extinction						
Taxon	Mainland	Island	Ocean	Total	Approximate number of Species	% of taxon extinct
Mammal	30	51	4	85	4000	2,1
Bird	21	92	0	113	9000	1,3
Reptile	1	20	0	21	6300	0,3
Amphibians	2	0	0	2	4200	0,05
Fishes	22	1	0	23	19100	0,1
Invertebrates	49	48	1	98	1000000+	0,01
Plants	245	139	0	384	250000	0,2

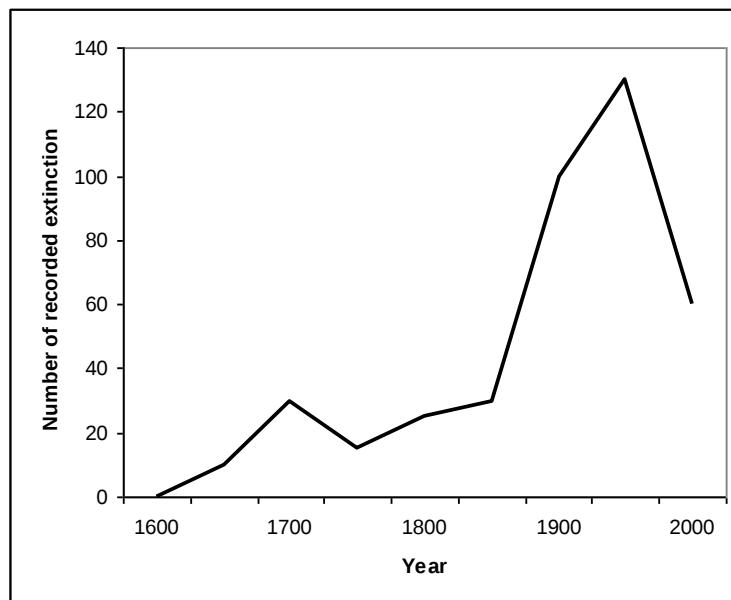


Figure 1.6 The number of recorded global extinctions of animal species since 1600 (Smith et al. 1993)

1.2.2 Threats on Biodiversity

Human population growth and their corresponding demand for natural resources are disrupted ecosystems of the Earth and lead to the overexploitation of resources. On the other hand, activities of this huge human population such as the rise of industrial development, agriculture, commercial activities and residential purposes are degraded and destructed the natural terrestrial and aquatic environments. Moreover, human activities are transformed biogeochemical cycles that results in climate change (Meyer and Turner 1994). Major threats of biodiversity can be examined as five titles including habitat destruction, fragmentation, degradation and pollution, climate change, overexploitation and introduction of species. And it is obvious that all these threats on biodiversity lead to the irreversible loss of components of biodiversity from genes to ecosystems (Mayer 1996, Figure 1.6).

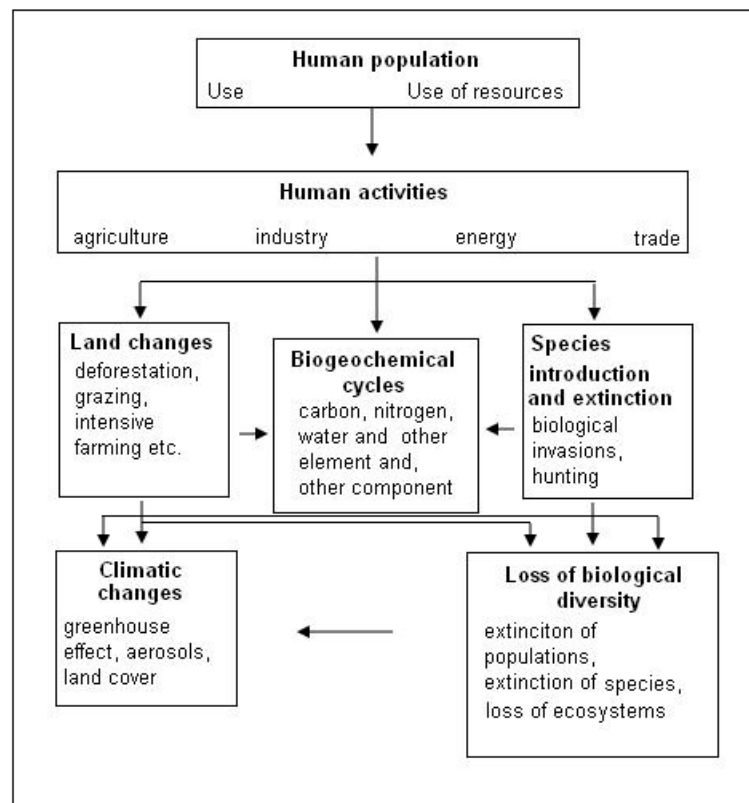


Figure 1.7 Effects of human population on biodiversity (Vitousek et al. 1997a)

1.2.2.1 Habitat Destruction

Habitat destruction is a process in which natural habitat is altered and become unable to support species survival.

Habitat destructions are result from expansion of human population and human activity. Major activities caused by habitat destructions are clearing habitats for agriculture and harvesting natural resources for industrial production and urbanization. Other important factors of destruction of habitats include mining, logging, trawling and urban sprawl (Arbault and Sastrapradja 1995).

The primary consequence of habitat destruction is decline in natural habitats of species. These results in reducing population size and facing species with extinction more likely since there is a systematic relationship between area of habitat and number of species. This means, how much habitat is lost, so much species have been driven to extinction. As many scientists; habitat loss is the greatest threat to organisms and biodiversity (Burke et al. 2000). For example, habitat destruction threatens over 86% of world's birds to goes extinction. Restricted range species that occupy limited areas are also most affected organisms by habitat destruction mainly because these organisms are not found anywhere else within the world and thus, have less chance of recovering (Temple 1986). Moreover, endemic species are among the most affected species from habitat destruction since endemic species obtain very specific requirement for their survival that can only be found certain ecosystems so deficiency of these result in extinction.

Earth's most destructed habitats are rain forests, tropical dry forest, grasslands, wetlands, aquatic habitats, mangroves and coral reefs. These are not only the most destructive habitats but also the habitats including the most diverse fauna and flora of the earth. Therefore, this is one of the reasons why recent rate of species extinction is higher than at any time in the past.

1.2.2.2 Habitat Fragmentation

Habitat fragmentation, as its names implies, describes the discontinuity of a habitat. When a large, continuous area of habitat is fragmented, it is reduced and divided into two or more pieces by roads, fields, towns and a broad range of any other human activities (Wilcove et al. 1986; Schonewald-Cox and Buecher 1992; Reed et al. 1996).

Habitat fragmentation can results in discrete phenomena. Common point of these phenomena is the probability of driving species to extinction. Habitat fragments differ from the original habitats in three ways: (1) reduction of the original habitat, (2) greater amount of the edge habitat for a given area and (3) reduced distance to nearest edge. And some problems may occur because of them.

First, fragmentation can restrict the dispersal and colonization ability of species. Habitat fragments create barriers to normal dispersal and colonization process. In an undivided habitat, seeds, spores and animals can move easily across the area, however when a habitat is fragmented the potential dispersal and colonization is reduced. Many birds, mammals and insects cannot pass very short distances of an open area (Bierregaard et al. 1992; Laurance and Bierregaard 1997). And species may go extinct within individual fragments due to natural succession and metapopulation processes are being unable to achieved, new species cannot be arrived because of barriers to colonization and the number of species present in the habitat fragment decline over time (Santos and Telleria 1994).

Second, fragmented habitats reduce the foraging ability of animals. Many animals need to move across large, undisturbed habitats to feed on widely scattered resources. But in fragmented habitats, animals confined to a small and divided habitat patches may not able to migrate for finding food. Also, barriers can restrict the mate finding capacity of species leading to loss of reproduction potential of many animal species (Laurance and Bierregaard 1997).

Third, habitat fragmentation may cause decline in population size by dividing an existing large population two or more subpopulations. These small subpopulations then become more vulnerable to inbreeding depression, genetic drift and any other problems related with small population size (Primack 1998).

Additionally, habitat fragmentation leads to edge effect that is the change in microenvironments of fragment edges. The most of important edge effect include microclimatic changes in light, temperature, wind, humidity and incidence of fire (Schelhas and Greenberg 1996; Laurance and Bierregaard 1997). Each of these cause significant effect about the vitality and composition of species present in fragments because species of plants and animals often cannot adopt the temperature, humidity and light level changes, and this results in elimination of species from fragments. Moreover, wind changes can have a significant effect in fragmented habitats. When a habitat is fragmented, wind can easily enter the habitat and move through the habitat. This raised wind and air turbulence damage the vegetation (Laurance 1991b, 1994). Also, increased wind means to increased drying of soil, lower air humidity and higher water loss from leaves. This water deficiency may create water stress in plants and leads to the kill of many plant species (Essen 1994). Furthermore, these increased wind, low humidity and higher temperature make more susceptible to habitat fragments. And it is a serious threat both for plant and animal species (Leigton and Wiravan 1986).

1.2.2.3 Habitat Degradation and Pollution

Habitat degradation is aspect of habitat destruction caused by humans that do not necessarily involve overt destruction of habitat, but result in habitat collapse (Geist and Lambin 2002). As a result of degradation, biological communities can be damaged and species driven to extinction. For example, keeping too many cattle in a grassland community can alter the species composition of that community and result in eliminating some native plant species. Also, too much boating and diving around coral reefs can destroy some sensitive coral species (Primack 1998).

Moreover, pollution is another degradation type and actually, it is the most irreversible one. It is generally caused by pesticides, industrial chemicals and waste, emissions from factories and automobiles. All of these pollutants corrupt air, soil and water quality and even cause global climate change. These are not only threatening for biodiversity but also harmful for human health.

Soil Pollution: It occurs when pollutants are released into soil. Among the most significant soil contaminants are hydrocarbons, heavy metals, herbicides, pesticides and chlorinated hydrocarbons. These chemicals can persist long term in

the soil leading to infertility and also unsuitability for survival of both plants and animals. Furthermore, these affect other organisms moving through food webs.

Water Pollution: Water pollution is the contamination of water bodies such as lakes, rivers, oceans and groundwater. Waste products and other pollutants are mixed into these water systems either by means of surface runoff or by using these systems as open sewers. All water pollution affects organisms and plants that live in these water bodies and in almost all cases the effect is damaging either to individual species and populations but also to the natural biological communities. Moreover, water pollution has serious consequences on human population because it destroys food sources and contaminates drinking water. These may cause long term harm on human health.

Air Pollution: Air pollution is the introduction of chemicals, particulate matter or biological materials that cause harm or discomfort to humans or other living organisms, or damages the natural environment. Atmosphere is a complex, dynamic natural gaseous system that is essential to support life on Earth. And its depletion due to air pollution has long been recognized as a threat to human health as well as to the Earth's ecosystems. Pollutants that lead to the air pollution can be in the form of solid particles, liquid droplets, or gases. In addition, they may be natural or man-made. Industry is the main contributor to air pollution (WRI 1994; 2008). Many times factories release greenhouse gases like carbon dioxide, chlorofluorocarbons (CFCs), methane, and nitrous oxide into the atmosphere. Greenhouse gases contribute to a phenomenon called the greenhouse effect or more simply put, global warming. There also other harmful gases are released when fossil fuels are burned. These gases have significant negative health and environmental effects. These are Carbon Dioxide, Carbon Monoxide, Sulfur Oxide, Nitrogen Oxide, Hydrocarbons (Benzene, Terpene, etc.) and Particulates (Kaufman and Franz 2000).

Environmental impacts of greenhouse gas pollutants: Greenhouse gases are gases in an atmosphere that absorb and emit radiation. This process is the fundamental cause of the greenhouse effect. The greenhouse effect is the heating of the surface due to the presence of an atmosphere containing greenhouse gases (Karl and Trenberth 2003). Main greenhouse gases found in the Earth's atmosphere are water vapor, carbon dioxide, methane, nitrous oxide and ozone. Without these gases, Earth's surface temperature would fall dramatically on

average about 33°C (59°F) colder than at present (Claussen, Cochran and Davis 2001). However, today, concentrations of these gases are increasing so much as a result of human activity. This creates an episode that is called as global warming. It is the increase in the average temperature of the Earth and oceans since the mid-20th century (Hansen 2005). As IPCC (Intergovernmental Panel on Climate Change) declared, most of the observed temperature increase results mainly from burning fossil fuels and deforestation. Also, variation in natural phenomena such as solar radiation and volcanoes contribute increase in Earth's temperature (Gates 1993, IPCC 1996).

Many scientists believe that the increasing concentrations of green house gases have already affected the earth's climate. The best evidence for this is the warming of the earth's climate between 0.3 °C and 0.6 °C during the last century. And this warming will continue to increase in future. Even predicting future weather pattern is a complex and difficult task, estimates made by meteorologist about warming earth's temperature is range between about 1°C and 3.5°C over the next century (Myneni et al. 1997; IPCC 2001) Beside of an increase in global temperature, global warming also results in rising sea level, change the amount and pattern of precipitation, and continues to retreat of glaciers, permafrost and sea ice with strong warming in the Arctic. Other likely effects include increases in the intensity of extreme weather events, species extinctions and changes in agricultural yields (Karl et al. 1997; Lu, Vecchi and Reichler 2007).

Although, global warming is not a new phenomena with at least 10 cycles of global warming and cooling histories during the past 2 million years, today's human induced global warming quite different from past's natural climate shifts. Recent global warming occurs more rapidly than any time in past. And as far as investigations about global climate change indicate, it is more likely that many species will be unable to adjust quickly enough this global climate changes to survive. Then the consequence of climate change from individual species to ecosystems is profoundly negative that means driving species to the point of extinction (Richard B. primack 1998).

1.2.2.4 Overexploitation of Biodiversity

Exploitation of biological resources is essential for continuum of existence of human population. This primarily refers to the harvesting and hunting for food and other resource that are needed for humans' survival. When human populations were small, methods used to meet their requirements were not sophisticated. Therefore, people could sustainably hunt and harvest plants and animals found in their around environment. However, as human population have began growing rapidly, their exploitation of natural resources became incredible levels by means of developing more sophisticated hunting and harvesting techniques (Redford 1992; Fitzgibbon et al. 1995).

With the development of these methods, guns are began to use instead of arrows or spears for hunting and powerful motorized boats harvest fish from the world's oceans. All of these developments allow to harvest through the wider areas more rapidly that means overexploitation of biological resources (Fitzgerald 1989).

Overexploitation has been currently threatened world's one third of the endangered, vulnerable and rare species (WCMC 1992). Legal and illegal trade in wildlife is among the most harmful exploitation leading to the decline in many wild life species (Poten 1991). One of the most pervasive legal trades is for fur. Species such as chinchilla, vicuna, giant otter and numerous cat species are hunted for their fur and have been reduced to low numbers. Overharvesting of butterflies, orchids, cacti and other plants, tropical fish are further examples that are targeted to trade in international market (Jones 1990).

Many of the species that have been overexploited in long time have been reduced to low numbers. If these species have not been harvested any more, perhaps their populations can have a chance to recover. However, unfortunately populations of many species such as rhinoceros and certain wild cat already have been reduced too severe number so they may not able to recover their population. Therefore, finding solutions to protect and manage the remaining individuals of such species should be the major goal of conservation efforts (Kendrick 1995).

1.2.2.5 Introduction of Exotic Species

An introduced species is a species that is not live in their native range. Geographic range of species is determined by geographic isolation and patterns of evolution. However, Humans have altered this pattern moving species throughout the world. In preindustrial time, generally cultivated plants and domestic animals were carried place to place in order to provide food for new colonies. And in modern time, many species have been introduced either deliberately or accidentally into their non-native areas (Drake et al. 1989; Vitousek et al. 1996).

Deliberate Species Introduction: the most common reason for introducing a species into a new place is the economic gain. For example in Alaska, foxes were introduced to many islands to create new populations for the fur trade (Naylor, Williams and Strong 2001). Introductions have also been important in supporting recreation activities or otherwise increasing human enjoyment. Numerous fish and game animals have been introduced for the purposes of sport fishing and hunting (Riley et al. 2003). Also, many plants have been introduced to improve public recreation areas or private properties. Intentional introductions have also been used with the aim of regulating environmental problems. For instance, some introduced species can be used to cope with their natural enemies so that to reduce and control their numbers (Moritz 1999). A special case of introduction is the reintroduction of a species that has become locally endangered or extinct, done in the interests of conservation. Examples of successful reintroductions include wolves to Yellowstone National Park in the U.S.

Accidental Species Introduction: Unintentional introductions occur when species are transported by human. Over 200 species have been introduced to the San Francisco Bay in this manner making it the most heavily invaded estuary in the world (Cohen and Carlton 1998). Increasing rates of human travel are providing accelerating opportunities for species to be accidentally transported into areas in which they are not considered native.

Although, Introduced species have some benefits to meet requirement of rapidly growing human population, these species can damage the ecosystem, in which they introduce, negatively affect the agriculture and other human use resources, or impact health of plant and animal species (Foster and Sandberg 2004). Even, the great majority of introduced species can not establish in their new area due to

unsuitability of the area for their needs, a small percent of introduced species can establish in their new home and become abundant. Then, these species may display with native species by competing for scarce amount of food. And ultimately, they may kill and eat native species to the point of extinction or may alter the habitats in which native species are not able to persist (Hedgepeth 1993).

1.3 Conserving Biodiversity

Biodiversity loss that is because of extinctions and threats on biodiversity is the current and growing problem all over the world. And it may have very serious consequences for human being because biodiversity is fundamental to all life on Earth. People depend on biodiversity for their many basic requirements such as food, air, water, medicine and raw materials. Also biological diversity provides many services that support life. For instance; wetlands filter pollutants from water, trees and plants reduce global warming by absorbing green house gases and bacteria and fungi break down organic materials and fertilize soil (De Groot 1992; BSC 2004; Sharman 2005).

On the other hand, biodiversity can provide opportunities to make economic profit by means of recreation and tourism. Furthermore, it is a field for research and education and these brings knowledge and insight for human.

Briefly, it is clear that biodiversity is the cornerstone of human' existence and there is a strong relation between biodiversity and sustainable future of people. Then, it is reasonable to protect it because the cost of not conserving biodiversity will be substantial for present and future generations. For example, decline in soil structure, decreased water quality, pest and weed invasion have increasing impacts on agriculture through loss in productivity and increased costs.

Conservation of biodiversity can be best achieved by understanding the issues that lead to the biodiversity loss and finding appropriate solutions to reduce their impacts. There have been two main approaches for biodiversity conservation that are to protect biodiversity either outside from their original habitat, **ex-situ conservation** or within their original habitat, **in-situ conservation**.

1.3.1 Ex-situ Conservation

Ex-situ conservation means "off-site conservation ". It is the process of protecting an endangered species of plant or animal by removing part of the population from native habitat and placing it in a new location (Soulé 1986, Conant 1988).

Ex-situ conservation can be applied when species decline and go extinct in the wild for any reasons that have been already discussed; habitat fragmentation, destruction, introduction of exotic species, spread of disease, excessive hunting and collecting. In such circumstances, remnant populations may become too small to maintain the species in the wild so the best approach is to protect them in artificial conditions which may be a wild area or within the care of humans (Griffith et al. 1989; Reading and Kellert 1993; Minkley 1995). There have been a number of species that are extinct in the wild survive in captivity such as the Pere David's deer (*Ela-phurus davidianus*) and Przewalski's horse (*Equus caballus przewalski*) (Falk and Olwell 1992).

Ex-situ facilities for animal preservation include zoos, game farms, aquaria and private breeders, while plants are maintained in botanical gardens, arboreta and seed banks. All these make the ex-situ conservation very expensive. For instance, the cost of maintaining African elephants and black rhinos is 50 times greater than protecting the same number of individuals in East African national parks (Leader-Williams 1990, Jeffries 1997). Nevertheless, it is an important part of the integrated conservation strategy that is the combination of both ex-situ and in-situ conservation. Ex-situ and in-situ conservation should not be thought as alternative of each other. These are complementary strategies so ex-situ conservation should be linked with in-situ conservation in order to increase individuals of remaining populations or establish new ones (Primack 1996; Falk et al. 1996).

Although, ex-situ conservation is an efficient way to protect endangered species, it cannot be applied for some taxa that are impossible to maintain in captivity such as large whales (Jeffries 1997). This is not only problem of ex-situ conservation, but also it has other certain limitations in comparison with in-situ conservation. One of the major problems for ex-situ conservation is small population size. In captivity the size of populations must be kept in finite number and this result in small population problems like genetic drift, inbreeding depression and population bottleneck. Also, Ex-situ populations can alter some of their genetic adaptation in artificial

conditions. For example, animal species kept in captivity for several generations may exhibit changes in their digestive enzymes due to the diet and when these animals are returned to the wild, they may have difficulty eating their natural diet. Another limitation is scarce genetic variability. Captive populations may represent only a small portion of genetic variation of species (Kleiman 1989; Waples and Tell 1990; Gipps 1991; Bowles and Whelan 1994; Kleiman et al. 1996; Phartyal et al. 2002). For instance, a captive population in which individuals are collected from warm lowland may be unable to adapt to the colder highland area that is formerly occupied by species (Olney et al. 1994; CIAT 2007). Lastly, individuals in ex-situ conservation may lose their learning skills which they need to survive in the wild. Generally captive animal cannot recognize edible foods and water resources around them when they are released into the wild. This is especially seen among social mammals and birds because their juveniles learn their survival skills and locations of critical resources from their adults (McLean et al. 1996; Sranley-Price 1989; Curio 1996; Wolf et al. 1996; Clemmons and Buchholz 1997).

In spite of some limitations of ex-situ conservation, it is indispensable together with in-situ conservation to protect species that are extinct or remain limited number in the wild

1.3.2 In-situ Conservation

It is on-site conservation and this is a process of protecting an endangered plant or animal species in its natural habitat. In-situ conservation is based on protecting natural areas and this is done by means of establishing protected areas (Soulé 1986). And these are recognized as fundamental tools for safeguarding biodiversity from genes to ecosystems in Convention on Biodiversity (CBD 1992).

In-situ conservation is a cost effective conservation strategy and it provides preservation of a significant number of indigenous species and systems. Also, in-situ conservation allows natural selection and maintenance of evolutions that result in producing new community systems and genetic materials. Furthermore, it enables to store specific examples of biodiversity for both present and future economic benefits (Soulé 1986; Burley 1988; WCMC 1992; Eisner 1990 and 1992; and Reid 1993; Jarvis et al. 2000).

Although in-situ conservation provides maintenance of biodiversity with its all levels and ecological processes, it is not sufficient to establish protected areas and assume its biodiversity preserved automatically without any risk (Bibby 1992) because protected areas may be exposed to many risks both natural and man-made. For example, demographic uncertainty may be occurred in protected areas due to the unexpected events in survival and reproduction of individuals. Also, environmental uncertainties resulting from unpredictable changes in weather, food supply, and the populations of competitors, predators, and parasites may be observed. Another important risk is natural catastrophes such as floods, fires, or droughts, which may occur at random intervals (Shaffer 1981; Riklefs et al. 1984; McNeely, 1990). An extreme example of this was the destruction of the entire remaining habitat of the golden lion tamarin (*Leontopithecus r. rosalia*) in 1992 by fire (Dietz et al. 1994; Castro 1995). Moreover, genetic uncertainty or random changes in genetic make-up due to genetic drift or inbreeding that alter the survival and reproductive probabilities of individuals may be seen (Shaffer, 1981; Reid 1993). However, the greatest uncertainty is generally man-made. The elimination of habitat because of human settlements and associated development activities is the most important factor contributing to the diminishing structure of biodiversity (Wilson 1984). The way to accomplish these uncertainties is not only to establish protected areas but also to apply an integrated conservation programs including identifying protected areas so as to provide effective conservation for all endangered species and systems, application of effective management strategies and performing appropriate ex-situ methods in combination with in-situ conservation (Westman 1985; WRI/UNEP/UNDP 1992)

1.3.2.1 Protected Area Concept of World (from past to present)

Many definitions have been done for protected areas. The Rio Convention defines a protected area as “a geographically defined areas which is designated or regulated and managed to achieve specific conservation goals” (CBD 1992) while the International Union for Conservation of Nature (IUCN) define them as “clearly defined geographical space, recognized, dedicated and managed, through legal or other effective means, to achieve the long-term conservation of nature with associated ecosystem services and cultural values” (IUCN). Beside these considerations, other important issue that should be considered in protected area concept is human welfare. From this point of view, definition of protected areas can

be enlarged as these are legally designated areas that are governed by laws and rules to conserve genetic, species and ecosystem diversity and allow widely varying degree of commercial resources use, traditional use by local people and recreational use (Gadgil and Guha 1992; Western et al. 1994; Jeffries 1997; Primack 1998).

The first conscious effort to protect nature in the World was made by the kings of England in the middle ages. They allocated private preserves for both recreation and hunting purposes and protected these sites from illegal excessive hunting and overexploitation. After that, the first idea about protecting natural lands was recommended by George Catlin (1796-1872), a self-taught artist in 1832. He worried too much about the impact of human expansion on wildlife and wilderness and suggested to preserve these areas by some great protecting policy of government. However, the idea gained acceptance years later, when in 1864 Congress gave Yosemite Valley to California for preservation as a state park. And then in 1872, Yellowstone set aside as a first legal national park and administered by the federal government for the benefit and enjoyment of the people. Afterwards, the idea of protecting wild land began to gain great concern and this US concept of national parks was copied by other countries around the world (Borland 1975; Dunlap 1988; Reiger 2001; Taber and Wayne 2003; Dessecker and Mealey 2005). Since then, there has been a great increase in number and kind of protected areas. These alterations in number and kind are recorded by IUCN in a database that is the World database on Protected Areas (WDPA) and this database provides an inventory of the number and extent of protected areas (UNEP 2008; Figure 1.7).

The first database was drawn up in 1962 and listed over 1000 sites. In 1992, nearly 7000 parks and protected areas covering 6.5 % of Earth's total area had been established worldwide (WRI, 1992) and these areas represented all 8 natural realms and 14 biomes of world categorized by Udvardy (1975). Nevertheless, the participants in the IVth World Congress on National Parks and Protected Areas (Caracas, Venezuela, February 1992) and the 1992 Earth Summit concluded that although progress had been made in conserving samples of these biogeographic provinces, coverage was still insufficient. Then, scientific committee decided that the total expanse of protected areas needs to be increased in order to maintain the earth's biotic resources (McNeely *et al.*, 1990). This meant that the establishments of additional protected areas properly funded and managed to ensure protection of broadest range of biotic resources (UNEP, 1992). Shortly after this, number of

protected areas was increased up to 12.754 covering 8.82 percent of Earth's total area. By 2003 this number reached 102.000 and as of 2008, number of protected areas are around 120.000 in the world with more added daily, representing a total area of 21.1 million km² or approximately 12.2 percent of the world's land surface area (IUCN and UNEP 2003; IUCN and UNEP 2007; UNEP 2008, Jenkins and Joppa 2009) (Figure 1.8, Table 1.4).

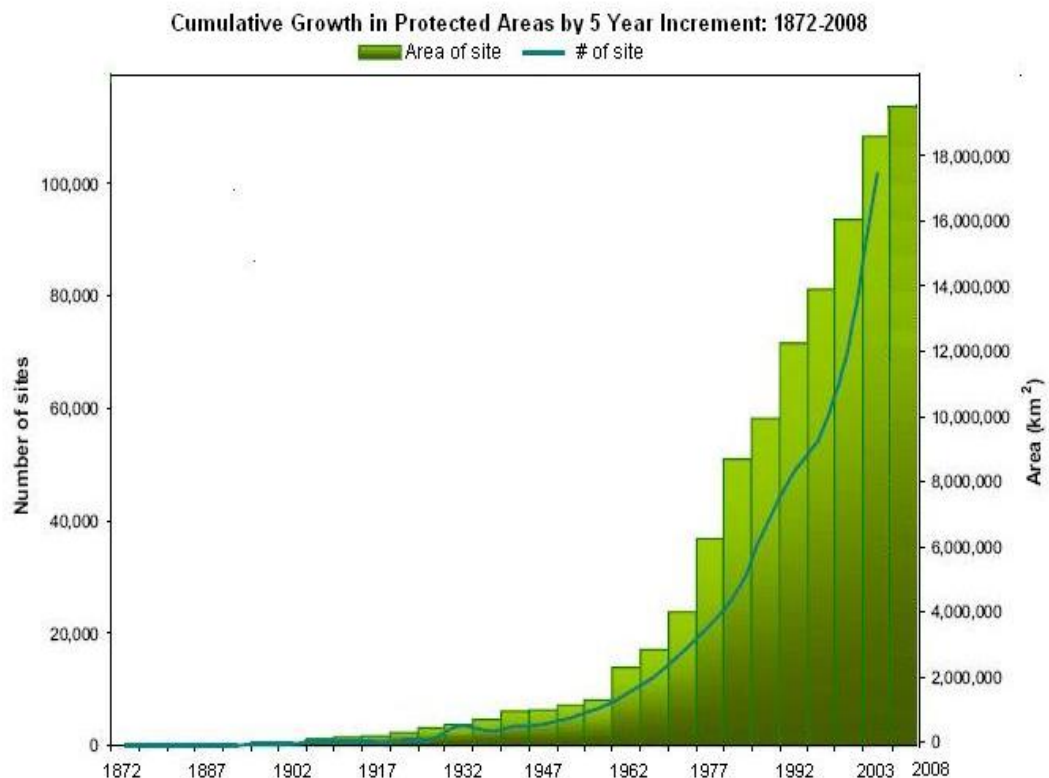


Figure 1.8 Global extent of protected areas measured by number and extent (IUCN 2008)

Table 1.4 Number and % of protected areas according to years (UNEP 2003, 2008)

Year	Number	Global land area protected (%)
1962	9214	2,4
1972	16394	4,1
1982	27794	8,8
1992	48388	12,3
2003	102102	18,8
2008	122512	21,2

Although numerous protected areas had been established until 1973, there was not any international conformity about their kind and management strategies. In 1973, Dr. Ray Dasmann prepared a system of protected areas categorization to provide an international association for management strategies. This was published by IUCN. Later on, this categorization system was improved by updating many times. Ultimately, its last form was given through Commission on National Parks and Protected Areas (CNPPA) and declared by IUCN as protected area management categories in 1994 (CNPPA; IUCN; WCMC 1994; Table 1.5).

This categorization system includes 6 different protected area management categories and these define right compromise between protecting biological diversity and ecosystem function and satisfying the immediate and long term needs of local human community (Western et al., Primack 1998). Moreover, this categorization system provide international standards to help global and regional comparisons among protected areas and reduce confusion that is due to the adaptation of many different terms describing different kind of protected areas. Also since it is a common system, generally it facilitates communication and understanding among countries with regard to conservation (IUCN; CNPPA and WCMC 1994). Most importantly, using this protected area management categorization appropriately is the first step to provide effective conservation because these categories are constituted by considering necessities of protected areas. Then, assigning appropriate protected area category for a site is too crucial for proper management and conservation.

Table 1.5 IUCN protected areas management categories and definitions (IUCN; CNPPA and WCMC 1994; OECD 1996 Jeffries 1997; Primack 1998)

IUCN protected area management categories	
I Strict Nature Reserve and Wilderness Area:	These areas include representative samples of biodiversity to protect natural organisms and processes. They are established in undisturbed areas for scientific study, education, environmental monitoring and maintenance of genetic variation. It includes two subcategories. (I-a) primarily includes nature reserve established for scientific research and monitoring. (I-b) primarily includes wilderness area protected and managed so as to preserve its natural condition.
II National Parks:	These are large areas to preserve scenic and natural beauty that are of national or international importance, maintained for scientific, educational and recreational use. Usually, they are not used for commercial purposes.
III Natural monuments and landmarks:	These are small areas or entities that are designed to protect unique, special national interest.
IV Habitat/ Species Management Areas:	These areas are exposed too much intervention for management purposes and designed to maintain habitats and also to meet the requirements of species.
V Protected Landscape /Seascapes:	These are areas that represent the harmonious interaction between people and environment. Also, they are the best representative for traditional and nondestructive use of natural resources while providing opportunities for tourism and recreation.
VI Managed Resource Protected Areas:	these allow for the sustained production of natural resources including water, wildlife, grazing for livestock, timber, tourism and fishing in a manner that ensure the preservation of biological diversity. These areas are often large and may include both modern and traditional uses of natural resources.

1.3.2.2 Current Conditions of Protected Areas in TURKEY: Status and Legislations

Biodiversity loss and habitat destructions that result from human activities have been the major threats of nature in whole world, as well as in Turkey. And as expressed before, their consequences may be too severe for human being. Therefore, countries all around the world have developed their own strategies to overcome these problems and to protect biodiversity since 1800s. Turkey have been a part of these efforts for approximately last fifty years too by improving its

legislations and protected area status. In Turkey, The first attempt to protect biodiversity began with the establishment of Yozgat Çamlığı National Park in 1956 and as a consequence of gradually raised concern of governments, non-governmental organizations (NGO's) and public, today more than 3,5 million ha area have been protected and managed legally with different protected area status (Table 1.6). Also, General Directorate of Nature Protection and National Parks that is the related part of ministry of environment and forestry still has been maintained their studies to expand protected lands and to improve efficiency of currently existing protected areas by applying appropriate management plans.

Today, there are 15 different protected area status in Turkey. 11 of them are regulated with national legislations of Turkish government while the rest 5 are regulated by international conventions of which government of Turkey became partner (Table 1.6). Although, these 10 protected area status and their management objectives are determined according to national legislations of Turkish government, additionally these are matched with the protected area management categories of IUCN in order to provide international conformity and to facilitate communication in international platform (Table 1. 7, MoEAF/GDoNPANP, NCC 2003-2005, MoCAT).

Table 1.6 Protected Area Status governed by either national legislations or international conventions (source; MoEAF/GDoNPANP, NCC 2003-2005, MoCAT)

Protected Area Status Governed by National Legislations			
Protected Area Status	# of site	Total Area (ha)	Legislation
National Parks (Milli Park)	40	797.366	
Nature Protected Area (Tabiatı Koruma Alanı)	35	84.049	National Parks Legislation-Milli Parklar Kanunu (9 August 1983)
Natural Monument (Tabiat Anıtı)	105	5286	
Nature Park (Tabiat Parkı)	30	79047.4	
Wildlife Protected and Refinement Site (Yaban Hayatı Koruma ve Geliştirme Sahası)	108	1.755.013	Terrestrial Hunting Legislation- Kara Avcılığı Kanunu (5 May 1937)
Conservation Forest (Muhafaza Ormanı)	61	231301.43	
Gene Conservation Forest (Gen Koruma Ormanı)	193	27735.60	Forest Legislation- Orman Kanunu (August 1956)
Seed Stance (Tohum Meşceresi)	338	46080.04	
Seed Garden (Tohum Bahçesi)	174	1158	
Natural Preservation Site (Doğal Sit)	789	-	Cultural and Natural Entities Protection Legislation-Kültür ve Tabiat Varlıklarını Koruma Kanunu (21 July 1983)
Protected Area Status Governed by International Conventions			
Protected Area Status	# of site	Total Area	Convention
World Heritage Site (Dünya Kültürel ve Doğal Miras Alanları)	9	-	Convention of World Heritage (14 April 1982)
Areas for Special Conservation Interest or	9	716.529	Bern Convention(9 January 1984)
Special Environment Protection Site (Özel Çevre koruma Alanı)	13	1.046.350	Barcelona Convention (7 October 1988)
Ramsar Area (Ramsar Alanları)	13	130.450	Ramsar Convention (17 May 1994)
Natura 2000	-	-	EU Habitat and Species Protection Rules- AB
Biosphere Reserve	1	25.274.58	

Table 1.7 Twining of IUCN Protected Area Management Categories with Protected Area Status of Turkey (Source; MoEAF/GDoNPANP, IUCN 1994, NCC 2003-2005, MoCAT)

Twining of IUCN Protected Area Management Categories With Protected Area Status of Turkey	
IUCN Protected Area Management Categories	Protected Area Status of Turkey
<u>Category I-a Strict Nature Reserve;</u> these are areas that represent important samples of ecosystems, geological or physiological features and species. And these areas are mainly managed for scientific purposes.	<u>Nature Protected Area (Tabiatı Koruma Alanı);</u> these areas includes rare and endangered ecosystems and species. These areas are absolute protected sites and can only be used for scientific purposes.
<u>Category I-b Wilderness Area;</u> These are nearly intact and natural areas and do not include any settlement around them.	No Matching are found
<u>Category II National Park;</u> National parks are designed to ensure ecological integrity of ecosystems and to protect them from inappropriate occupations and degradations. They also provide scientific, recreation and visiting services.	<u>National Park (Milli Park);</u> They have national and international importance with regard to science, esthetic and natural beauty. And These are not only protected for their biodiversity features but also for their natural, cultural and tourism resources.
<u>Category III National Monument and Lanmark;</u> These are entities that are unique and have esthetic and cultural importance.	<u>National Monument (Tabiat Anıtı);</u> Special entities and they have scientific and cultural importance.
<u>Category IV Habitat/Species Management Area;</u> They protect special habitats or species and managed actively.	<u>Wildlife Protected and Refinement Site (Yaban Hayatı Koruma-Geliştirme sahaları);</u> These areas are absolute preservation sites to protect and refine specific species.
<u>Category V Protected Landscape/Seascape;</u> There is a harmonious interaction between people and nature in these areas. And They have rich biodiversity and aesthetic beauty.	No Matching are found
<u>Category VI Managed Resources Area;</u> Aim of them to protect biodiversity while providing traditional and sustainable utilization of local people.	No Matching are found
No Matching are found	<u>Nature Park (Tabiat Parkı);</u> Recreation sites including specia plants, vegetation and wild life and having landscape beauty.
No Matching are found	<u>Special Environment Protected Area (ÖÇK);</u> They have historic, natural and cultural integrity and have national and international importance.
No Matching are found	<u>Natural Preservation Site (Doğal Sit);</u> these are extraordinary sites and have universal value

1.3.2.3 Deficiencies of Protected Area Systems

Establishment of protected areas is the most effective way to decrease the global biodiversity loss. Today, observed rate of extinction of plant and animal species due to human activities is approximately 1000 times greater than at any time in past (Lawton and May 1995; Pimm et al. 1995). And concurrently, governments do not have enough time and resources to protect rare and endangered species or ecosystems one by one. In such a case, protected areas should be carefully selected and designed so as to provide the most effective return from conservation investment. However, at present limited number of protected areas has been identified with a systematic biodiversity conservation strategy and generally protected areas include few number of species that are really needed protection (Pressey 1994). Also, protected areas that were established in the past usually designed as their visual beauty, recreation and tourism value and many studies indicated that these sites are valueless especially for biodiversity conservation (Runte 1976, 1979; Mosley 1978; Harris & Whinam 1994; Mendel & Kirkpatrick 1999). Furthermore, a study that was conducted by Scott et al. in 2001 showed that protected areas are located in high altitudes and poor lands in U.S. Actually, this situation is not different for the rest of the world. In recent years, areas that are not valuable with regard to biodiversity and have little economic value have been set aside as protected areas (Fearnside & Ferraz 1995; Bojorquez -Tapia et al. 1995; Ramesh et al. 1997; Powell et al. 2000). All these make conservation efforts inadequate and ineffective in terms of biodiversity conservation.

In 1993, IUCN suggested that at least 10% of total area of major terrestrial biomes should be represented within protected area network to ensure protection of most of the terrestrial biodiversity. Currently, protected area network cover 21% of these terrestrial biomes. However, as global evaluations indicated that there are still large gaps in protected area network especially in Tropics (Brooks et al. 2004, 2006; Ferrier et al 2004; Rodriguez 2004; Soutullo et al 2008). Then, it is apparent that explicit, measurable, applicable and repeatable conservation targets should be determined to fill these gaps.

Moreover, although many protected areas have been formally designed for conservation, they receive no, little or limited protection in practice. These are often termed as paper parks. For instance, Gronne Ejland in Greenland is a such kind of protected area. It was declared as a Ramsar site in 1987 because of having the

world's largest Arctic terns (*Sterna paradisaea*) colony. But this designation never had any practical significance because in the summer of 2000 there was not any remaining breeding pair of terns (Hansen 2002). Also, effectiveness of protected areas often depends on the level of management activities and funds that are used to apply conservation strategies. And this is generally insufficient to perform effective management and conservation activities (Bruner et al 2001a, b; Vanclay 2001; James et al 1999, 2001).

Although there have been many attempts such as establishing protected areas, applying conservation conventions and developing different management strategies to ensure maintenance of earth's biodiversity, sometimes these may not be enough to effective conservation. Therefore, it should be required to increase number and effectiveness of protected areas and rapidly generalize conservation efforts. For these purposes many approaches have been developed. Some of these approaches have been used GIS (Geographic Information System) and RS (Remote Sensing) in natural resource management and nature conservation. Both of these tools provide to evaluate efficiency of protected area network, identify new protected areas and effective planning for existing protected areas system (NCC 2003-2005).

1.3.3 GIS in Biodiversity Conservation

As already indicated above parts, the growing human population and its demands on the earth's resources generate depletion on natural resources. Therefore, it is required to preserve earth's natural landscape and sustain biodiversity because these are crucial for biodiversity conservation. Geographic Information System (GIS) is one of the tool that have been used in natural resource management and biodiversity conservation since 1980s. It is used to integrate, manage, analyze and visualize different format data from multiple sources. In natural resource management and nature conservation, it provides opportunity to identify protected areas, monitor habitat change, track wildlife demographics and predict future land and resource use. And all these are essential parts of conservation goals and practices. Also, as a data management and analyze tool, GIS has the ability to take decision based on environment data in order to better conserve its resource and its biodiversity (Jones 1997; Funk 1999; Groves et al 2002; NCC 2003-2005; Salem 2003; Balram 2004).

Due to all of these advantages in biodiversity conservation applications, it became a widespread tool in many national and international nature conservation programs. Previously, it was only used to determine priority conservation sites through the application of **Gap Analysis** and **Complementarity Approach** (Jenning 1999; Kirkpatrick 1983; Margules et al. 1988; Scott et al 1989; Margules 1989; Pressey and Nicholls 1989a, b; Scott et al 1993; Edward et al 1993; Sætersdal et al. 1993; Rebelo 1994). However, later on it became an essential part of **Systematic Conservation Planning (SCP)** (Margules and Pressey 2000; Groves et al 2002; Sarkar 2005; Margules and Sarkar 2007). With a simple perspective, Gap Analysis is an analysis that is worked in complementarity manner and used to determine species and communities that are not represented or inadequately represented within existing protected area network. Both Gap Analysis and Complementarity approach constitute base of SCP. SCP is a process that is explicitly defined conservation goals in order to identify effective conservation area network for providing long term and permanent maintenance of biodiversity. Actually, Gap Analysis is only a small part of SCP. However, it is more popular and more commonly used than SCP because Gap Analysis is historically older and SCP is a more complex process and includes several stages that require long and detailed studies. And generally foundations that are conducted conservation studies have not had enough fund and expert people for such a complex process. Then, they usually prefer Gap Analysis that is less demanding than SCP in protected area studies (NCC 2003-2005).

1.3.3.1 Gap Analysis and Complementarity Approach

Both Gap Analysis and Complementarity Approach were begun to use at the beginning of 1980s to identify protected areas. Gap Analysis briefly can be defined as an analysis that is utilized to determine the gaps within existing protected area system (Scott et al 1989; Edward et al 1993; Jennings 1999, 2000). It uses species, community types and vegetation categories as data in the form of digital layers and provides to analyze and evaluate these digital biodiversity data layers in terms of conservation in short time.

Gap Analysis was firstly used by The Nature Conservancy (TNC) in 1982 with national heritage program. Afterwards, it was used by Scott et al in 1985 to determine protected areas for birds in Hawaii. And later on, it was utilized for

several regional and international conservation programs and studies (Diamond 1986; Noss 1987, 1990; Austin 1991; Scott et al 1993; Powell et al 2000; Oldfield et al. 2004; Rodrigues et al. 2003, 2004; Mathur et al 2006). Although Gap Analysis was commonly used for several conservation studies, it was thought that it has some disadvantages. Especially using sites that have high species diversity to fill conservation gaps is not an effective conservation approach because this species rich areas generally have same biological composition and this lead to the protection of some species a few times within the protected area network while some other species especially threatened and rare species may not be represented in this network. Because of this, some scientist preferred to utilize Gap Analysis together with complementarity approach. With this approach, maximum numbers of target species that are needed to preserve are protected at least number of sites and each site that are selected during the process is the complementary of each other in respect to biodiversity composition (Pressey and Nicholls 1989b; Williams et al 1994; Margules and Pressey 2000; Valutis and Müllen 2000; Sarkar and Margules 2002; Justus and Sarkar 2002; Vassiliki *et al.* 2004; Williams et al. 2006). Complementarity Algorithms was developed in Australia (Kirkpatrick 1983; Margules et al 1988; Margules 1989; Pressey and Nicholls 1989a, b), South Africa (Rebelo 1994) and Europe (Sætersdal et al. 1993) independently from each other. Therefore, there have been several complementarity algorithms that are used to determine protected areas. Some of them are based on rarity while some others use richness. Deciding which kind of algorithm is the best one and give the most reasonable results is not an easy task. And this very much depends on data on hand and purpose of conservation programs (Pressey et al 1997).

Also, Complementarity Approach has three important fundamental features that bring its effectiveness. These are;

Complementarity; Priority protected areas that are selected during the process complete each other with regard to biodiversity composition (Jenning 2000; Justus and Sarkar 2002).

Flexibility; Sometimes, some of the sites that are selected as a result of analysis may be used for other purposes. Then, these cannot be established as protected areas. In such situations, alternative areas can be determined instead of these unavailable sites by using flexibility feature of the algorithms (Bedward et al 1992).

Irreplaceability; If species or taxa are unique and if they cannot be replaced with other species or taxa. Then, they have to be had in the selected priority conservation sites. In such circumstances, these species or taxa must be defined before running algorithm in order to guarantee selection of these species during the process (Margules and Pressey 2000; Ferrier et al. 2000; Carwardine et al 2007).

There are also some examples of complementarity based GAP analysis in TURKEY. These studies were carried out Southeast Anatolia, Mediterranean, Lesser Caucasus and Coastal Aegean respectively in cooperation of Nature Conservation Centre, Baku-Tbilisi-Ceyhan (BTC) Pipeline Environmental Investment Programme, the Turkish Foundation for Combating Soil Erosion, for Reforestation and the Protection of Natural Habitat (TEMA) and Middle East Technical University. Each of these Gap analysis projects were carried out in order to fill conservation gaps within the related regions and provide more effective and sustainable biodiversity conservation with scarce resources.

1.3.3.2 Systematic Conservation Planning

Systematic conservation planning (SCP) is a process of deriving protected area network for a region (Margules and Sarkar 2007). Systematic conservation approach began with the application of GAP analysis and Complementarity studies that were conducted separately in USA and Australia. Although, these studies constitute very little part of the today's conservation approaches, these are the corner stone of the systematic conservation planning. And systematic conservation planning was developed in the light of these applications with the studies of Margules and Pressey 2000, Groves et al. 2002; Cowling and Pressey 2003 and Sarkar 2004, 2005. Since then, there have been many applications of systematic conservation planning all over the world. And for sure, due to the difference in region, conditions, facilities and implementers, a variety of perspectives and applications have been developed in order to able to carry out systematic conservation in distinct parts of the world. Even, all these cause some discrepancies in practice applications of systematic conservation, the essential and common thing in systematic conservation planning that wants to be accessed is to achieve effective sustainable biodiversity conservation. Therefore, variability in systematic conservation applications would remain insignificant when thinking the

main goal of this conservation approach, alike as being many different systematic conservation planning classifications would not able to change the main aim of the studies. This means that, different conservationist can classify each steps of systematic conservation process according to their own view. This forms many classifications for systematic conservation planning. In this thesis one of them that was classified by Margules and Sarkar (2007) and gathered within 11 different conservation steps is presented. The steps of this systematic conservation planning classifications are below;

- Identify stakeholders for the planning region.
- Compile, assess, and refine biodiversity and socio-economic data for the region.
- Identify surrogates for region.
- Establish conservation targets and goals.
- Review existing conservation areas.
- Prioritize new sites for potential conservation action.
- Assess prognosis for biodiversity for each potentially selected site.
- Refine networks for sites selected for conservation action.
- Examine feasibility using multiple criteria analysis.
- Implement conservation plan.
- Periodically reassess the network

Although, each of these systematic conservation planning stages have their own importance in conservation applications, in this thesis the attention was paid on the third stage that is related with the identification of the surrogates since one of the objective of the thesis is to obtain the most reliable and effective surrogates for detecting protected areas network of Lesser Caucasus Region in which most effective biodiversity conservation can be achieved. The third stage of this classification including surrogate identification is the most critical and crucial stage of systematic conservation planning in this aspect since it is the first step to be able to detect the most effective protected areas network of an area.

1.3.3.2.1 Surrogate Concept and Environmental Surrogates in Systematic Conservation Planning

Surrogates have to be used in conservation planning in order to represent biodiversity and provide a full measure of biodiversity since if biodiversity is defined

as the diversity of life at every level of structural, functional and taxonomic organization; it becomes all of biology (Takacs 1996). Therefore, it is too difficult to quantify biodiversity of a region for the purpose of conservation planning. Herein, identifying surrogates so as to represent full range of biodiversity of a region as far as possible is an important step in SCP in order to set effective protected area network for biodiversity conservation (Sarkar 2002; Sarkar and Margules 2002).

Since 1980s to 1990s, only biodiversity objects such as species, community types and vegetation classes utilized as surrogates in conservation planning to identify protected areas even though it was known that this may lead to the some misspecifications in protected areas network due to the bias in data. However later on, environmental diversity (ED) such as topography, climate, soil etc. have begun to use in conservation planning as surrogates instead of biodiversity surrogates because many conservation planners assume that there is a positive relationship between biodiversity and environmental diversity. Then, Environmental diversity can be used as surrogate in SCP so as to substitute biodiversity surrogates while detecting priority protected areas.

That is, by means of today's advanced data gathering techniques, conservation planners are able to use both biodiversity and environmental diversity in conservation planning. But the decision about which one is the most efficient to identify protected areas is very much depend on the reliability of the surrogate data on hand. And in this point, the general opinion is that there may be too much bias in biodiversity data. Then, the usage of environmental diversity in conservation planning may become more suitable and more preferable. Actually, preferring environmental diversity instead of biodiversity as surrogate in conservation planning results from some necessities. These necessities that make the usage of environmental diversity more suitable can be listed and explained with the following statement.

- The scarcities of data on patterns of species occurrence in some of the most important regions of the world affect the selection of proper priority conservation areas. Thus, incorporation of environmental diversity which acts as an effective surrogate for pattern of biodiversity have been suggested for conservation planning (Belbin 1993; Folke et al. 1996; Noss 1996a, b; Cowling et al. 1999; Fairbanks and Benn 2000; Faith 2003).

- There are neither resources nor time to carry out detailed inventories before priority conservation areas are selected. Thus, environmental diversity can be used as surrogates in order to cope with these difficulties (Araujo et al. 2001).
- Generally, there can be bias between real occurrence of species and collected samples of species data. This means that collected samples can not reflect real species diversity so results might be unreliable.
- Complete representation of overall species diversity cannot be achieved by area selection based on indicator groups, and then it may be wise to incorporate environmental diversity within systematic conservation planning to capture all rare and endemic species whose occurrence may correlate with special environmental characteristic of their habitat (Gaston and Rodriguez 2003).
- Diversity explicitly defined as a hierarchical concept with genetic, species and ecosystem diversity and ecosystems are interacting systems of biotic and abiotic components. Therefore, it is important to protect not only the species diversity but also the non-living environment. Maximizing environmental diversity within conservation area network, that is maximizing the range of suitable living conditions for different species, should guarantee the representation of a diversity of species (Faith and Walker 1996). Therefore, integrating the use of environmental diversity in systematic conservation planning is important to achieve conservation targets and goals.

1.3.3.2.2 How to Use Environmental Surrogates or Environmental Diversity (ED) in SCP

Although, many conservation biologist have suggested that environmental diversity can be used as surrogates in conservation planning to detect protected areas instead of biodiversity, there have been still debates about this opinion and about methodologies that have been applied to investigate efficiency of environmental diversity in SCP. Nevertheless, several different methodologies have been

improved to examine and prove efficiency of environmental surrogates for representing biological diversity.

First studies to investigate the efficiency of environmental surrogates in respect to represent biodiversity was begun with Belbin (1993) and Faith and Walker (1993; 1994; 1996a, b; 1996). These scientist applied p-median location allocation algorithm in their studies in order to indicate biodiversity representativeness of environmental surrogates (1993; 1994; 1996a, b, 1996). And these studies performed by the mentioned scientist were the starting point of longstanding discussions about the applications of p-median because later on some other conservation biologist who applied one of the different forms of the p-median algorithm began their studies in order to figure out efficiency of biodiversity representativeness of environmental diversity (Araujo et al 2001, 2003, 2004). Reason of the discussion among these implementers is because while Belbin, Faith and Walker (1993; 1994; 2003; 2004) applied continuous form of p-median algorithm and argued that it is the most appropriate form for using in conservation planning, the second team used discrete p-median algorithm to identify protected areas with environmental surrogates and defended its efficiency. But, after their long debate, Hortal and Araujo (2009) compared these two forms and concluded that one of these algorithms is not consistently superior to the other.

Also, roughly at the same time, some other location- allocation algorithms were tried in order to investigate the usefulness of environmental diversity as surrogates in conservation planning (Gerrard et al 1997; Church 2002).

Besides of mentioned location-allocation approach, ordination analyses such as detrended correspondence or canonical correspondence in conjunction with spatial autocorrelation have been used as a methodology in order to figure out efficiency of environmental diversity in conservation studies, especially in detection of priority protected areas (Pressey et al. 2000; Fairbanks et al. 2001; Reyers et al. 2002).

Another method that has been applied for conservation area selection with environmental diversity was recommended by Ferrier et al in 2002. It is Generalized Dissimilarity Modeling (GDM). This is the form of distance regression and it is a nonlinear method. It models dissimilarities in a region. In this way, it can prioritize and select protected areas (Ferrier 2002a, b).

Other widely used application to demonstrate the efficiency of environmental diversity for representing biodiversity is clustering techniques. Many scientists have performed different types of clustering analysis such as k means, ward's minimum variance and cenroid algorithms in order to indicate usefulness of environmental diversity as surrogate while detecting protected areas (Trakhtenbrot and Kadmon 2006, Kent and Carmel 2010).

As is seen, there have been several techniques and so many studies that were performed with these techniques in order to exhibit the utility of environmental diversity in conservation planning. Although, some of these applications are not hopeful in order to demonstrate biodiversity representativeness of environmental diversity, some others are too encouraging to use environmental diversity as surrogate for representing biodiversity in conservation studies instead of biodiversity surrogates

1.4 Objective of the Thesis

As specified above parts, earth's biodiversity exposures serious threats due to the increasing demand of human population. And as a result of these great pressures on biodiversity, biodiversity loss and extinctions become inevitable. In this case; to provide sustainable conservation of biodiversity, either existing protected areas system should be revised so as to ensure conservation of threatened and rare species or new protected areas should be established in order to expand existing protected areas network. For latter case, one approach is to detect effective protected areas for biodiversity conservation by performing complementarity based gap analysis with reliable biodiversity surrogates. The crucial and critical step in this analysis is to identify the most proper biological surrogates to be able to represent full measure of biodiversity of an area. Due to the importance of surrogate identification in conservation of biodiversity, this point has been attracted too much attention and many studies have been carried out in order to investigate efficiency of different taxa or taxon as surrogate. One of the aims of this thesis is to examine surrogate efficiency of different biological taxa or taxon for Lesser Caucasus region too. For this purposes a biological database including records and information for breeding birds, butterflies, amphibians and reptiles, highly threatened endemic plants, large mammals and ecological communities were used and their surrogate efficiency was quantified by performing a complementarity

based gap analysis. Moreover, cross-taxon congruence for species richness and for complementarity was investigated among these taxa in order to determine the most appropriate biodiversity surrogate for Lesser Caucasus region.

In the second part of the thesis, the aim is to evaluate the efficiency of environmental surrogate for representing biodiversity. Although, biodiversity surrogates have been frequently and effectively used in conservation area planning, sometimes they may have some deficiencies during area identification and these may render biodiversity surrogates useless in conservation planning. Due to this, another alternative that is environmental diversity can be used as surrogate in order to represent biodiversity of an area by assuming that there is a positive relationship between environmental diversity and biodiversity. Even though, many studies have been carried out in different part of the world to clarify surrogate efficiency of environmental diversity, any example of such a study was not performed for Turkey up to now. In this sense, this thesis is the first applied example of the environmental surrogate approach for Turkey and when considering using biodiversity data as surrogate in conservation planning is how costly and time consuming, environmental surrogate approach and studies examining this approach become more important in respect to provide acceleration and cost efficiency in biodiversity conservation.

CHAPTER 2

MATERIALS AND METHODS

2.1 Study Area

2.1.1 Geographic Location

Study area is in the north-eastern part of Turkey and is about 35.000 square kilometres. The area includes all of Ardahan, south and east part of Artvin, north-eastern of Erzurum and some parts of Kars. However, it excludes northern part of Kaçkar Mountains, coastal Artvin and Aras valley because these parts are biogeographically and climatically different from the rest of the area.

The study area is known as lesser Caucasus ecoregion since the area is continuum of north Caucasus Mountains and occupies lesser part of Caucasus ecoregion. The area is quite remarkable with its geographic features. It is mainly characterized by high Eastern Black Sea Mountains, broad plateaus and deep valleys and has an altitude range of roughly 50 m. to 3900 m (Figure 2.1). All of these geographic features determine interesting ecological characteristics of the area. It is divided into two main parts by Karçal and Kaçkar mountain ranges so as to formalize the area with old humid temperate forests and dry high mountain step-alpine meadows. Also, deep valleys pass through the area and separate it as composing different ecological units. These parts are dominated by Mediterranean vegetation including typical Mediterranean maquis and stone pine (*Pinus pinea*) especially in Çoruh valley.

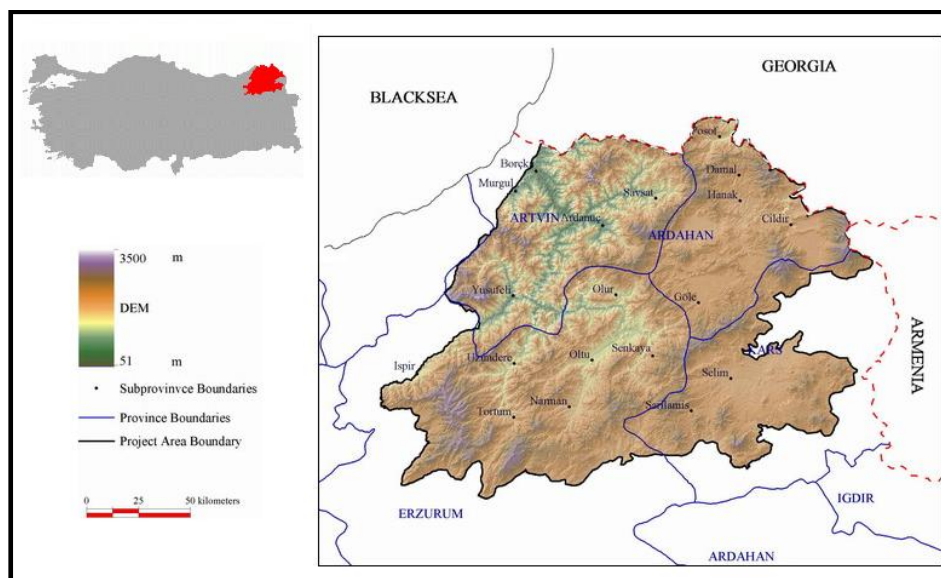


Figure 2.1 Geographic position of study area

2.1.2 Biodiversity

Study area has considerable rich biodiversity. It occupies both the Colchic flora sector of Euro- Siberian Phytogeographic Region and eastern part of Irano-Turanian Phytogeographic Region. It demonstrates high plant diversity and endemism. 3650 plant taxa of which 376 are endemic have been determined in area (Table 2.1; Kaya 2006).

Table 2.1 Distributions of plant taxa according to location, systematic classification and endemism status

	Artvin		Erzurum		Ardahan		Kars	
	Endemic	Non Endemic	Endemic	Non Endemic	Endemic	Non Endemic	Endemic	Non Endemic
Family	26	112	34	89	10	48	21	80
Genus	67	502	107	445	14	166	52	378
Species	100	1200	200	1300	16	250	70	900

Moreover, area hosts several animals. Many large mammals like Brown Bear, Gray Wolf, Eurasian Lynx, Roe Deer, Wild Goat (*Capra aegagrus*), and Wild Boar (*Sus scrofa*) and also small mammals such as Red Fox, Stone Marten, and Marbled Polecat are observed in the area (Ambarlı 2006).

Since this area is on the one of the most important bird migratory routes of the Earth, several bird species inhabit in the region. The most known one among them is Caucasian Black Grouse (*Tetrao mlokosiewiczi*) because it is an endemic and threatened bird species. Also, there are many wetlands like Lake Aktaş in the area. These provide home for many breeding colonies of White and Dalmatian Pelicans (*Pelecanus onocrotalus* and *Pelecanus crispus*), Armenian Gull (*Larus armenicus*), Velvet Scoter (*Melanitta fusca*) and rare waterfowl such as White-headed Duck (*Oxyura leucocephala*) and Ferruginous Duck (*Aythya nyroca*) (Atkin 2007).

Study area also has significantly rich reptile fauna and demonstrates high rate of reptile endemism. The most prominent reptile species are the endangered Clark's Lizard (*Lacerta clarkorum*), Caucasian Viper (*Vipera kaznakovi* = *Vipera pontica*) and the rare Orsini's Viper (*Vipera. [ursinii] eriwanensis*).

Moreover, high species endemism and species richness are quite common among invertebrate species, especially for butterflies.

2.2 Data and Working (Mapping) Units

Biodiversity and environmental diversity data were used as surrogates in the analysis part of this thesis respectively in order to identify priority biodiversity protected areas and environmental diversity (ED) sites. First of all, Study area was georeferenced with UTM north 37 zone map projection system and mapped so as to compose of 336 of 10*10 square kilometres resolution UTM grids (Figure 2.2). Afterwards all biological and environmental data used as surrogates were obtained, produced and analyzed according to those grid cells.

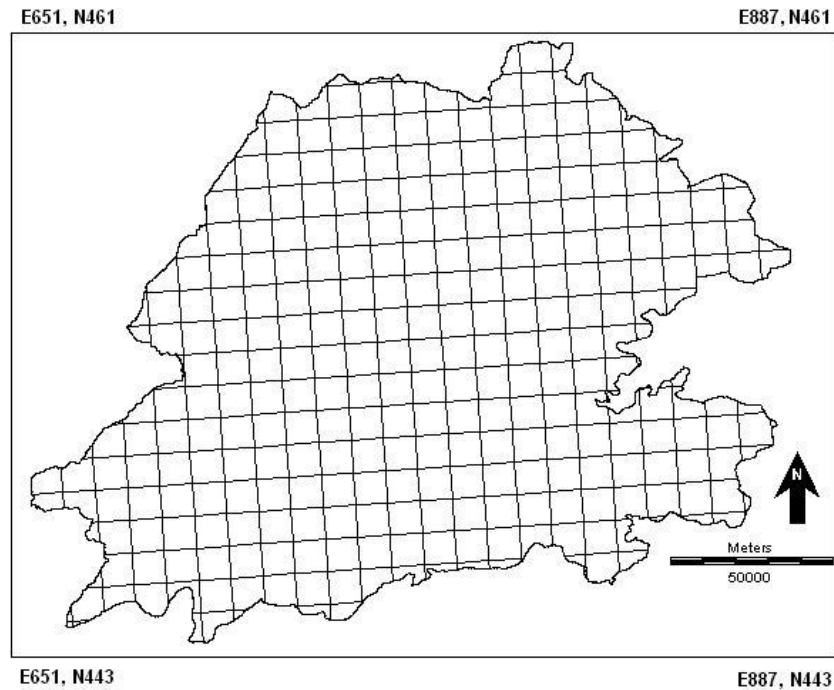


Figure 2.2 Map showing UTM-37 grid cells and border coordinates

2.2.1 Biodiversity Data

Six different taxonomic groups, endemic and non-endemic highly threatened plant species, globally important amphibian and reptile species, butterflies, breeding birds, ecological community types and large mammals were used as biological surrogates to determine priority biodiversity protected sites. This biological data set was composed within the scope of “TEMA-METU Gap Analysis of Lesser Caucasus Forest Project” funded by Baku-Tbilisi-Ceyhan (BTC) Pipeline Environmental Investment Programme (Atkin 2007). Required field works for obtaining biological data were carried out by researchers who are expert in their own research field between 2003 and 2005. While performing field studies for taxonomic groups, endemic and non-endemic highly threatened plant species, globally important amphibian and reptile species, breeding birds, and large mammals, presence of predefined species of the study area were searched for each UTM grid cells and if the investigated species was in the grid cell, then it was recorded along with lower left coordinates of the related UTM grid. In this way, present data set were prepared for taxonomic groups mentioned above. Also,

literature search, questionnaire applications and negotiations with local authorities were done to verify occurrence information and threatened categories of species.

To obtain butterfly data, a butterfly book, “Die Tagfalter der Türkei”, was used. This book consists of 3 volumes and was published by G. Hesselbarth, H. Van Oorschot and S. Wagener in 1995. It has been the only study including all systematic, habitat and location information for all defined butterfly species of Turkey. Location records are given with maps in the book therefore presence data of butterfly could be easily prepared using these location records for the study area. As doing for other taxonomic groups, data were recorded again together with lower left coordinates of UTM grids.

Community data was produced using satellite images. These images were Landsat TM images and processed before using. First of all, applying unsupervised image classification technique, a vegetation map including 15 different vegetation classes was produced for the area and then with the help of co-variables such as slope, altitude and hard copy stance maps, a community map that contains 39 community types was composed (Domaç 2005). Afterwards, this map was overlaid with 10*10 square kilometres resolution grid cells in order to convert the community map into the 10*10 square kilometres resolution.

Mentioned biodiversity database includes 11,932 records of occurrences for 54 endemic and non- endemic, highly threatened plant species, 42 breeding bird species, 10 large mammals, 238 butterfly species, 6 globally threatened reptile and amphibian and 39 community types (Table 2.2), (Appendix A). And all occurrence records of species of taxonomic groups are in accordance with mapping units, 10*10 square kilometres UTM north 37 zone grids (Figure 2.3).

Table 2.2 Distributions of biodiversity data according to number of records of taxonomic groups.

308 records for the 54 endemic and non-endemic highly threatened plant species.
1572 records for the 42 breeding bird species.
1240 records for the 10 large mammal species.
376 records for the 6 globally important amphibian and reptile species.
2833 records for the 238 butterfly species
5603 records for the 39 ecological communities.

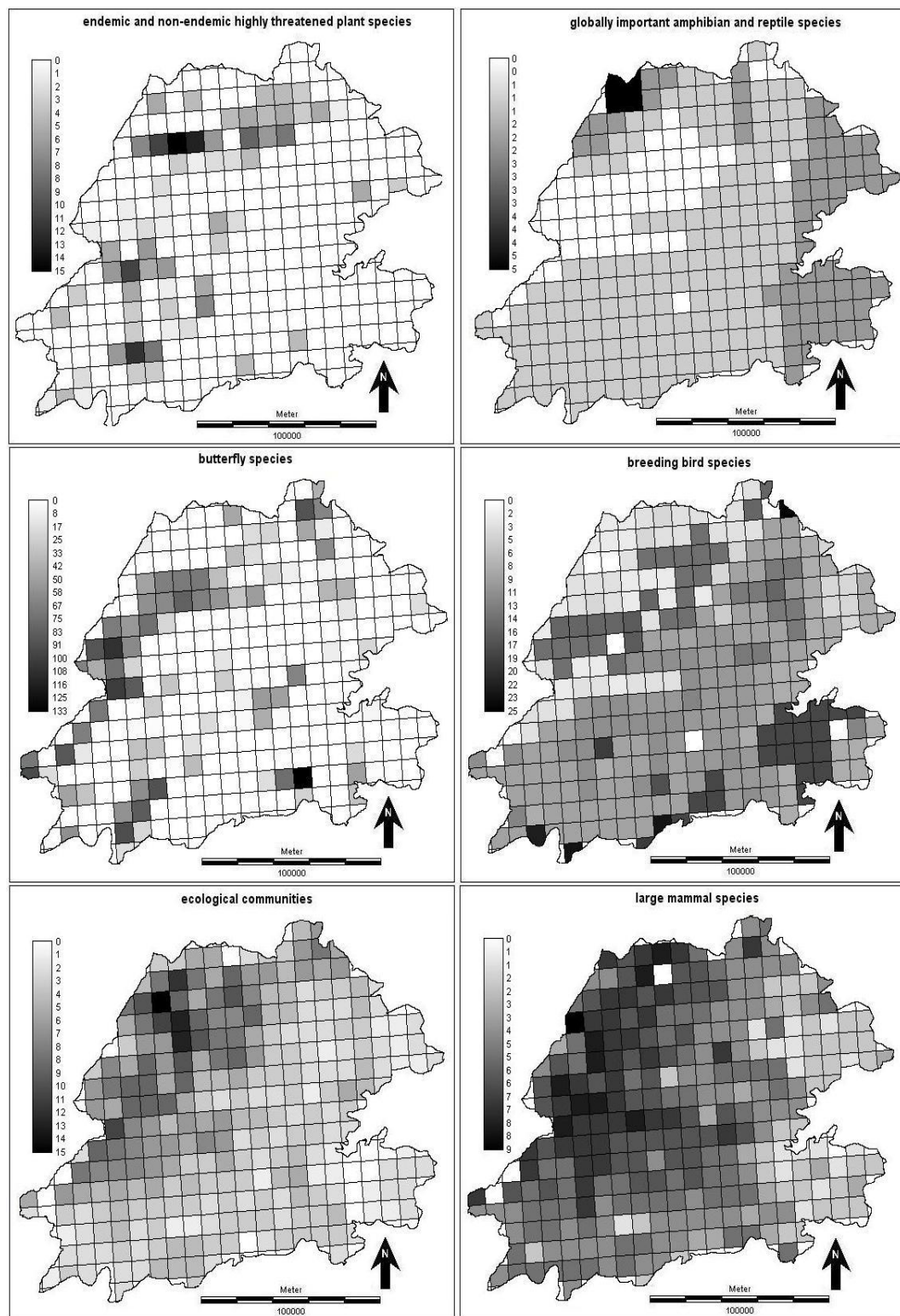


Figure 2.3 Maps showing distributions of numbers of species for each taxonomic group according to UTM grids

2.2.2 Environmental Diversity Data

Totally, 23 environmental input layers belonging three main environmental determinants that are topography, climate and physical features were used as surrogates in order to identify environmental diversity (ED) sites. Each of these environmental variables was produced or edited using different GIS software and processes. Each of these techniques is explained in detail below.

2.2.2.1 Topography Data

Altitude, aspect, slope and ruggedness were selected to use as topography variables. Altitude data is a Shuttle Radar Topography Mission (SRTM) digital elevation model (DEM) and directly was obtained from official web page of U.S Geological Survey (USGS) (<http://dds.cr.usgs.gov/srtm/>). It is a 90*90 m. resolution map and used as a base map to produce other topographic data layers. Aspect and slope were generated using Dem directly in TNT mips RS/GIS software. Afterwards, aspect was reorganized by dividing as northern and eastern aspect. And ruggedness was produced applying a ruggedness index on digital elevation model. This index calculates standard deviation of altitude for each UTM grid cell (Pelikan 2001). In conclusion, 5 different topographic data layers that are Dem, northern and eastern aspect, slope and ruggedness were directly acquired or produced to utilize as topographic environmental surrogates (Table2.3, Figure2.4).

Table 2.3 Topographic data layers.

Name of layer	Source	Resolution	Georeference system	Software (used to generate data layer)
Altitude (DEM)	SRTM	90*90m.	UTM 37. zone WGS 84	Obtained from USGS official web site.
Northern aspect	Aspect	90*90m.	UTM 37. zone WGS 84	TNT-mips RS/GIS software and IDRISI- Andes
Eastern aspect	Aspect	90*90m.	UTM 37. zone WGS 84	TNT-mips RS/GIS software and IDRISI- Andes
Slope	DEM	90*90m.	UTM 37. zone WGS 84	TNT-mips RS/GIS software
Ruggedness	DEM	90*90m.	UTM 37. zone WGS 84	TNT-mips RS/GIS software and IDRISI- Andes

2.2.2.2 Climate Data

In total, 15 climate surface belonging temperature, precipitation, humidity and solar radiation variables were utilized as climatic environmental surrogates in this thesis. These climate layers were generated using data obtained from Turkish State Meteorological Service (TSMS). This data set includes data belonging 38 climate stations situated in the study area for years between 1970 and 2000 (Appendix B). Last 10 years data were excluded from data set while producing climate surfaces because of abnormal climate shifts after 2000 (Türkeş and Sümer 2004).

11 of the climate layers were composed interpolating data with different kriging or co-kriging techniques while the rest 4 were generated applying mathematical formulas on some of these 11 layers. In order to produce mentioned 11 layers, firstly model fitting were done for data after implementing standardization according to 0 mean and 1 variance. The purpose of the model fitting is to determine visually and mathematically the most appropriate continuous surface model that represent spatial variability of data well (Eastman 2006). This was done by means of designing a semivariogram model and calculating R (coefficient of determination) and p values which indicate success of the selected semivariogram model. When computing p values, 25% of the data points that is almost equal to 9 of 38 climate stations were left for testing success of the model. All of these procedures were performed in Gamma Design GS+ (version-9) software (Handcock and Wallis 1994, Brown and Comrie 2002, Janis And Robeson 2004, Robertson 2008). After deciding the best semivariogram model for data that have R values greater than 0.80 ($R > 0.80$) and p-values smaller than 0.001 ($P < 0.001$), models were applied in ESRI/Arc-GIS 9.3 Geostatistics analyst tool in order to produce continuous climate data layers. Other 4 continuous climate surfaces that are isothermality (isotm), annual temperature range (an_temp_rng), diurnal range (drn_rng), and precipitation seasonality (pr_sea) were created using some of these climate layers generating with interpolation as mentioned above (Table2.4, Figure2.5).

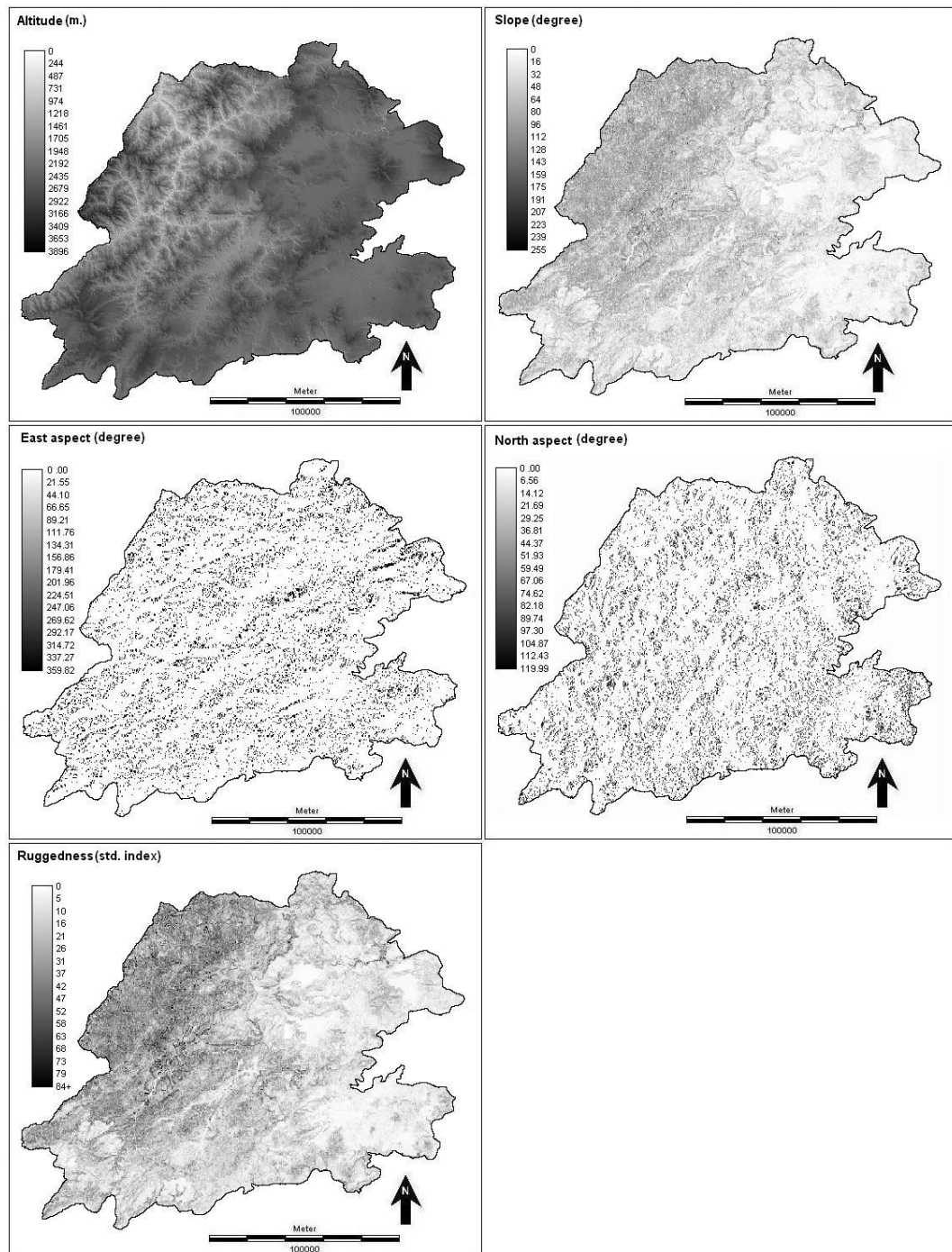


Figure 2.4 Maps showing topographic features of the study area

Table 2.4 Climate data layers

Name of Layer	Methodology	Co-variables	Software
Annual temperature	Co-kriging, Model: Gaussian, R²=0.861, p<0.001	Altitude	Gamma Design (GS+)version 9 ESRI/ Arc-GIS 9.3 Geostatistics analyst
Average maximum temperature of hottest month	Co-kriging, Model: Gaussian, R²=0.835, p<0.001	Altitude	
Average minimum temperature of coldest month	Co-kriging, Model: Gaussian, R²=0.811, p<0.001	Altitude	
Annual precipitation	Co-kriging, Model: Spherical, R²=0.942, p<0.001	Aspect	
Precipitation of hottest month	Co-kriging, Model: Spherical, R²=0.915, p<0.001	Aspect	
Precipitation of coldest month	Co-kriging, Model: Spherical, R²=0.918, p<0.001	Aspect	
Annual relative humidity	Co-kriging, Model: Spherical, R²=0.829	Aspect	
Relative humidity of coldest month	Co-kriging, Model: Spherical, R²=0.813, p<0.001	Aspect	
Relative humidity of hottest month	Co-kriging, Model: Spherical, R²=0.846, p<0.001	Aspect	
Solar radiation of hottest month	Kriging, Model: Gaussian, R²=0.911, p<0.001	-	
Solar radiation of coldest month	Kriging, Model: Gaussian, R²=0.889, p<0.001	-	
Name of Layer	Co-variables		Application
Annual temperature range	Average temperature of coldest and hottest month		Applying mathematical formulas (from bioclim)
Diurnal range	Mean monthly temperature, min temperature and max temperature		
Isothermality	Mean diurnal range, annual temperature range		
Precipitation seasonality	Precipitation of coldest and hottest month		

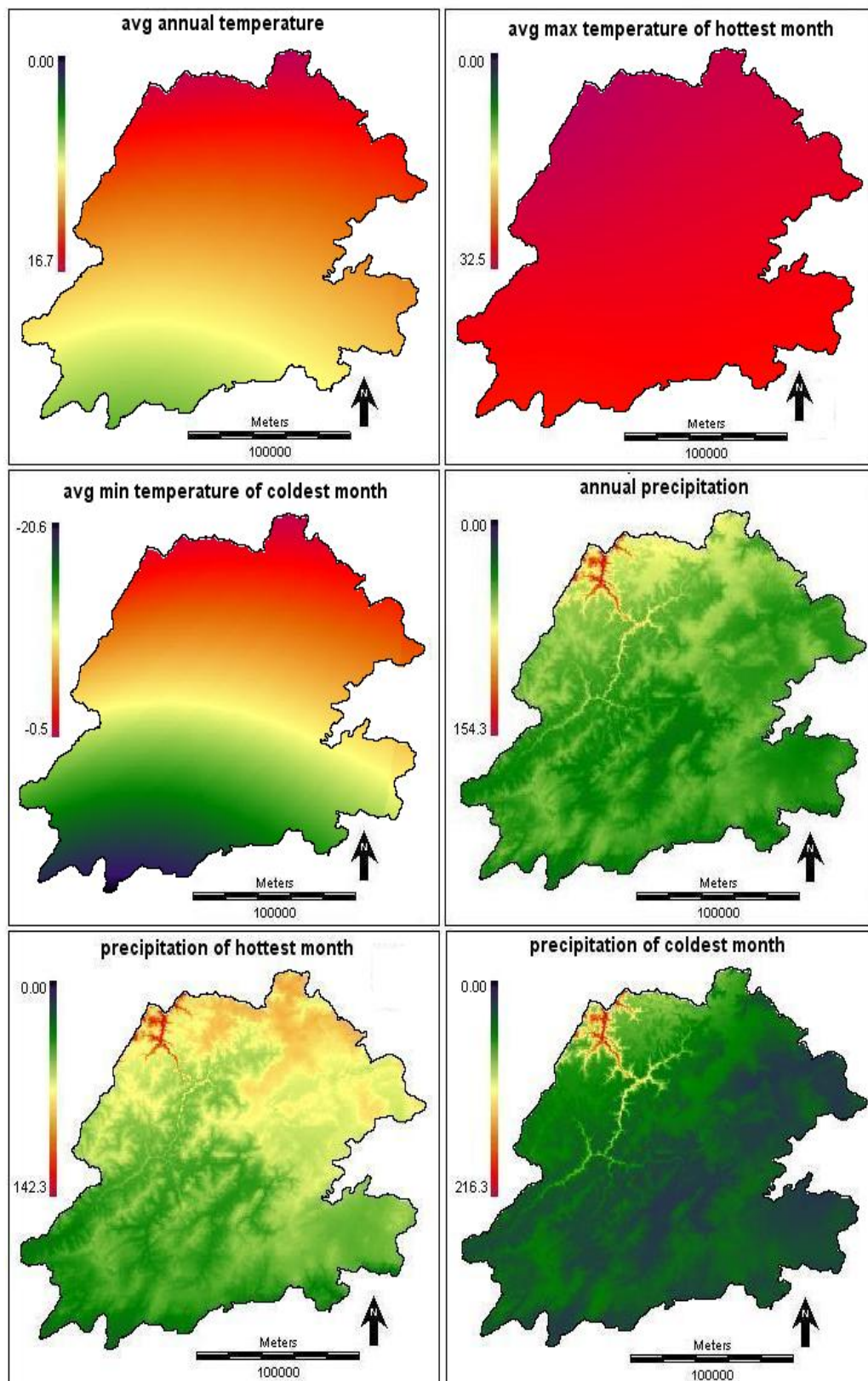


Figure 2.5 Maps showing different climate parameters of the study area

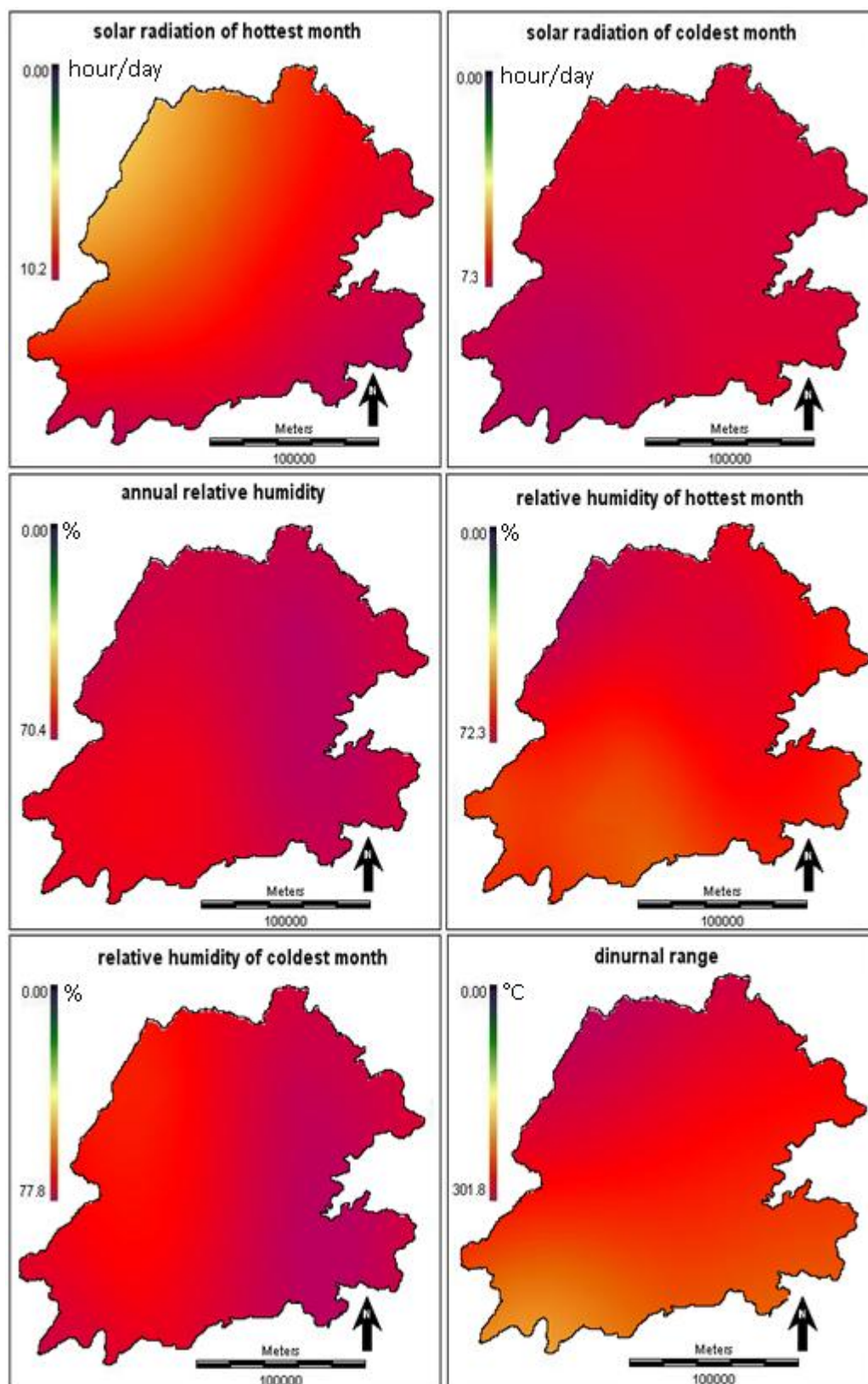


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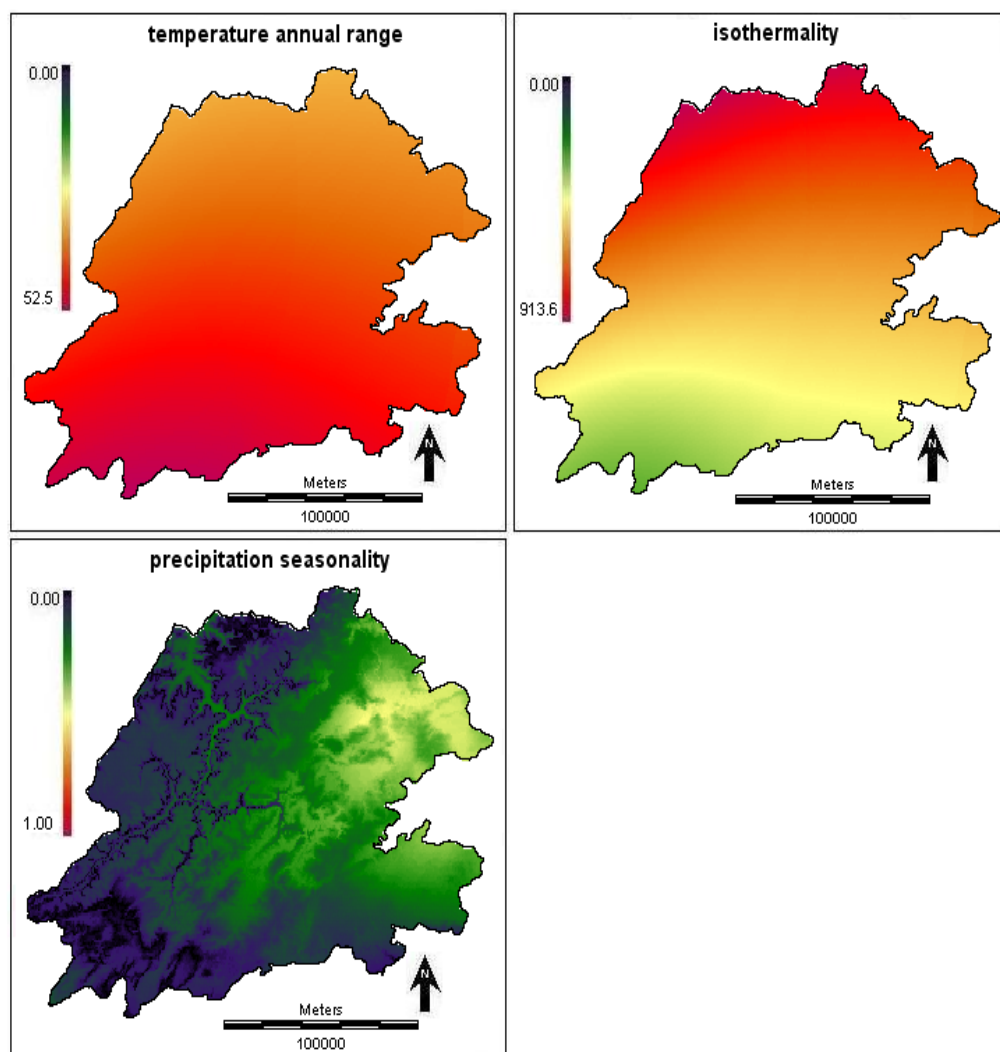


Figure 2.5 con't

2.2.2.3 Physical Data

River systems, lakes and soil type variables were used as physical environmental surrogates. Initially, these data layers were obtained from related ministry or company. Afterwards, they were edited in order to update the data and remove some digitizing errors such as silver polygons or dangling nodes. All of these editing processes were performed both in TNT-mips RS/GIS and Idrisi-Andes software. Later on, these layers were transformed as river intensity, lake shore line and soil heterogeneity layers by measuring length of rivers, length of lake shore line and heterogeneity of soil types respectively within each grid cells (Table2.5, Figure2. 6).

Table 2.5 Physical data layers

Name	Source	Editing	Transformed as	Resolution	Software
River system	Hat GIS company	Removing dangling nodes	River Intensity (calculating length of rivers)	1/25000	TNT-mips RS/GIS & Idrisi-Andes
Lake		Removing dangling nodes and sliver polygons	Lake Shore Line (calculating length of lake shore)		
Soil type	Ministry of forestry	Removing sliver polygons	Soil Heterogeneity (calculating heterogeneity of soil types)		

As expressed above after composing all environmental surrogates concerning topography, climate and physical features of the study area, all of them were overlaid with 10*10 square kilometres resolution grids by calculating their required values for each grid cells. Table that is below indicate all of these environmental variables and their summary calculations (Table 2.6).

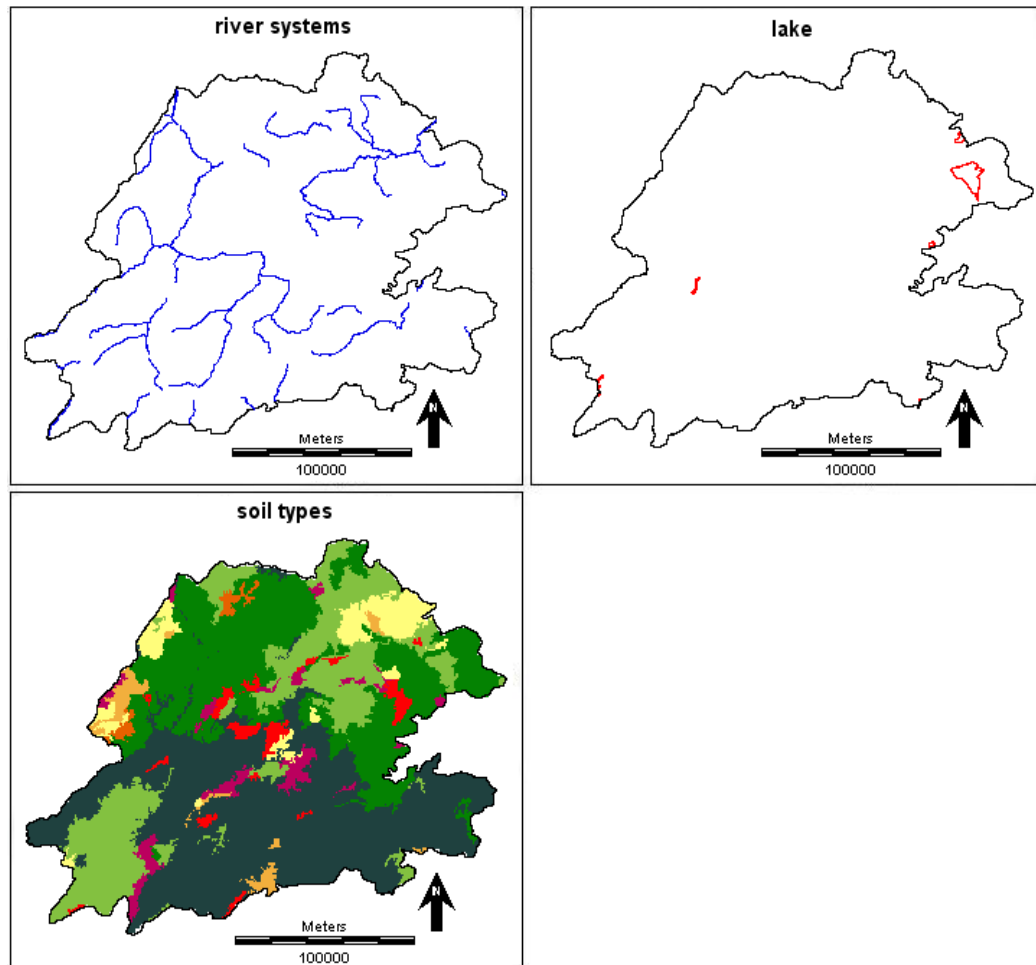


Figure 2.6 Maps showing physical features of the study area

Table 2.6 All environmental variables used for analysis

Topographic Features		
Variable Name	Definition	Source
Digital elevation model (dem)	Average altitude	USGS official web site
Ruggedness (rgd)	Standard deviation of altitude	
Slope (slp)	Average slope	
Eastern aspect (e_asp)	Average eastness	
Northern aspect (n_asp)	Average northness	
Climatic Features		
Variable Name	Definition	Source
Annual temperature (an_temp)	Average annual temperature	Turkish State Meteorological Service
Average maximum temperature of hottest month (max_temp_hm)	Average maximum temperature of July	
Average minimum temperature of coldest month (min_tmp_cm)	Average minimum temperature of January	
Annual temperature range (an_temp_rng)	Seasonality between hottest month and coldest month	
Diurnal range (drn_rng)	Mean of monthly (max temp - min temp))	
Isothermality (isotm)	(Mean diurnal range / Temperature annual range)* 100	
Annual precipitation (an_pr)	Average annual precipitation	
Precipitation seasonality (pr_sea)	Coefficient of variation	
Precipitation of hottest month (pr_hm)	Average precipitation of July	
Precipitation of coldest month (pr_cm)	Average precipitation of January	
Annual relative humidity (an_rl_hmd)	Average annual relative humidity	
Relative humidity of coldest month (rl_hmd_cm)	Average relative humidity of January	
Relative humidity of hottest month (rl_hmd_hm)	Average relative humidity of July	
Solar radiation of hottest month (rdt_hm)	Total solar radiation of July	
Solar radiation of coldest month (rdt_cm)	Total solar radiation of January	
Physical Features		
Variable Name	Definition	Source
Lake shore line (shr_ln)	Total lake shore line length	Hat GIS Company
River intensity (r_int)	Total river intensity	Hat GIS Company
Soil heterogeneity (s_htr)	Total soil heterogeneity	Ministry of agriculture

2.3 Analysis

2.3.1 Biodiversity Analysis

2.3.1.1 Identifying Priority Biodiversity Protected Areas using Marxan Software

Marxan is site selection software. That means it is used to design priority protected areas network. Early version of the software is Spexan (Spatially Explicit Anneling). It was developed for Phd Thesis of Ian Ball in 2000 supervised by Professor Hugh Possingham (Ball and Possingham 2000). Afterwards, it was modified in 1999 as Marxan that have more advanced functions (Game and Grantham 2008) and since then it has been used by protected area agencies of governments and Non-governmental organizations (NGOs) in order to design protected areas network or rearrange existing protected areas network. Also, the Ecology Centre of University of Queensland still continues its studies to develop the software (Ardron et al. 2008).

The purpose of the usage of Marxan is to determine sites providing most efficient biodiversity conservation among several numbers of potential sites by achieving user defined biodiversity targets (desired representation of biological features) for protected areas network (Ball and Possingham 2000, Possingham et al 2000). While performing site selection with marxan, one of the goals is to realize design of protected areas network at least possible cost (McDonnell et al 2002). However, generally information about actual cost of the sites can not be reached therefore size of the sites may be used instead of cost considering knowledge that the larger the protected areas network the most expensive its protection (Game and Grantham 2008). From this point of view, it can be said that representing maximum numbers of biological features inside minimum size or minimum number of protected areas is the most efficient way in order to compose protected areas network with minimum cost. Second goal of the software is to determine complementarity protected areas. That means each site in protected areas network should include different biological features in order to complete each other in term of biodiversity (Kirkpatrick 1983, Vane-Wright et al. 1991, Pressey et al. 1993). This provides composing a comprehensive protected areas network containing

every biodiversity features of area of interest (Noss 1990). Shortly, aim is to identify minimum number of complementarity sites while arranging protected areas network. To achieve all these, marxan uses heuristic algorithms. These algorithms provide a number of near optimal solutions quickly (McDonnell et al 2002, Cabeza 2001, Game and Grantham 2008). Among these, simulated annealing that is more powerful than other heuristic solutions of marxan with regard to find closer solutions to the optimal solutions was used to identify priority protected sites of the study area. This algorithm uses both representing maximum biological features within minimum number of sites and complementarity principles while detecting protected areas. Another important point is to design a compact network by reducing the edge to area ratio because compactness has many advantages like less management cost, more viable populations and ecosystem functions (Wilson et al. 2006). This was implemented by using Boundary Length Modifier (BLM) tool of marxan which allow conservation planners to design a compact protected areas network.

As running the marxan algorithm, a number of alternative solutions are determined as priority protected areas network. In order to select best protected area network among them, software calculates a mathematical objective function for each solution set. Objective function is the total of the cost of the selected protected areas set and penalties that is the value for not achieving user defined biodiversity target. Shortly, objective function indicates the suitability of the determined protected areas network and lower objective function means the most desirable protected areas network (Game and Grantham 2008). That is to say, algorithm tries to keep objective function in minimum. Procedure works similarly the heating and cooling principles of materials. Temperature increase during detecting sites indicates negative changes in network while decrease means positive changes and is accepted as efficient design for protected area network. When running the software, complementarity based simulated annealing algorithm performs user defined number of iterations (1000000 for the thesis). During each iteration, a site is selected randomly among all sites and added in the network. Afterwards, change in the objective function value of the network is evaluated. Moreover, this information is merged with temperature decrease or increase information and then all of these results are compared with the results of other randomly selected sites. And, depending on this comparison, the site may be added or removed from the network. With this procedure, previously defined number of solution sets is produced as protected areas network. After completing process, software decides

the most efficient protected area network for the area of interest by assessing their objective functions (Ardron et al. 2008, Game and Grantham 2008).

Formula of objective function in Marxan;

$$\underbrace{\sum_{PU_i} Cost}_{\textcircled{1}} + \underbrace{BLM \sum_{PU_i} Boundary}_{\textcircled{3}} + \underbrace{\sum_{Cons Value} SPF \times Penalty}_{\textcircled{2}} + \underbrace{CostThresholdPenalty(t)}_{\textcircled{4}}$$

1. The total cost of the reserve network (required)
2. The penalty for not adequately representing conservation features (required)
3. The total reserve boundary length, multiplied by a modifier (optional)
4. The penalty for exceeding a preset cost threshold

Marxan User Manual

In order to perform priority biodiversity protected area selection of the study area with marxan, required five input data files were prepared firstly. These are input parameter file, conservation feature file, planning unit file, planning unit versus conservation feature file and boundary length file.

Input parameter file; this file includes all parameter settings and control how the selected algorithm works. In brief, it is the management file of marxan. First of all, using this parameter file all parameters that are needed to run the marxan was adjusted. 20 repeated runs with 1000000 iterations were performed using simulated annealing algorithm as indicated above. Also, normal iterative improvement were applied after simulated annealing algorithm in order to confirm the selected solution is the best one for representing biological features of the study area. And as expressing previously, BLM was implemented to design a compact protected areas network.

Conservation feature file; it can be also called as species file. It contains all species information of taxa like species name, conservation targets or representation target and penalty factor. Species file used during the process includes 11,932 records of 402 species belonging 6 different taxonomic groups, their names, conservation targets and penalties.

Planning unit file; it is grid information file and includes grid id numbers, UTM 37 east and north coordinates and costs (area of grids) of each of 336 UTM grids.

Planning unit versus conservation feature file; this file contain species distribution information for each grids. The file that was used in the analysis demonstrates distribution of 402 species according to each of 336 UTM grids.

After doing all required parameter settings and preparing input data files, complementarity based simulated annealing algorithm was applied to identify priority protected areas. Software produced 20 solution sets and determined the best solution among them as priority protected areas network of the study area by comparing objective functions. In the next step, measurements that are explained later were calculated to compare results of complementarity based selections with the results of environmental diversity analysis and simulated random null model and also to demonstrate the surrogate performance of each taxonomic group.

2.3.1.2 Detecting Priority Biodiversity Protected Areas for Different Taxa to Test Efficiency of Them as Surrogate

In the second part, effectiveness of different taxonomic groups as surrogates in conservation area planning and cross-taxon congruence among taxonomic groups used for the thesis were investigated. Again Marxan site selection software was used to perform analyses. Firstly, different combination taxonomic group sets were determined and prepared. In total, 12 different combination sets that are shown in below were composed (Reyers et. al 2000, Warman et. al 2004, Tushabe et. al 2006), (Table 2.7). Afterwards, conservation feature and conservation feature versus planning unit files were reorganized as these new combination sets. Any changes were not done on the planning unit and input parameter files. Later, complementarity based simulated annealing algorithm were run for these combinations. Again, 20 solution sets were produced for each of these taxonomic group combinations as doing before while detecting priority protected areas network of the study area. And then the best one among these 20 solution sets were determined by software and described as the priority protected areas of the related run. Afterwards, selected best result of each taxonomic group combinations were mapped using IDRISI-Andes GIS software. One of the features of obtained results, these include optimum number of protected areas for each combination

sets. Although, this approach is an appropriate way to evaluate the surrogate performance of taxa, it is not sufficient in order to test the ability of taxon or taxa for representing overall biodiversity of the study area and to decide efficient surrogates of the study. Therefore, another approach was also applied to investigate the surrogate performance of taxa once more and also to test efficiency of taxa is a chance or not. In this stage, Marxan was rerun to detect equal number of protected areas for each combination sets (Howard et. al 1998, Jaarsveld 1998, Lund and Rahbek 2002). To do this, appropriate threshold cost values were determined for each combination in order to not exceed this value while detecting protected areas. By this way, 19 equal number of protected areas were determined for each combination sets. 19 sites were detected for each combination since it the optimum number of priority protected areas of taxonomic group combination including all taxa as surrogate. This means, detecting less or more site than 19 number of site as protected areas can lead to inefficiencies while representing biodiversity of the area. Therefore, selecting optimum number of site as priority protected areas is very reasonable to achieve efficient conservation for biodiversity of the area. In the next step, required measurements that are explained later in detail were calculated in order to compare results of each run and evaluate the effectiveness and performance of taxonomic groups as surrogates.

Table 2.7 Table showing species and record distributions of each taxonomic group combinations

Taxonomic Group Combinations			
Only One Taxon			
Group no	Taxon	Total # of species	Total # of records
1. group	endemic and non-endemic highly threatened plant	54 species	308 records
2. group	globally important amphibian and reptile	6 species	376 records
3. group	butterfly	238 species	2833 records
4. group	breeding bird	42 species	1572 records
5. group	ecological communities	39 communities	5603 records
6. group	large mammal	10 species	1240 records
Two Taxa			
Group no	Taxon	Total # of species	Total # of records
7. group	Butterfly + ecological communities	238 sp + 39 communities	8436 records
8. group	breeding bird+ ecological communities	42 sp + 39 communities	7175 records
9. group	endemic and non-endemic highly threatened plant + ecological communities	54 sp + 39 communities	5911 records
10. group	Butterfly + endemic and non-endemic highly threatened plant	251 sp + 54 sp	3141 records
Four Taxa			
Group no	Taxon	Total # of species	Total # of records
11. group	globally important amphibian and reptile + breeding bird + butterfly + large mammal	6 sp + 42 sp+ 238 sp + 10 sp	6021 records
All Taxa			
Group no	Taxon	Total # of species	Total # of records
12. group	endemic and non-endemic highly threatened plant + globally important amphibian and reptile + butterfly + breeding bird + ecological communities + large mammal	54 sp + 6 sp + 238 sp + 42 sp + 39 communities + 10 sp	11932 records

2.3.2 Environmental Diversity Analysis

In the ED part, Analyses were carried out in order to detect ED in other words, P median sites. These analyses were performed within 4 different steps. First of all, correlation analysis was applied and variance influence factors (VIF) were calculated in order to prevent bias in the rest of the analyses. Secondly, Geographically Weighted Regression (GWR) was implemented to identify environmental variables indicating significant spatial variation for each taxonomic

group. Subsequently, to investigate variation pattern of the remaining environmental variables, principle component analysis (PCA) was applied and then using results of it, a dissimilarity matrix was produced. Lastly, p-median algorithm was run in order to determine environmental diversity sites by using dissimilarity matrix as an input.

2.3.2.1 Correlations and Variance Influence Factors (VIF)

Before starting to perform geographically weighted regression analysis, a preliminary global correlation analysis was applied in order to detect least correlated environmental variables since implementing such a preliminary analysis would prevent multicollinearity among predictor variables. Multicollinearity is one of the assumptions of regression models and violation of it might cause less precise parameter estimates, high standard error in parameter coefficients and parameter redundancies that result in over fitting in regression analysis (Graham 2003, Farrar and Glauber 2010, Haitovsky 2010). Additionally, unexpected spatial variation which may lead to the unreliable significance level, among variable coefficients can be seen. Due to these undesirable effects in regression analysis, multicollinearity should be detected and remedied (<http://webhelp.esri.com>). Beside of correlation analysis, variance influence factors (VIF) were also quantified. It is another measurement to examine multicollinearity among variables and it is used in order to figure out how much the variance of estimated regression coefficients is increased because of collinearity. Both of these statistical evaluations were done by using 23 different environmental variables before geographically weighted regression analysis and highly correlated variables and variables that have high VIF values were removed among the environmental variables in order to obtain valid results for the rest of the analyses.

2.3.2.2 Geographically Weighted Regression (GWR)

Geographically Weighted Regression is a statistical regression model and it is based on ordinary least square principle as all other regression types. Difference of GWR from other regression types, it concentrates on spatial data analysis. This means that it is a local regression and models local relations. That is, it is used to estimate local parameters not global parameters.

GWR model is expressed as;

$$y_i = \beta_0(u,v) + \beta_1(u,v) x_1 + \dots + \beta_n(u,v) x_n + \varepsilon$$

Where y_i is the dependent variables, x_1 to x_n are independent variables (environmental variables), β_0 is the intercept, β_1 to β_n are estimated parameter coefficients, ε is random error term and (u,v) s are the locations at which data are collected. This provides to do separate estimation for each data point while in normal regression types; a global average estimation is done for all space (Fotheringham et al 2002). Shortly, GWR allows investigating spatial heterogeneity of the area by including the coordinate information of data points in the analysis (Anselin 1988, Anselin and Griffith 1988, Brunsdon et al 1996, Fotheringham et al 2000 and 2002). This spatial heterogeneity is called as spatial non stationarity and defined as the variation of processes or relations over space (Brunsdon et al 1996, Fotheringham et al 2000 and 2002). Another spatial effect that is considered in GWR model is spatial autocorrelation (Anselin 1988, Shi and Zhang 2003, Shi et al 2006). Spatial autocorrelation is the situation of closer points is more similar than points that are further (Shi et al 2006, Osborne et al 2007) and this relation among points is incorporated in the analysis by defining a kernel bandwidth while predicting local model parameters. Kernel bandwidth is a distance in which all neighbour points have effect on the estimation of model parameters. In other words, model parameters are predicted by weighting values of previously defined number of neighbour data (Fotheringham et al 2002, Shi et al 2006 and Osborne et al 2007).

GWR not only provides to consider both of these mentioned spatial effects while modelling real life situations, but also provides to detect local estimators demonstrating significant spatial variation. This is achieved by performing Monte Carlo simulation while running GWR analysis. In this simulation, the coordinates of observations are randomly permuted against variables for a given number of times. Thus, n values of variance for the coefficients of variables that are used as an experimental distribution are obtained. Finally, this list including n values of variance are compared with the actual value of the variance to acquire an experimental significance level (Fotheringham et al 2002). This approach allows detecting significance of the variability of the coefficients. In other words, it provides to determine non-stationary variables. Therefore using this approach, environmental variables indicating significant spatial variation were detected for

each taxonomic group respectively. GWR.3 software was used to conduct all required analyses. First of all, desired files were organized and settings were done. As a GWR model, Gaussian was selected since dependent variables (taxonomic groups) are in the density form and a suitable fixed type kernel was used as kernel bandwidth because data points are regularly distributed across the study area. (Paez et al. 2002a, 2002b and Fotheringham et al. 2002). Afterwards GWR analyses were run by determining each taxon as dependent variable and all environmental variables as independent variables. Eventually, significant environmental variables of each taxon were identified and these were defined as environmental surrogates in order to use subsequent parts.

2.3.2.3 Principle Component Analysis (PCA) & Dissimilarity Matrix

Principle component analysis is an eigenvector based ordination analysis and mainly used to reduce the number of highly correlated variables or to explore variation pattern of the data. In this study, it was used to demonstrate and summarize the variation of non-stationary environmental variables obtained as results of GWR into PCA axes. In this way, variation pattern of environmental variables for each of the 336 grid cells of the area was investigated. Afterwards, dissimilarity matrix including pairwise distances of grids was produced using variation scores of PCA axes. This matrix indicates similarities between each grid pairs in terms of environmental variation (Araujo et al. 2001, Bonn and Gaston 2005). This matrix is a 336 by 336 matrix and was composed in PAST software using Bray-Curtis type dissimilarity measure (Faith et al 1987, Belbin 1993, Faith et al. 2004). Later, these distance values were used to determine ED areas by applying P-median algorithm.

2.3.2.4 Performing ED model (P median Algorithm) to Detect Environmental Diversity (ED) areas

The purpose of the ED model is to sample variation of the environmental pattern for measuring environmental diversity. And desired thing is to access maximum variation within sampling units in order to increase environmental diversity since it is assumed that the greater the environmental diversity, the greater the species diversity (Faith and Walker 1996a, Araujo 2001, 2003, 2004, Faith 2003, Faith et.

al. 2004). Another important point, ED model covers the complementarity principle (Williams 2001). That is, if pattern variation is high within the selected sites, this means that there are different compositions of environments and this results in many different species as expected in complementarity principle. To achieve these objectives of ED model, p median algorithm is one of the most widely used approach. P median algorithm is a location allocation algorithm and it is used for any type of location problems like using to detect environmental (ED) diversity sites (Church and Sorenson 1996, Church 2002). There are two types of p median algorithms, optimum and heuristic. Heuristic gives sub-optimal results. In this study, a heuristic greedy algorithm was used. The algorithm applied for the analysis used by Faith and Walker (1996a, 1996b), Araujo et al. (2003), Hortal and Lobo (2005) and Hortal et al. (2009) in their studies. This algorithm selects the p areas one by one. At each selection step, algorithm searches the area and defines appropriate p areas sequentially among m candidate sites. When passing the next step, it only takes into account the remaining m candidate sites (Hortal et al. 2009).

When operating p-median algorithm, distance matrix that had been calculated in the previous step was used as input file and while the algorithm detects the ED areas, it selects the areas so as to minimize the sum of the distance of determined sites because this is equal to increasing variation of environmental pattern, in other words equal to maximizing environmental diversity within determined p sites.

In each area selection step, p median algorithm calculates p- median scores for each of the candidate sites (m_i). This score is the sum of dissimilarities between a candidate site and remaining candidate sites. And if this score is minimum for a candidate site, then it is added among p selected sites and dropped among the candidate sites. Afterwards, matrix was reorganized in order to calculate p-median score again for remaining candidate sites. This process repeats until determined number of sites included in the p selection set.

The p-median score for each candidate sites was calculated using the following formula (Faith and Walker 1996a, 1996b, Araujo et al. 2003, Hortal and Lobo 2005 and Hortal et al. 2009);

$$P \text{ median} = \sum_{i=1}^{i=m} d_{m,r}$$

$$d_{m,r} = \min \text{dist}(m, r+m_i)$$

Where;

m is the number of candidate sites (for this study, it is 336).

m_i is the i'th site.

d_{m,r} is the minimum distance between m_i candidate site and the remaining non selected candidate sites.

In this study, 19 ED sites were identified with p-median algorithm because it was the optimum number of sites for the complementarity based area selection. And to detect equal number of sites for both, biodiversity and environmental analysis, is important to do meaningful comparison during further assessments. After implementing site selection, effectiveness values of the ED sites explained in detail later were calculated.

2.3.3 Simulated Random Null Model

Random null model was set to evaluate the performance of both complementarity based priority protected areas and ED areas approaches with regard to biodiversity conservation and to test efficiency of these approaches whether is a chance or not (Araujo 2001, 2003) and also to investigate the cross-taxon relations among taxa of the study. Initially, optimum number of random selection for the random null model was determined. Optimum number of random selection is the point where efficiency of random selections is not change anymore. In order to detect this number, different number of random selections that begins from 200 and increasingly continue till 5000 were performed. Each of these random selection sets includes 19 sites since random null model should contain equal number of sites with complementarity based priority protected areas and ED areas approaches in order to do meaningful evaluations about their performance. Afterwards, efficiency values were calculated as average representation value for each random selection set to decide which random selection set is the optimum number for the random null model. Calculations of these values are explained later in subsequent parts.

2.4 Statistical Analysis and Measurements to Evaluate performance of both Biodiversity and Environmental Diversity Analyses

As expressed above parts, required effectiveness calculations were done after performing analysis. These calculations can be gathered into two main titles. In the first part, calculations were applied to assess the success of each taxonomic categories as surrogates and to indicate relations (cross-taxon congruence) among taxonomic groups with regard to different measurements like richness and complementarity. And in the second part, effectiveness values were calculated in order to compare performance of complementarity based area selection and ED based area selection in terms of biodiversity conservation. However, before doing these calculations, following the same procedure, appropriate number of random selection were determined in order to describe success of these methodologies are a chance or not.

2.4.1 Identifying optimum number of random selections for simulated random null model

In order to determine optimum number random selections, efficiency of each run was calculated as average representation. Average representation is the average number of species for each run. This was calculated using the following formula.

$$\text{Average representation} = \frac{\sum_{i=1}^j (19 \times \text{total number of species in each site})}{\text{number of random selection}}$$

Where; j is the number of random selection

After calculating these values for each run, curve was prepared to identify optimum number for random null model. This curve was plotted as average representation versus number of random selection and the point where the average representation have not showed any increase or decrease was determined as optimum number of random null model.

2.4.2 Measuring performance of each taxonomic group and taxonomic group combinations as surrogates

As explained in the analysis part, to evaluate the surrogate performance of taxon or taxa, combination sets were prepared and priority protected areas were identified for these sets. Afterwards, in order to test their efficiencies, different measurements were applied. Firstly, percent representations of each combination sets were calculated. **Percent representation** is percentage of the total number of species of related taxonomic groups within determined priority protected areas network. Although it is a quite simple calculation, it provides to evaluate surrogate efficiency of each taxon or taxa and also informs about how well surrogate taxon or taxa can represent taxonomic groups. Moreover considering result of percent representation calculations, it can be decided that which taxon or taxa can be used instead of others. Nevertheless, it is not a sufficient way in order to decide which taxon or taxa is the most powerful with respect to represent all taxonomic groups of the study area and to compare performance of each combination set with each other and random null model. Therefore, cumulative representations were calculated using results of priority protected area selections that include equal number of sites (19 sites) for each combination sets and species accumulation curves were produced for each set. **Cumulative representation** is the cumulative number of species inside designated priority protected areas network of each combination set (Howard et. al 1998, Reyers et al 2000, Lund and Rahbek 2002, Beger et al 2003). With cumulative representation, it can be demonstrated that which taxon or taxa is more efficient for representing taxonomic groups of the area than the others.

Except these two measurement approaches, congruence among taxonomic groups was also investigated as indicated previously because this information is substantially valuable in order to evaluate efficiency of each taxon as surrogate. First of all, Jaccard coefficient was calculated as pairwise among taxonomic groups. It is a similarity coefficient and was used to measure percentage of overlapped sites of priority protected areas network of each taxon. Through this, similarity between taxa can be revealed. Following formula was used to calculate Jaccard values (Howard et. al 1998, Warman et. Al 2004)

Jaccard coefficient = [number of shared sites/ (number of additional sites selected for taxon A+ number of additional sites selected for taxon B)] *100

Furthermore in order to lead while assessing efficiency of each taxon as surrogate, cross taxon congruence in terms of species richness was examined. For this, species richness were calculated firstly for each taxon as the total number of species in each site and then using spearman rank correlation coefficient, cross taxon congruence in species richness were tested (Howard et. al 1998, Lund and Rahbek 2002, Warman et. Al 2004, Sue et. al 2004,). Finally, Monte Carlo simulation with 1000 permutations was applied to demonstrate the significance level of the correlation results.

Ultimately, complementarity scores were calculated using Colwell and Coddington's formula (1994) to investigate the cross taxon congruence in complementarity (Colwell and Coddington 1994, Howard et. al 1998, jaarsveld et. al 1998, Lund and Rahbek 2002). Complementarity score is another perspective for indicating surrogate efficiency of taxon or taxa. The formula used during calculations measure the compositional distinctiveness of taxon within two sites and it is equal to the complementarity concept. By this means success of taxon or taxa with respect to complementarity can be evaluated and compared.

Formula is; $C_{ij} = U_{ij} / S_{ij}$

$$U_{ij} = S_i + S_j - 2V_{ij}$$

$$S_{ij} = S_i + S_j - V_{ij}$$

Where; S_i = Total species richness of site i.

S_j = Total species richness of site j.

V_{ij} = Common species of site i and j

Applying the formula, pairwise complementarity scores of grids were calculated and matrices for each taxon including these scores were produced. Afterwards, mantel correlation test was applied to demonstrate the congruence of complementarity. Mantel test evaluates the null hypothesis that assumes no

relationship between two matrices. Significance test after mantel test was performed again with 1000 Monte Carlo simulation (Manly 1997, Oliver et al 1998).

2.4.3 Comparing Complementarity based priority protected areas, environmental diversity areas and random null model

While performing comparisons among complementarity based biodiversity areas, ED areas and random null model in order to evaluate their efficiencies, three different measurements were followed. Firstly, percent representations were calculated for each approach as the percentage of total number of species of each taxon in selected sites and then, a graph was plotted in order to indicate and compare performance of them in respect to representing each taxon. Secondly, Cumulative representation that is the cumulative number of species in determined sites were calculated separately for complementarity based priority protected areas, environmental diversity areas and random null model. These representation values were then used to produce accumulation curves. In this way, efficiency of approaches can be assessed in terms of biodiversity conservation. And finally, complementarity scores for mentioned three approaches were calculated. Complementarity score is the sum of unique species occurring in one or the other two sites is divided by the combined total of species in the same sites. It is calculated in order to demonstrate which approaches is the most powerful in terms of biodiversity complementarity. These scores also were expressed as percentage complementarity to provide a general sight during comparison.

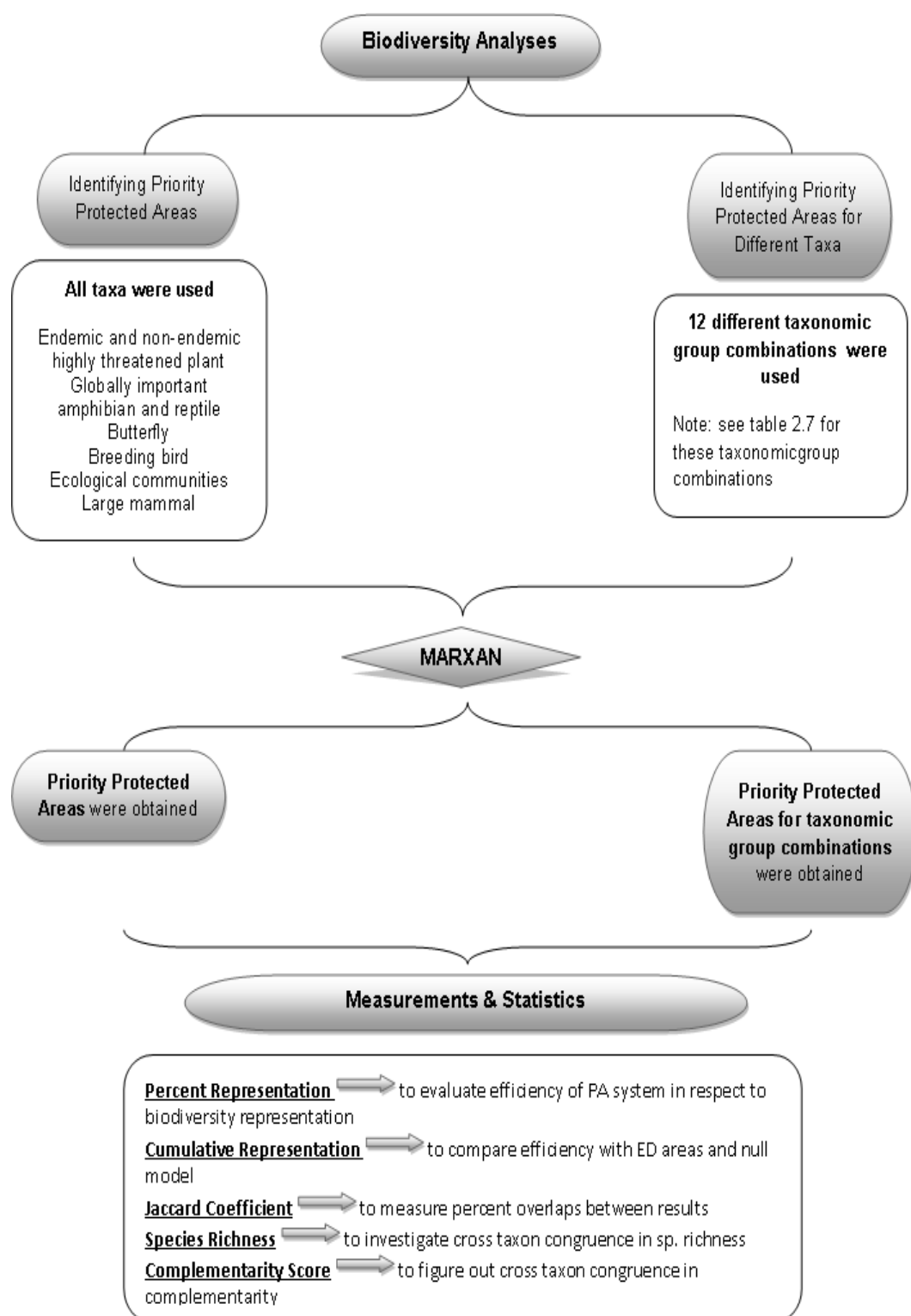


Figure 2.7 Schematic presentation of all biodiversity analyses together with related measurements and statistics

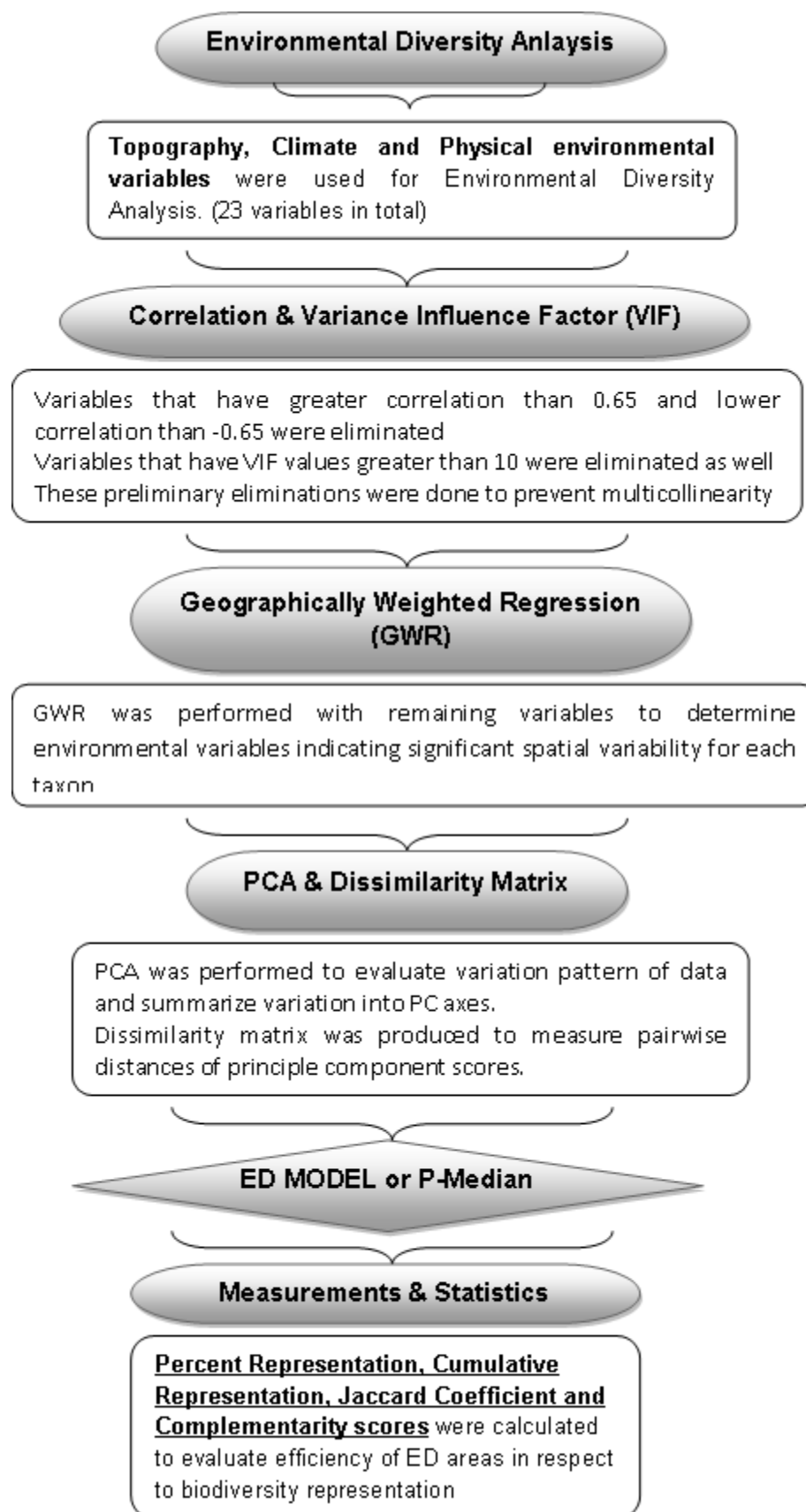


Figure 2.8 Schematic presentation of environmental diversity analysis together with related measurements and statistics

CHAPTER 3

RESULTS AND DISCUSSION

3.1 Biodiversity Analysis

3.1.1 Priority Protected Areas of the Study Area Detected by Using Marxan Software

Priority protected areas of the study area was determined by using marxan site selection software. As indicated before in methodology part, 20 solution sets were produced and the best one among them was selected as priority protected sites of the area. Table that is below shows results of each of these 20 solution sets with their values required to evaluate them (Table 3.1). And as it is seen from table, run 2 that is highlighted with grey colour was determined as the best solution by software since it has the lowest score value which is the objective function of the related run. Moreover, this run has the lowest cost, lowest boundary length and lowest penalty factor. Beside these, it is also conspicuous with its missing value because it is lower than the others. This value indicates number of species that can not be included in the determined protected area network. And lower missing values mean greater number of conserved species and communities within the protected areas network. Due to these reasons and assessments, run 2 was detected as the best solution set among other runs and described as the priority protected areas network of the study area.

Table 3.1 Table showing results of 20 solution sets of Marxan software

Run no.	Score	Cost	Planning Units	Boundary Length	Penalty	Shortfall	Missing Values
1	15048.67	1737.99	19	582	12728.68	65.2	68
2	14696.07	1700.83	19	531	12464.24	68.8	63
3	15867.65	1720.03	19	610	13537.62	65.8	70
4	15016.51	1710.49	19	595	12711.02	58.8	65
5	15672.26	1730.78	18	607	13334.48	61.5	73
6	15860.49	1725.62	19	597	13537.87	62.8	72
7	15201.03	1756.83	19	605	12839.29	57.5	67
8	15078.3	1723.92	18	591	12763.38	58.5	70
9	15643.75	1718.26	19	587	13338.49	61.8	67
10	15317.4	1743.78	19	611	12962.62	58.5	71
11	15722.6	1763.22	19	672	13287.38	63.5	67
12	14881.64	1734.71	19	568	12578.93	56.8	72
13	15674.04	1746.92	19	593	13334.12	65.8	68
14	15690.04	1724.78	18	598	13367.26	67.5	71
15	14958.66	1765.38	19	546	12647.28	65.6	68
16	15783.66	1738.27	19	578	13467.39	67.6	70
17	15263.59	1729.32	19	567	12967.27	58.8	71
18	16164.34	1730.78	19	611	13822.56	65.5	67
19	15183.05	1727.43	19	598	12857.62	67.2	72
20	15564.25	1711.68	18	568	13284.57	65.8	71

Map that is below shows distributions and locations of sites of this priority protected areas network (Figure 3.1). When this map was investigated, it was seen that sites are generally distributed in the most valuable and important biodiversity parts of the study area. Especially, sites that are in northwest part of the area and highlighted with red circle occupy the most attractive part of area in respect to biodiversity features. This section of the study area includes deep Çoruh valley and high Kaçkar mountain ranges. Because of these distinct topographic structures, this part has substantially rich and diverse biodiversity together with many endemic and relict organisms. This part also includes several legally established protected areas like Kaçkar Mountains National Park (NP), Hatila Valley NP, Yusufeli Çoruh Valley Wildlife Development and Reserve Area and Vercenik Çat Wildlife Development and Reserve Area. Second section that is highlighted with green colour is around Ispir and Erzurum. And it is particularly prominent with its butterfly species since this part is dominated by high step-alpine meadows and such vegetation types compose very appropriate habitats for butterfly species. Other sites, in blue circle, are in the portion of the area that is important for bird species since these three

sites are very close to the lake Aktaş and Çıldır and also river Kura. And it is known that these lakes provide home for many bird colonies.

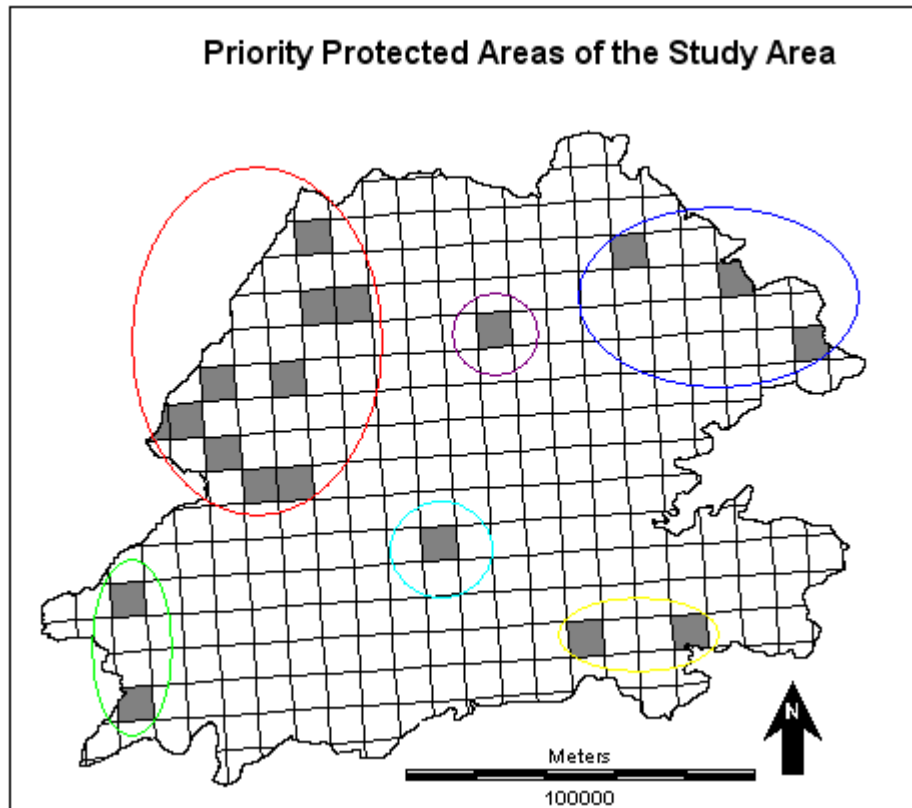


Figure 3.1 Map showing distributions and locations of priority protected areas network

Another site which is in the middle part of the area and highlighted with purple circle is around the southwest edge of the Yalnızçam Mountains. This mountain range is one of the important plant areas (IPA) of Turkey. It was declared as a result of studies and collaboration of World Wildlife Fund (WWF), Flora and Fauna international and pharmacy faculty of Istanbul University because high alpine and subalpine meadows including rich and diverse plant species cover the mountains and also several rare, endemic and threatened plant species inhabit in this part of the area. Another two sites that are in south-eastern part and signed with yellow are characterized by high and broad Kars plateaus. These two sites are dominated with pastures and coniferous forest. The site that is on the left hand side of the yellow circle also includes some part of the Sarıkamış NP. Although, this national park was established mainly because of its historical importance, its uninterrupted scotch pine (*Pinus sylvestris*) forest is very impressive and important in respect to harbouring many different species. Also, these scotch pine forests are the forests where Scotch pine reaches the highest altitude in all Europe. Furthermore, this part

of the area hosts many large mammal, bird and reptile species. There is also one more site which is in lower middle part of the study area. Although this site selected due to its endemic and threatened plant species, the site also covers the some part of Oltu wildlife development and reserve area and this protected area host many wildlife species like ibex goat (mountain goat).

Moreover, efficiency of the determined priority protected areas in terms of representing all taxonomic groups used during the analysis was evaluated. This was implemented by calculating percent representations of each taxonomic group and plotting a graph that is percent representation versus taxonomic groups. As the plotted graph shows, most of the percent representations are around 90 % and/or greater than 90 % except endemic and non-endemic highly threatened plant species (Figure 3.2). Although, plant taxa has the lowest percent representation, its representation is quite enough when considering such species have too narrow distributions and capturing them within the determined priority protected areas network is too difficult. Therefore, it can be said that determined priority protected areas network by marxan site selection software is sufficiently efficient in order to represent taxonomic groups of the study.

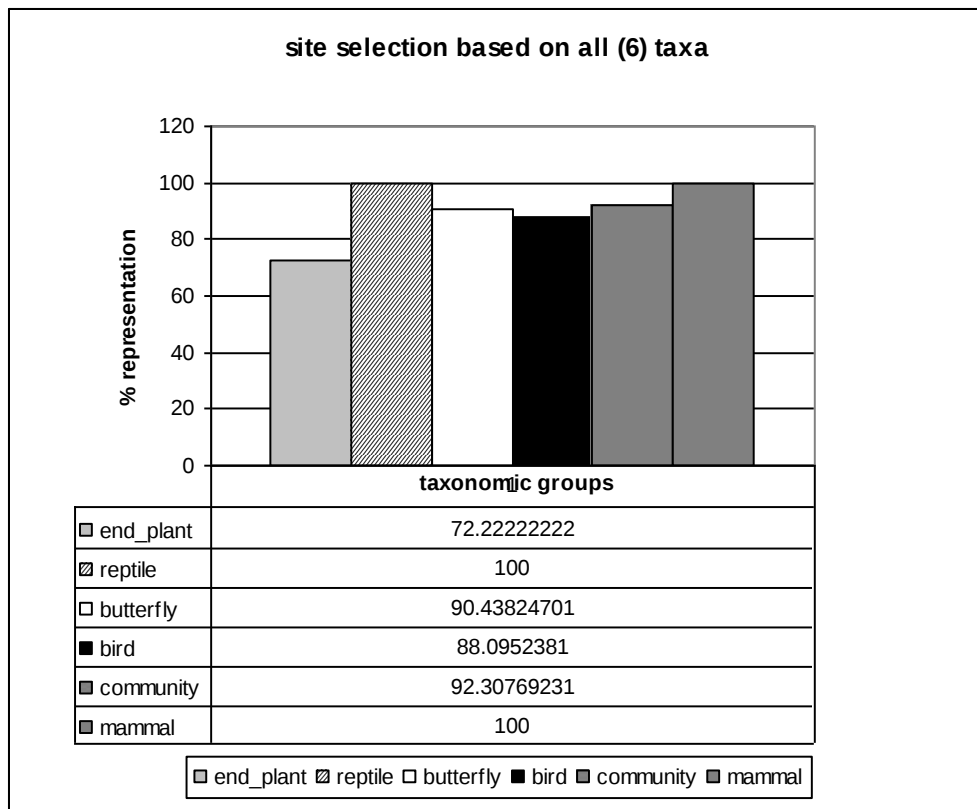


Figure 3.2 Graph showing percent representations of each taxonomic group

As it is seen, evaluations about marxan results were done with three steps. Firstly, values that were obtained from marxan were qualified in order to demonstrate and determine the most efficient priority protected areas network of the study area. Afterwards, distributions and locations of sites of the priority protected areas network were assessed according to real field observations and literature knowledge. Lastly, results were evaluated with regard to representing taxonomic groups of the study. Consequently, as far as all of these results and evaluations indicate, it can be said that complementarity based site selection algorithm of marxan gives very much consistent site selection results with reality. In order to deduce this conclusion, not only numerical results of analysis, distributions of sites and percent representation values were investigated and evaluated but also overlap between currently existing protected areas and determined priority protected areas network of the study area were examined (Figure 3.3) (Appendix C).

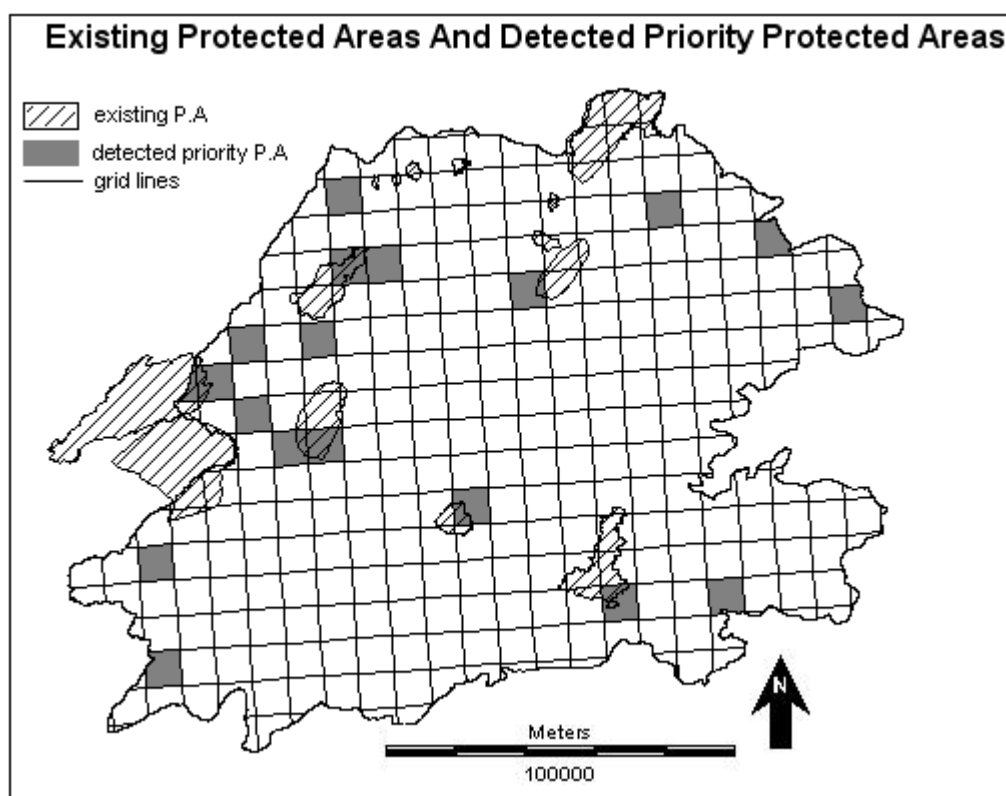


Figure 3.3 Map showing overlap between existing P.A and detected priority P.A

As above map indicates, there are many overlap between existing protected areas of the study site and priority protected areas network detected by using marxan. This is evidence both for efficiency of complementarity based site selection algorithm and adequacy and accuracy of biodiversity database used during marxan site selection analysis. Consequently, based on similarities among existing protected areas and detected priority protected areas, it cannot be a mistake to define this selected network as priority protected areas network of the area within the scope of this thesis.

3.1.2 Efficiency of Each Taxonomic Group as Surrogate

As indicated in methodology part, 12 different taxonomic group combinations were prepared (Table 2.7) and marxan was run to detect optimum number of priority protected areas for each of these combinations. After, software detected the best solution for each taxonomic group combination among their 20 solution sets, these

best solutions were described as the priority protected areas of the related run and percent representation values were calculated for them as explained in methodology part in order to investigate surrogate efficiency of taxon or taxa and determine the most efficient taxonomic group combination as surrogate. The 20 solution sets that were obtained from Marxan for each of the taxonomic group combinations can be seen in appendix D (Appendix D1-12). Afterwards, maps and graphs that are in below prepared for the priority protected areas of the taxonomic group combinations. While these maps show distribution of priority protected areas of each combination, graphs demonstrate the percent representation of the taxonomic group combinations for each taxon (Figure 3.4 and Figure 3.5).

First maps and graphs are for taxonomic group combinations including only one taxonomic group as surrogate. These taxa are endemic and non-endemic highly threatened plant, globally important amphibian and reptile, butterfly, breeding bird, ecological communities and large mammal (Figure 3.4). When distributions of priority protected areas of these taxa are investigated, it is clearly distinguished that their distributions and locations are not very much compatible with the distributions of priority protected areas network of the study area (Figure 3.1 and Figure 3.5 F). Even though this evaluation is not directly related with the surrogate efficiency of taxonomic group combinations, it gives some idea about success of these taxa as surrogate. Nevertheless, in order to do more formal qualification about their compatibility, also overlap among priority protected areas of each taxon demonstrated in Figure 3.4 and priority protected areas network of the study area indicated in Figure 3.5 F were examined by calculating Jaccard coefficient (Howard et. Al 1998, Warman et. Al 2004). Table 3.2 indicates these results (Table 3.2). And as this table shows, Jaccard coefficient percentages are very low for taxa. This means that site overlap between priority protected areas of taxa and priority protected areas network of the study area are too low. Even, by looking at these results, it can be roughly said that priority protected areas determined using only one taxon is not as successful as priority protected areas network of the study area in order to efficiently represent all taxa, these evaluations are not enough to reach a certain conclusion. Therefore, percent representation values of taxa were also investigated in order to assess surrogate efficiency of them. And as the graphs demonstrate, percent representation values of taxa reveal differences in respect to represent taxonomic groups (Figure 3.4).

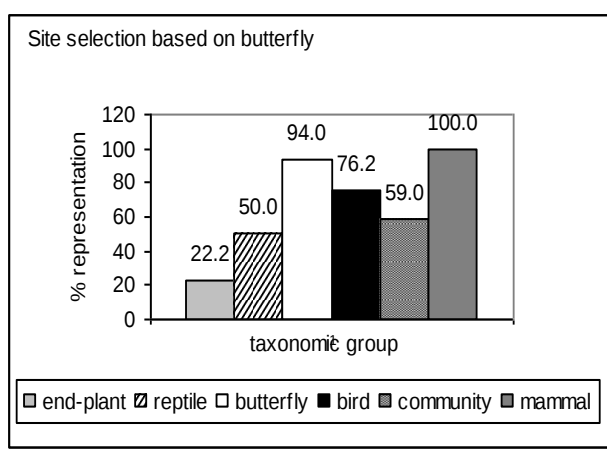
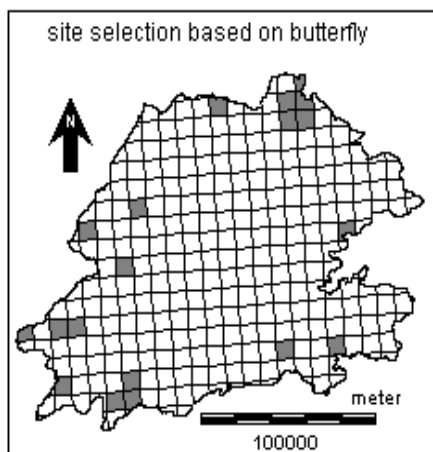
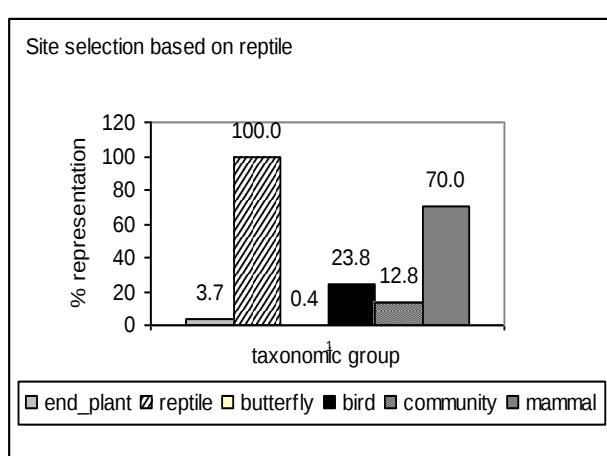
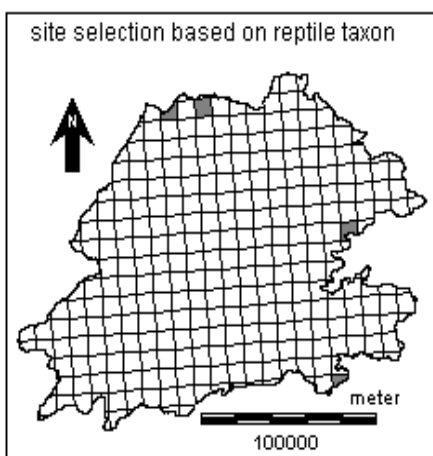
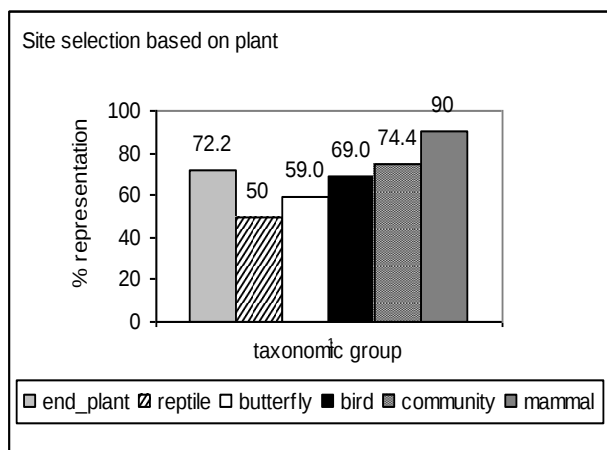
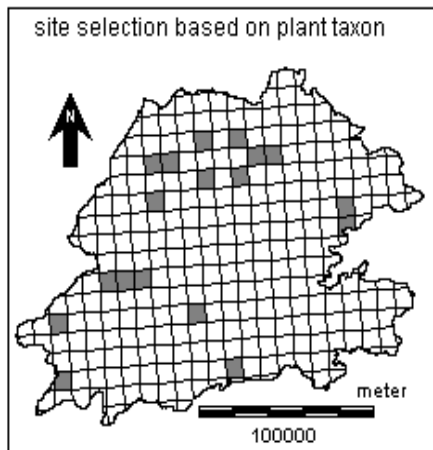


Figure 3.4 Maps and graphs showing distributions and percent representations of taxonomic group combinations including one taxon

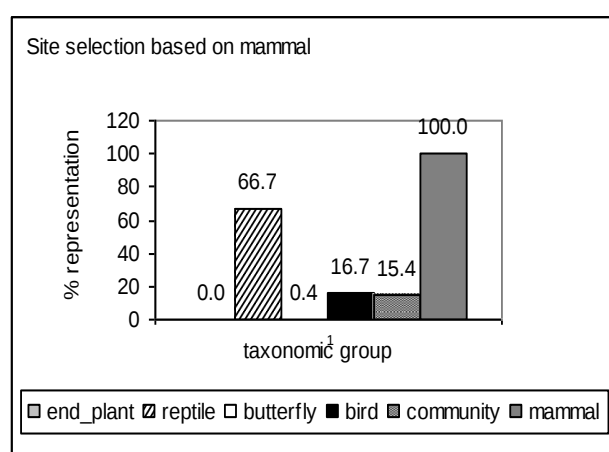
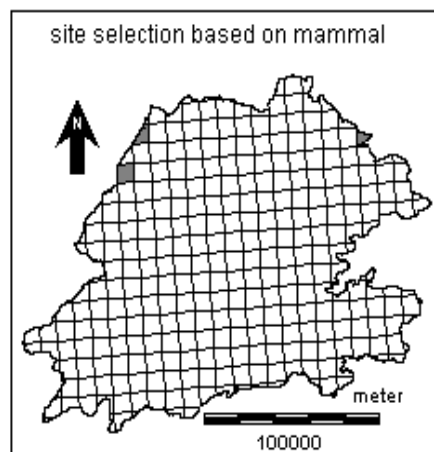
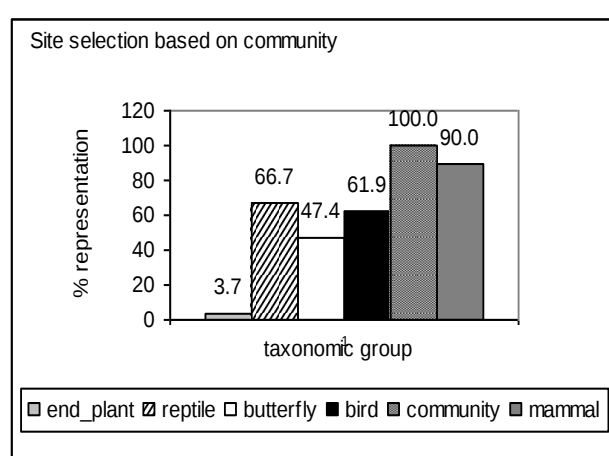
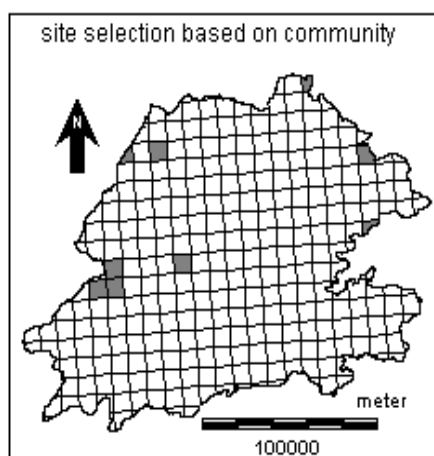
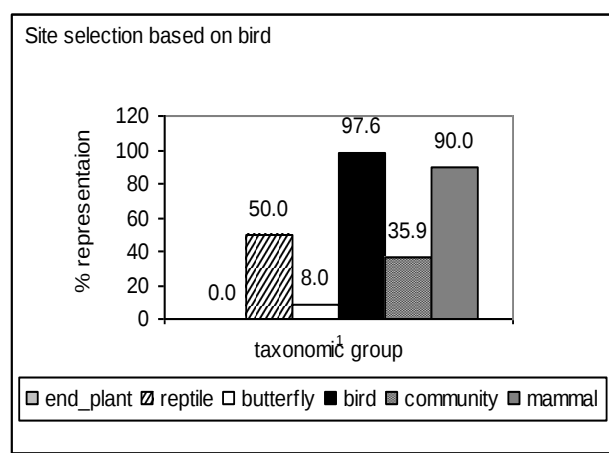
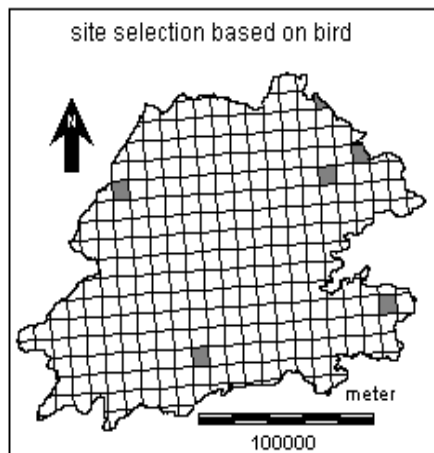


Figure 3.4 Maps and graphs showing distributions and percent representations of taxonomic group combinations including one taxon

Table 3.2 Table showing results of Jaccard coefficient for taxonomic group combinations including only one taxon as surrogate

Site selection based on	Plant	Reptile	Butterfly	Bird	Community	Mammal
All taxa	14.28%	0%	29.16%	4.34%	3.84%	0%

Among these six taxa, the most powerful one to represent other taxonomic categories is endemic and non-endemic highly threatened plant. It has the highest representation values for all taxonomic categories and the second highest Jaccard coefficient value, and then it is more successful than others for representing taxa. This is most probably related with the number of sites that were determined for plant taxon. Its number of priority protected areas is more than number of priority protected areas of other taxa and this makes plant taxon more successful while representing other taxa (Dobson 1997, Bonn et al 2002, Lawler et al 2003). Actually, distributions of plant species cause this situation (Warman et al 2004). Plant taxon includes endemic and non-endemic highly threatened plant species. These are very characteristic, narrowly distributed species and each of them prefers very different habitats from each other (Bonn et al 2002, Lawler et al 2003 and Warman et al 2003). This means each species has specific habitats and occupies different parts of the area (Warman et al 2003). Because of this, software determines many numbers of sites in order to conserve each of these plant species within priority protected areas. And when the number of site detected by software increase, its potential and probability to represent other taxonomic groups rise as well (Ryti 1992, Faith and Walker 1996a, Williams et al 2000 and Lund and Rahbek 2002). Other two taxa that are ecological community and butterfly are relatively well according to reptile, bird and mammal for representing all taxonomic groups except endemic and non-endemic highly threatened plant. While, both of them have low percent representation values for plant taxon, their representatives for other taxonomic groups are not too bad. Success of butterfly taxon as surrogate may be related with the number of butterfly species that are used during the analysis (Ryti 1992, Balmford 1998, Howard et al 1998, Lund and Rahbek 2002). There are 251 butterfly species with 2833 records. To protect such a high number of species within priority protected areas, sufficiently high number of protected areas should be determined. As indicated before, this provides to increase representation of other taxa so success of butterfly as surrogate becomes

unavoidable (Ryti 1992, Balmford 1998, Lund and Rahbek 2002). Another prominent taxon with respect to efficient representation is ecological communities as indicated above. It is not incredible while considering dependency of most animal species to plants and communities (Su et al 2004, Samraat 2006). Rest three taxa that are reptile, bird and mammal are not good surrogate for conservation area planning of the study area since their representation values are too low for most of the taxa. When their representation graphs are investigated, it can be observed that they are only good surrogates for themselves and for one another. Then it is not reasonable to suggest only them or their combinations as surrogate while detecting priority protected areas for study area (ICBP 1992, , Su et al 2004, Pawar et al 2006).

Maps and graphs that are in Figure 3.5 are for taxonomic group combinations including two and more than two taxonomic groups. These are butterfly-community, bird-community, plant-community, butterfly-plant and reptile-bird-butterfly-mammal taxonomic group combinations. As doing previously for taxonomic group combinations including only one taxon as surrogate, again surrogate efficiency for these taxonomic group combinations were evaluated by comparing distributions of their priority protected areas with the distribution of priority protected areas network (Figure 3.5 A, B, C, D, E and F), calculating Jaccard coefficients and investigating percent representation values. When distributions of priority protected areas of these taxonomic group combinations are compared with the distributions of priority protected areas network of the study area (Figure 3.5), it can be observed that although, distributions of sites of priority protected areas network are not same with each site of the priority protected areas of taxonomic group combinations one by one, There is a little bit compatibility among them, especially with regard to almost occupying same parts of the study area.

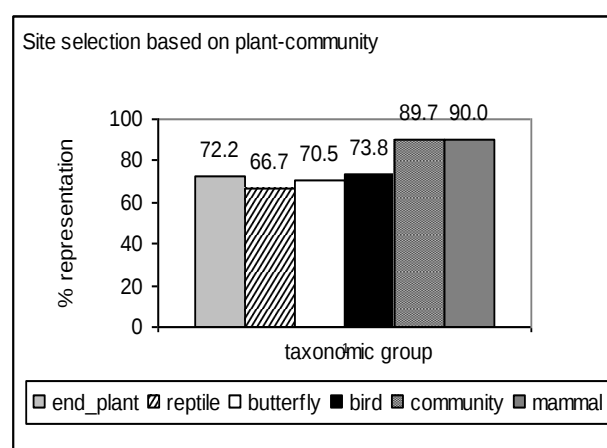
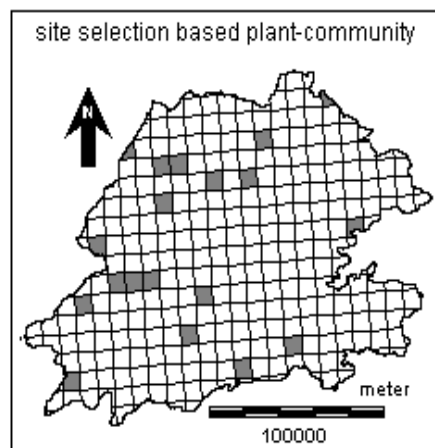
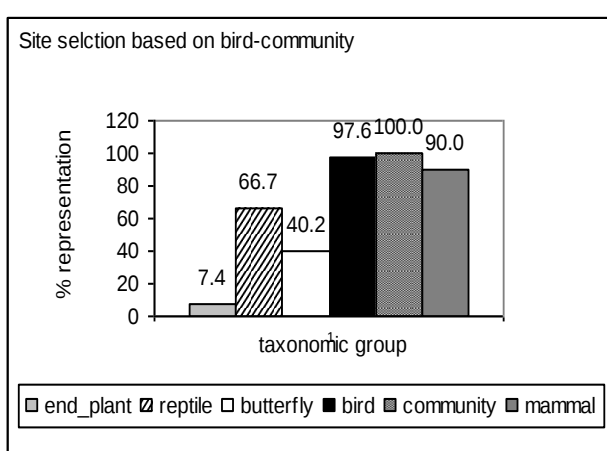
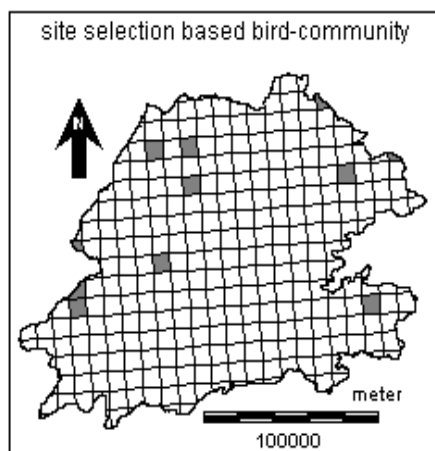
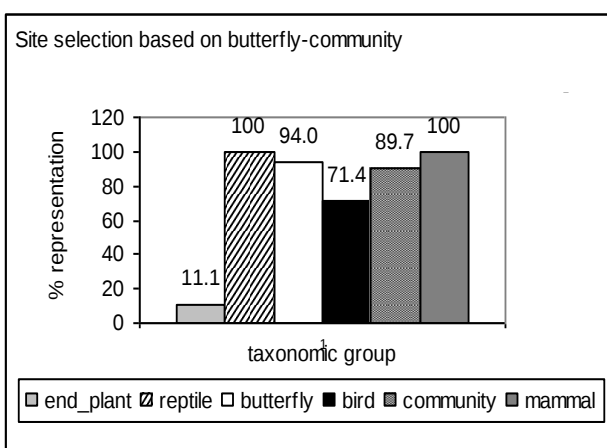
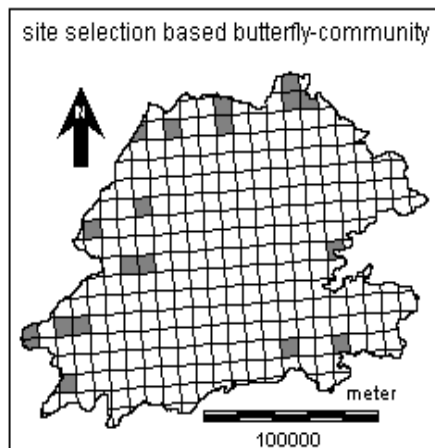


Figure 3.5 Maps and graphs showing distributions and percent representations of taxonomic group combinations including two and more than two taxa

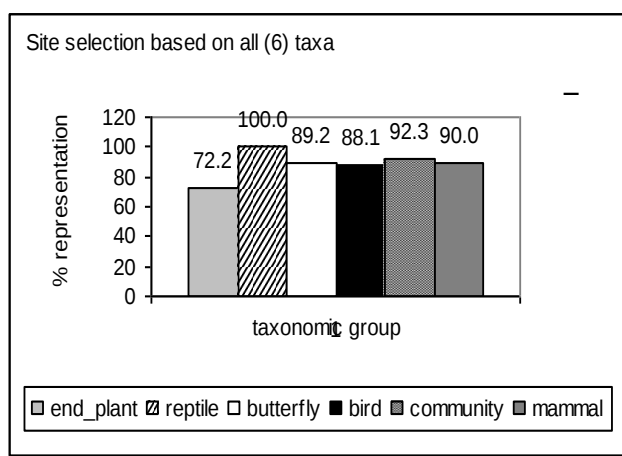
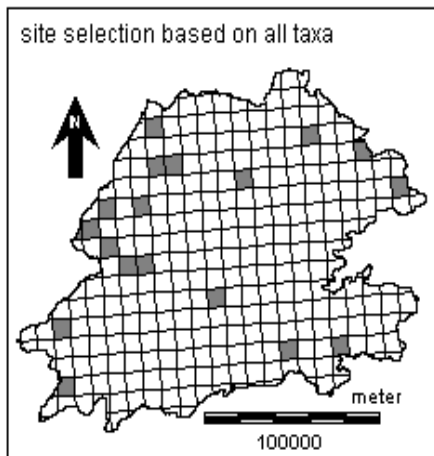
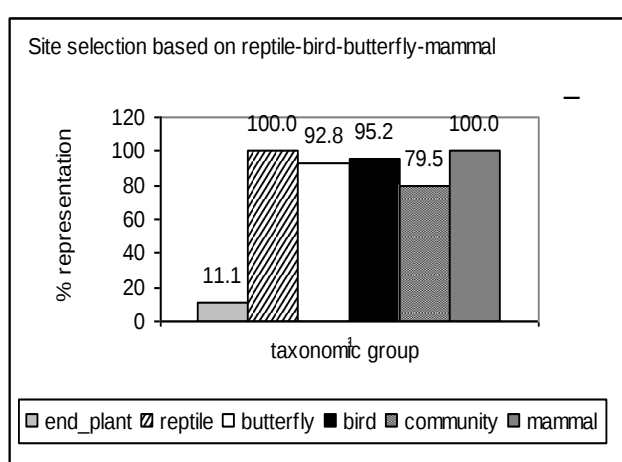
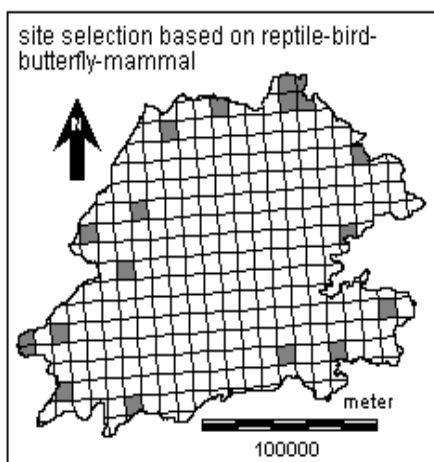
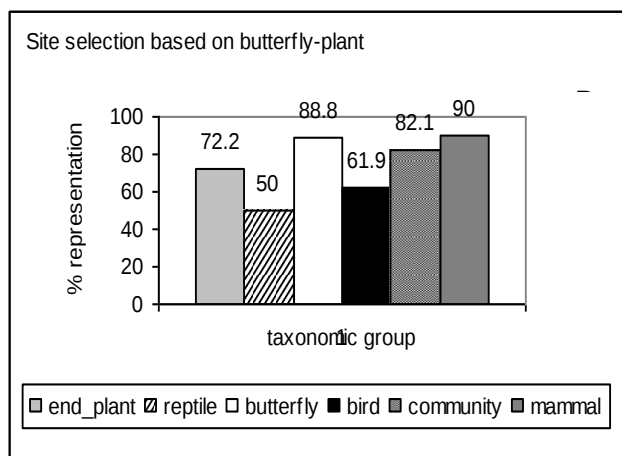
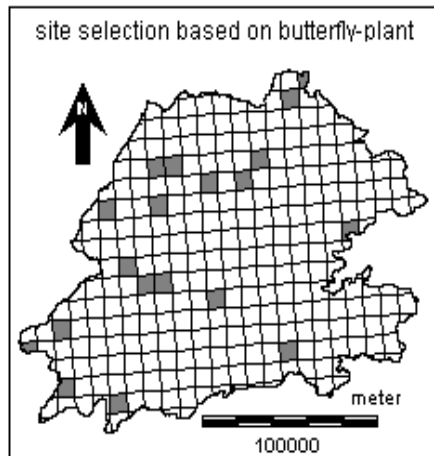


Figure 3.5 Maps and graphs showing distributions and percent representations of taxonomic group combinations including two and more than two taxa

Table 3.3 Table showing results of Jaccard coefficient for taxonomic group combinations including two and more than two taxa as surrogate

Site selection based on	Butterfly-community	Bird-community	Plant-community	Plant-butterfly	Reptile-bird-butterfly-mammal	Mammal
All taxa	29.16%	0%	17.85%	36.36%	30.43%	0%

As stated previously, even though this gives a general idea about surrogate efficiency of taxonomic group combinations, it is not sufficient. Hence, Jaccard coefficients are examined once again for taxonomic group combinations including two and more than two taxa in order to do more formal assessments. As observed from Table 3.3, Jaccard coefficients between priority protected areas network and taxonomic group combination including two and more than two taxa are greater than coefficients between protected areas network and taxonomic group combinations including only one taxon (Table 3.2 and Table 3.3). Therefore, it can be said that priority protected areas that were selected using one taxon as surrogate remain less efficient in order to represent all taxa of the study area than priority protected areas determined by using taxonomic group combinations that includes more than one taxon. However, before given a definite decision, examining percent representation values of these taxonomic group combinations is substantially useful.

As graphs indicate, percent representations of these combinations are more successful than taxonomic group combinations including one taxon (Figure 3.5). Even if, none of them are as efficient as priority protected areas network of the study area in order to represent all taxa of the area, plant-community and butterfly-plant taxonomic group combinations can be evaluated as the most successful combinations among others for representing taxa since these can represent all taxa approximately well while others, butterfly-community, bird-community, reptile-bird-butterfly-mammal, are not able to represent endemic and non-endemic highly threatened plants well.

By looking at both, results of priority protected areas determined with one taxon and results of priority protected areas detected using two and more than two taxa, it can be shortly said that in order to represent endemic and non-endemic highly threatened plant species efficiently within priority protected areas, itself of plant taxon should be absolutely used while detecting priority protected areas because as it can be seen from Figure 3.4 B, C, D, E, F and 3.5 A, B and E, when plant taxon is removed among surrogates, its representativeness decreases too much in detected priority protected areas. As indicated before, plant taxon includes endemic and non-endemic highly threatened plant species. This means these species occupy very special habitats or narrow areas. Hence capturing these species within priority protected area system is too difficult without using itself of plant taxon as surrogate (Bonn 2002, Lawler 2003).

Moreover, using only plant taxon or taxonomic group combinations including plant taxon as surrogate in conservation area planning of the area gives good results with regard to representativeness of not only itself of endemic and non-endemic highly threatened plants but also other taxa of the study. Actually, this situation is too normal since as it is known that many animal species very much depend on plant species for their survival. They provide their species specific requirements from plants like nutrition, progeny and nesting site. This results in compatibility and overlap among plant and animal distributions since animal species tend to disperse places where they can supply their requirements from plant species. Therefore, using plant taxon, vegetation classes or community types as surrogate in conservation area planning studies can most probably increase representation success of animal species in protected areas (Dobson 1997, Su et al 2004).

As indicated in methodology part, another analysis was performed in order to detect protected areas containing 19 sites for each taxonomic group combination. This was done to be sure efficiency of each taxon as surrogate, to compare surrogate performance of each taxon with each other and to test success of taxonomic group combinations as surrogate is a coincidence or not (Howard et. al 1998). In order to determine these 19 protected areas for each taxonomic group combinations, marxan was rerun (Appendix E1-12). Afterwards, cumulative representation values for each taxonomic group combinations were calculated in order to evaluate and compare surrogate performance of them. Results can be seen in below maps and graphs (Figure 3.6 and Figure 3.7) (Howard et. al 1998, Reyers et al 2000, Lund and Rahbek 2002, Beger et al 2003).

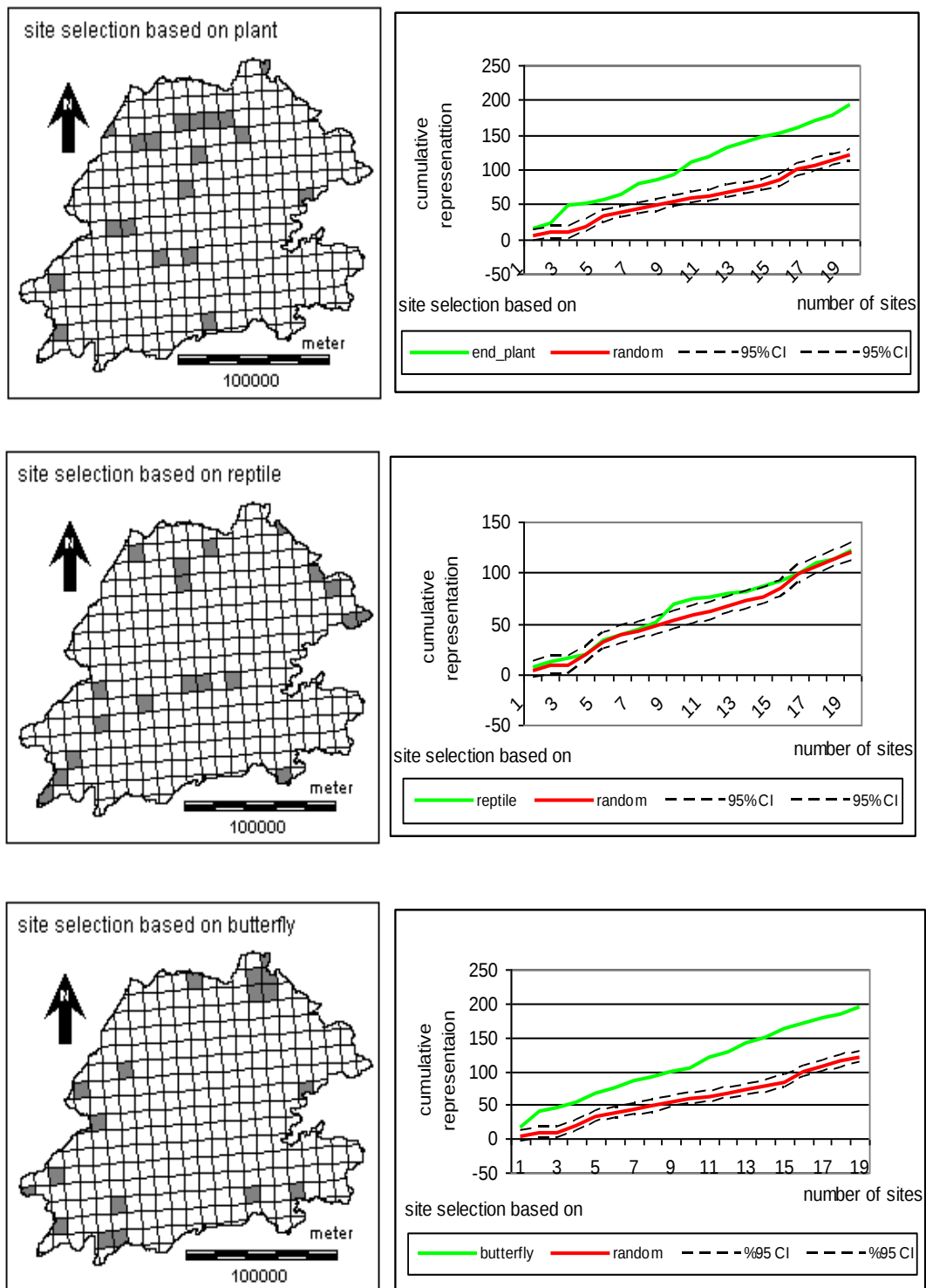


Figure 3.6 Maps and graphs showing distributions and cumulative representation of taxonomic group combinations including one taxon

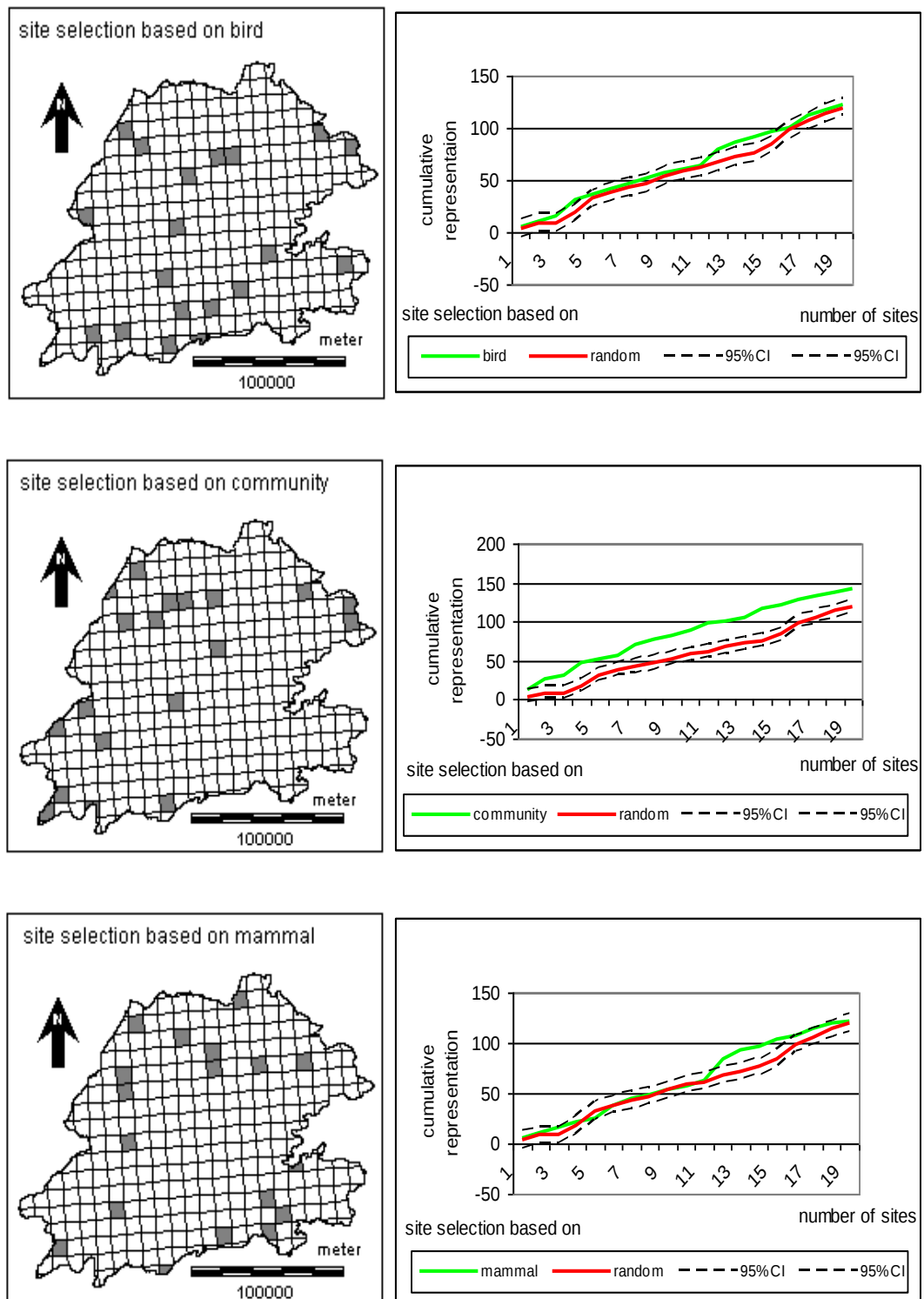


Figure 3.6 Maps and graphs showing distributions and cumulative representation of taxonomic group combinations including one taxon

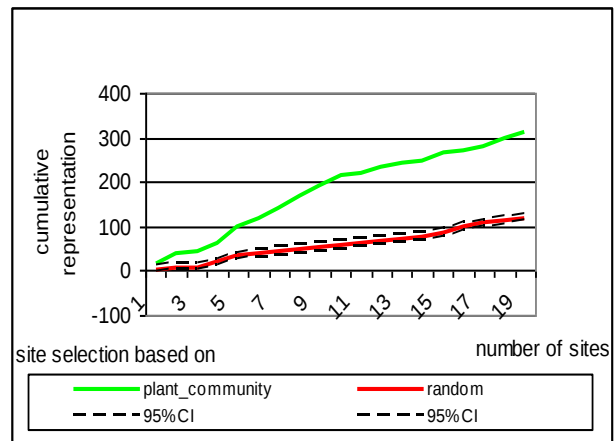
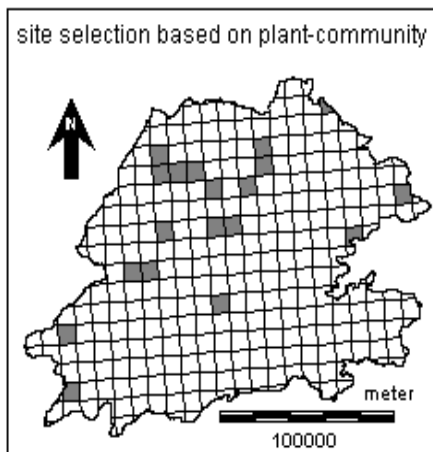
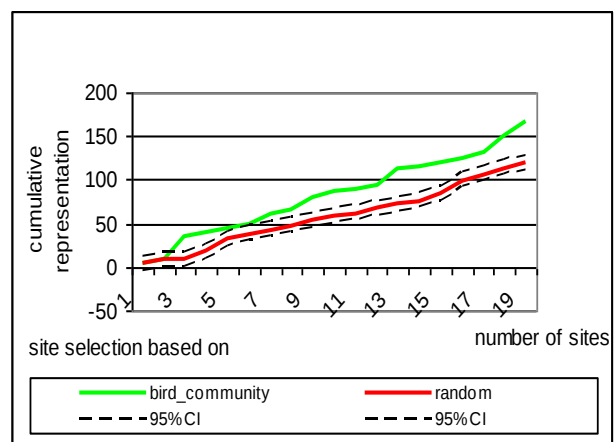
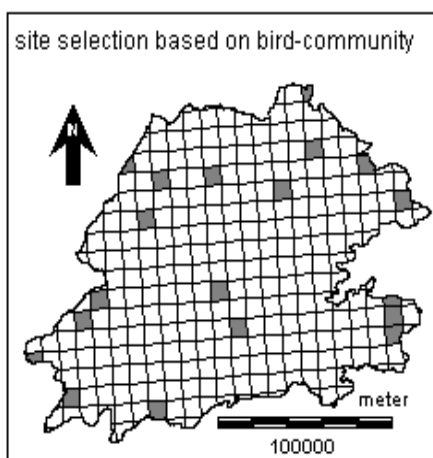
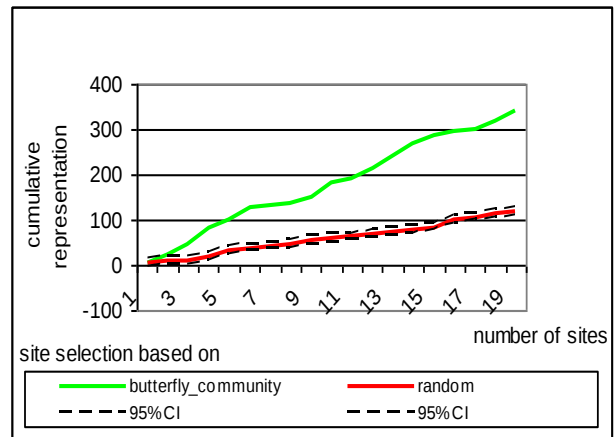
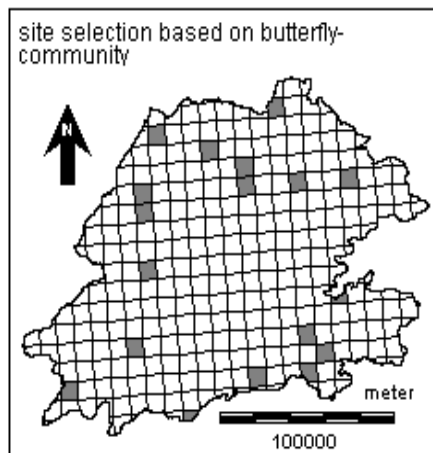


Figure 3.7 Maps and graphs showing distributions and cumulative representation of taxonomic group combinations including more than one taxon

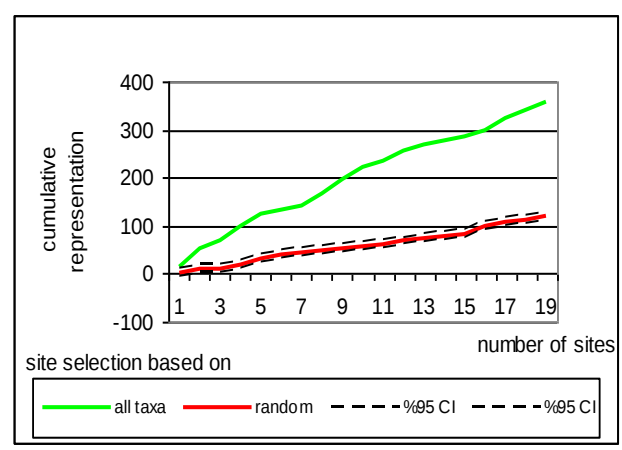
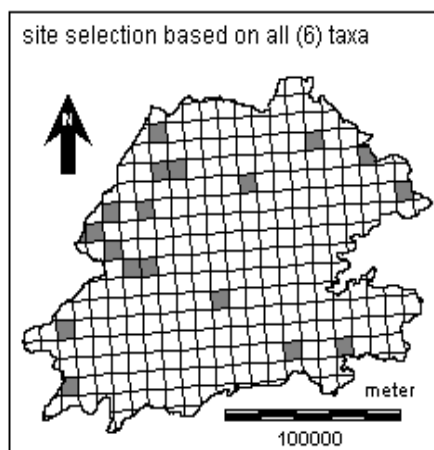
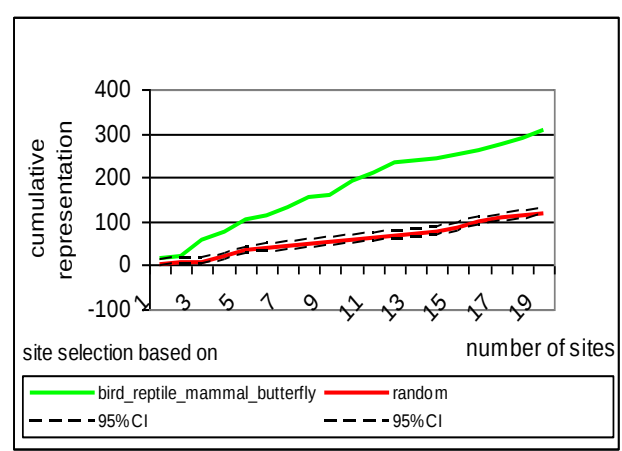
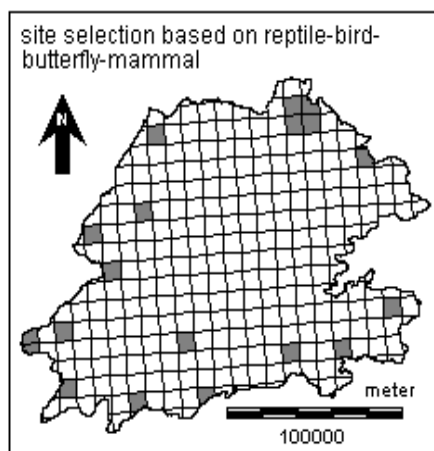
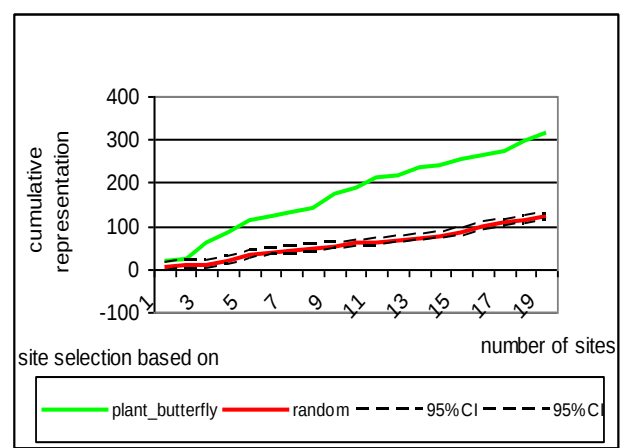
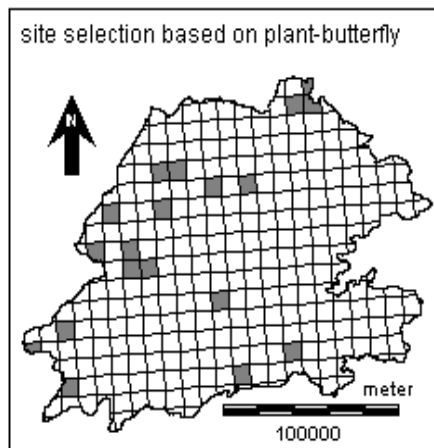


Figure 3.7 Maps and graphs showing distributions and cumulative representation of taxonomic group combinations including more than one taxon

As seen from these graphs, cumulative representation results are compared with random selection. This random selection includes 1000 run containing 19 sites for each. Reason about why to determine 1000 run as random selection is explained in detail later. With this comparison that is between taxonomic group combinations and 1000 random selection, it was tried to figure out that taxonomic group combinations as surrogate is really efficient in order to represent each taxon of the study or is this efficiency coincidence.

At first glance, it can be roughly said that taxonomic group combinations including one taxon is less efficient than taxonomic group combinations containing two or more taxa in respect to cumulative representation since their representation curves are generally around random selection curve while representation curves of taxonomic group combinations containing two or more taxa are always greater than random selection curve (Figure 3.6 and Figure 3.7). Although, this is a general statement, it is not valid for all one taxon group combinations because plant, butterfly and community taxon are remarkable with their greater cumulative representations. As their representation curves indicate, they are noticeably successful than random selection with respect to represent taxa of the study area. Then, it cannot be mentioned that their surrogate performance and representation success as surrogate are coincidence (Figure 3.6 A, C, E). However, it is not same for reptile, bird and mammal taxon since these have smaller cumulative representations and their representation curves remain under the upper tail of %95 confidence interval of random selection curve (Figure 3.6 B, D, F). This makes them as successful as random selection in order to represent taxa of the study. This means that they are not efficient as surrogate to use them in conservation area planning of the study area.

Taxonomic group combinations that include two or more than two taxa have greater cumulative representation values and their representation curves always remain over the upper tail of % 95 confidence interval of random selection (Figure 3.7). Therefore, it can be said that their success as surrogate is not a chance. Also, this indicates that these are more efficient than random selection in order to represent taxa of the study. Shortly, using taxonomic group combinations including more than one taxon as surrogate is more reasonable than using only one taxon in conservation area planning to represent all taxa of the study area efficiently. However, this doesn't mean that using only one taxon as surrogate to detect protected areas of the study area is a useless and time consuming evaluation.

On the contrary, analysis and evaluations about one taxon groups is too useful in order to realize the most efficient surrogate taxon and decide which taxon can be used instead of others in conservation area planning of the study area. Beside these, comparisons among all taxonomic groups were implemented by plotting a graph that shows their cumulative representation values in combination. This graph can be seen in below (Figure 3.8). As the graph demonstrates, cumulative representation curves of taxonomic group combinations compose two different parts on the graph. Generally, Curve of taxonomic group combinations including more than one taxon are in part I. These are butterfly-community combination, plant-community combination, bird-reptile-mammal-butterfly combination, plant-butterfly combination and taxonomic group combination including all taxa of the study. Only, bird-community combination including two taxa is not in part I, it is in part II.

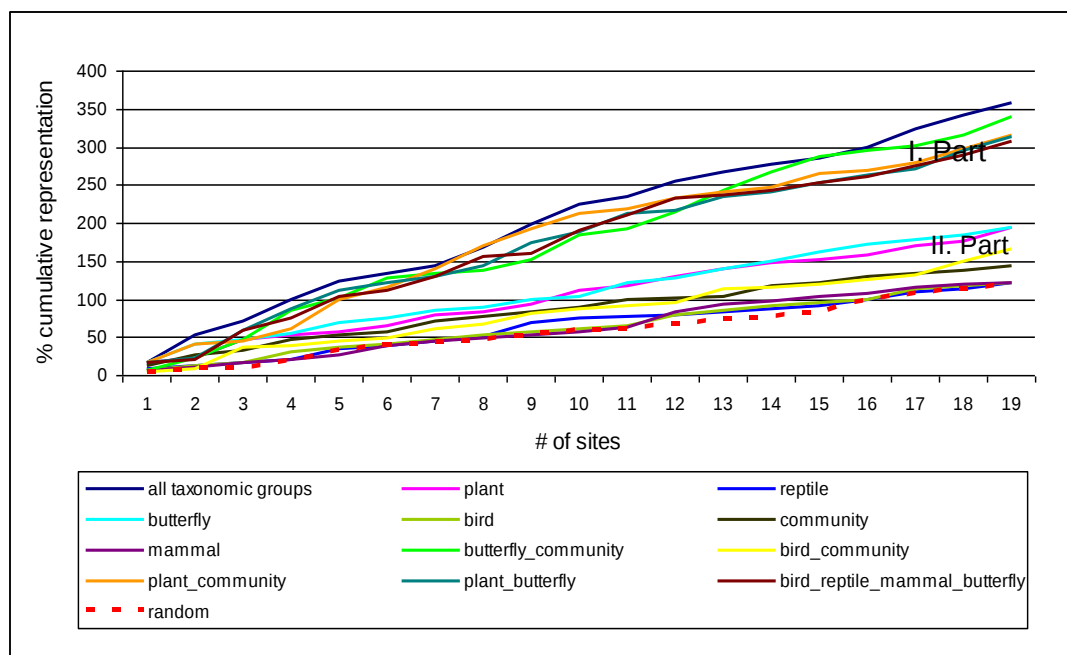


Figure 3.8 Graph showing cumulative representation of all taxa in combination

Also, all one taxon surrogates, plant, reptile, butterfly, bird, community and mammal are in part II. And the most powerful taxa among them are plant, butterfly and community as being in the previous parts since they have greater cumulative representation values than other one taxon surrogates (Figure 3.8). Although, this difference provides to reach general assessment about taxonomic group

combinations including two and more than two surrogate taxa are more efficient than taxonomic groups including one surrogate taxon in respect to represent all taxa, actually this success mostly depend on the taxon composing these taxonomic group combinations. This means, if taxonomic group combinations include more efficient surrogate taxon like plant, butterfly and community then their representation success increase (Figure 3.7 A, C, E and Figure 3.8) (Howard et al 1998, Van Jaarsveld et al 1998, Lund and Rahbek 2002, Su et al 2004,). However, if they contain less successful surrogate taxon like bird, then these combinations cannot provide efficient representation for all taxa (Figure 3.8) (Howard et al 1998, Van Jaarsveld et al 1998, Lund and Rahbek 2002).

In conclusion, depending on results of percent representation and cumulative representation of taxonomic group combinations including only one taxon and more than one taxon, it can be said that plant, community and butterfly taxon are more efficient as surrogates than others while representing taxa of the area (Pearson and Stevan 1999, Su et al 2004).

Even if, These analysis and evaluations are too important in order to determine surrogate efficiency of each taxon, these are not enough especially when considering other important aspects of conservation area planning like richness and complementarity (Prendergast et al. 1993, Lombard 1995, Williams et al. 1996, Flather et al. 1997, Howard et al. 1998, Van Jaarsveld et al. 1998). Therefore, other measurements that take into account them were applied in order to reveal cross taxon congruence among taxa in respect to richness and complementarity. As it is known, using surrogates in conservation area planning to represent overall biodiversity of an area is a very common approach because sampling and using whole biodiversity of an area is impossible (Kirkpatrick 1983, Pressey and Nicholls 1989, Vane-Wright 1991, Pressey, Possingham and Margules, 1996, Reyers, Van Jaarsveld and Krüger 2000, Lindenmayer et al 2000, Soberon et al 2000, Warman 2004). However, their use is only valid, when their richness and complementarity are correlated with the diversity and complementarity of other taxa. Otherwise, using surrogate to represent biodiversity of the area becomes a useless and unnecessary task (Noss 1990, McGeoch 1998). Due to this, investigating these two aspects is very useful in order to detect and use the most efficient surrogates in conservation area planning.

Table 3.4 Cross taxon congruence in total species richness

	Plant	Reptile	Butterfly	Bird	Community	Mammal
Plant		0.049 (>0.05)	0.52* (<0.05)	0.037 (>0.05)	0.67* (<0.05)	0.31 (>0.05)
Reptile			0.027 (>0.05)	0.42* (<0.05)	0.22 (>0.05)	0.08 (>0.05)
Butterfly				0.22 (>0.05)	0.46* (<0.05)	0.37 (>0.05)
Bird					0.26 (>0.05)	0.27 (>0.05)
Community						0.73 ** (<0.001)
Mammal						
Note: spearman's rho, (<i>p</i> value according to 5000 Monte Carlo simulation), * 95% and ** 99% significance level.						

Table that is above demonstrates correlation results of richness of taxa (Table 3.4). This table includes both spearman's rho values of richness and p values evaluating according to % 95 and % 99 of confidence levels. And as it is seen from this table, ecological communities has significant positive correlations with plant (sp rho= 0.67 p<0.05), butterfly (sp rho= 0.67 p<0.05) and mammal taxa (sp rho= 0.73 p<0.001). When considering place of communities in ecosystems, this situation is too normal since ecological communities provide home for most animal and plant species and supply requirements of animals. Therefore, high community richness means high animal and plant species richness. Another significant positive correlation is seen between reptile and bird taxa (sp rho= 0.42 p<0.05). This is quite usual appearance for reptile and bird since they have prey-predator relations. Therefore, they can demonstrate high species richness correlations among themselves.

Even if, all these correlation values are not as high as expected, finding species richness correlations among plant-butterfly, plant-community, bird-reptile and community-mammal are as expected and very much parallel with literature studies (Su et al 2004, Warman et al 2004, Tushabe et al 2005). Also, these correlations are substantially meaningful because they can explain ecological relations among taxa and indicate which taxon or taxa can be used instead of others as surrogate in conservation area planning. However, the disappointing thing is that there is not any significant positive correlation among other taxa. Nevertheless, ecological community, plant and butterfly taxa are prominent with respect to their surrogate efficiency as being in previous analysis and this is very pleasing due to demonstrate consistency between results of previous analysis and results of

species richness correlations. This compatibility among different analysis is significant since it enable to determine most accurate and efficient surrogate taxa of the study area by integrating different approaches in a common point.

Another important aspect of conservation area planning is complementarity as indicated above. It is significant as providing efficient and cost effective conservation by protecting a great number of different species within minimum number of protected areas (Pressey et al 1993, Margules et al 1994 and Williams et al 1996.). For this reason, investigating and revealing cross taxon congruence with regard to complementarity is useful since it enables to detect efficient surrogates that provide complementarity not only for themselves but also for other taxa of the study area.

Table 3.5 shows results of cross taxon congruence in complementarity (Table 3.5). This table includes both mantel correlation values of complementarity score of taxa and p values. As is seen from the table, there are significant positive correlations in terms of complementarity among plant-community (mantel= 0.35, $p < 0.05$), bird-reptile (mantel=0.48, $p < 0.05$), reptile-community (mantel=0.49, $p < 0.05$), bird-community (mantel=0.42, $p < 0.05$), bird-mammal (mantel=0.35, $p < 0.05$), and mammal-community (mantel=0.35, $p < 0.05$)

Table 3.5 Cross taxon congruence in complementarity

	Plant	Reptile	Butterfly	Bird	Community	Mammal
Plant		0.080 (>0.05)	0.29 (>0.05)	0.096 (>0.05)	0.35* (<0.05)	0.047 (>0.05)
Reptile			0.017 (>0.05)	0.48* (<0.05)	0.49* (<0.05)	0.24 (>0.05)
Butterfly				0.025 (>0.05)	0.21 (>0.05)	0.060 (>0.05)
Bird					0.42* (<0.05)	0.35* (<0.05)
Community						0.35* (<0.05)
Mammal						
Note: mantel correlation values, (<i>p value according to 5000 Monte Carlo simulation</i>), * 95% and ** 99% significance level.						

Positive significant correlation results among plant-community, bird-reptile and mammal community are very much familiar from previous species richness

correlation results. This compatibility between two different measurements for same taxa is very pleasing since this situation supports efficiency of these taxa as surrogate. Also, there are other positive correlation results among reptile-community, bird-community and bird-mammal taxa. When evaluating all these correlation results among taxa, it can be seen that once again ecological community is quite conspicuous as having significant positive correlation values with almost all other taxa.

In Conclusion, it was found that some taxa have effective percent representation and cumulative representation values for representing other taxa. And same taxa also exhibit cross taxon congruence in total species richness and complementarity. Therefore, these taxa can be used as surrogate of biodiversity in other taxa. Taxonomic groups that are plant, butterfly and ecological communities can represent other taxa of the study well and significantly different than random selection in terms of their cumulative representation values. Also, they demonstrate significant positive correlation in species richness with some taxa. However among them, only ecological community is efficient as having significant positive correlation in complementarity with other taxa. Therefore, while it is the most robust taxon as surrogate with providing high representation for taxa and representing other taxa in respect to richness and complementarity, plant and butterfly remain fairly robust due to their less cross taxon congruence in complementarity. Although, these taxa are remarkable as efficient surrogate, important point that must be emphasized are lower correlation values in species richness and complementarity (Oliver et al, 1998, Su et al 2004). As both tables indicate, even if there are significant correlation between these taxa and some others, these values are too low. This situation is very embarrassing since it may decrease surrogate reliability of these taxa. When thinking seriousness and importance of conservation area planning, it can be understood that ignoring these results can cause severe mistakes.

When it comes to bird, reptile and mammal taxa, they are not robust and not better than random selection in order to represent other taxa. However, they exhibit cross taxon congruence in species richness and complementarity with some taxa. This incompatibility between results makes these taxa less reliable as surrogate since this means that they may not be able to represent taxonomically broader range of biodiversity and protect all taxa together with all aspect of conservation area planning (Lund and Rahbek 2002). Actually, this inefficiency of birds, reptile and

amphibians as surrogate is very surprising since these are usually proposed and supported as effective surrogates in other taxa (ICBP 1992, Pearson and Stevan 1999, Su et al 2004, Pawar et al 2006).

Eventually, it is said that although plant, butterfly and ecological community are seem more efficient as surrogate than reptile and amphibian, bird and mammal, this may not be certain due to low significant correlation results in complementarity and species richness. This situation is very common in literature. And many scientists who are interested in conservation area planning and surrogacy approach and meet such a situation do not very much trust and determine them as efficient surrogate. Generally, they suggest that using as possible as great number of taxonomic groups while planning conservation areas is more useful than using finite number of surrogates to represent diversity of all other taxa (Dobson et al 1997, Howard et al 1998, Reyers et al 2000, Bonn et al 2002, Moore et al 2003). Nevertheless, these judgements should not create disappointment since significant positive correlations in species richness and complementarity is very encouraging in order to improve surrogate performance of taxa. Therefore, it is not thought that surrogacy approach is a useless and time consuming evaluation.

3.1.3 Detecting Optimum Number of Random Selection for Null Model

As it is explained in methodology part, in order to detect optimum number of random selection for null model, different number of selections that begins from 200 and maintain till 5000 was performed. Afterwards, average representation values of these random selections were calculated in order to measure their efficiency. And a graph that is average representation versus number of random selection was plotted. The graph demonstrating results of these random selections can be seen in below (Figure 3.9).

As is seen from the graph, 1000 random selections is the point where average representation, in other words efficiency of random selection do not exhibit any change (Figure 3.9). This means, there is not more or less any increase or decrease after this point. Then, 1000 random selection was accepted as the optimum number of random selection for null model and used as the random null model. The graph that is above demonstrates average cumulative representation values of random null model site by site with its %95 upper and lower tails (Figure

3.10). Random null model is used in this way while trying to figure out efficiency of surrogate taxa is a chance or not (Title 3.1.2, Figure 3.6, 3.7 and 3.8) and comparing result of complementarity based area selection with result of ED area approach.

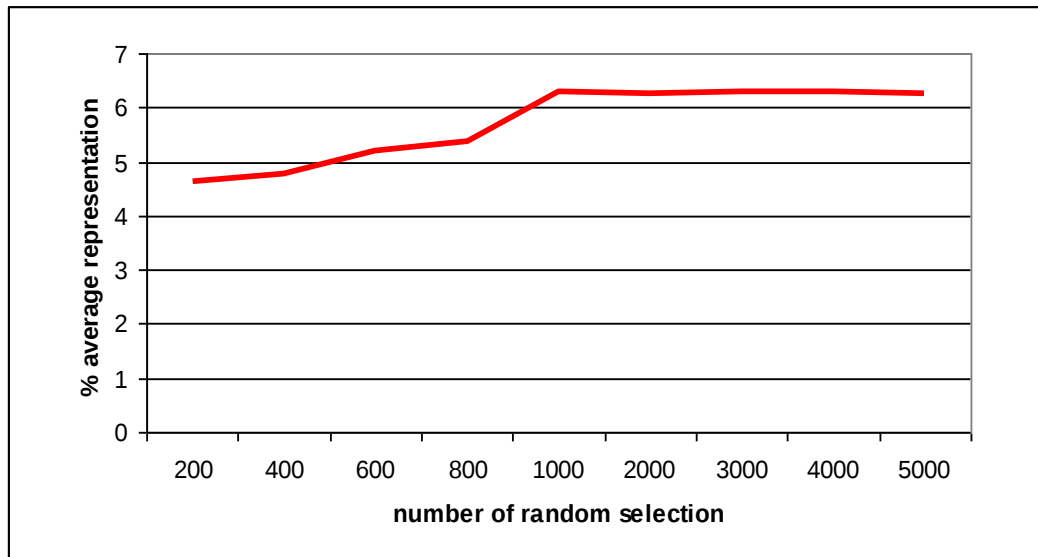


Figure 3.9 Graph showing efficiency of each random selection

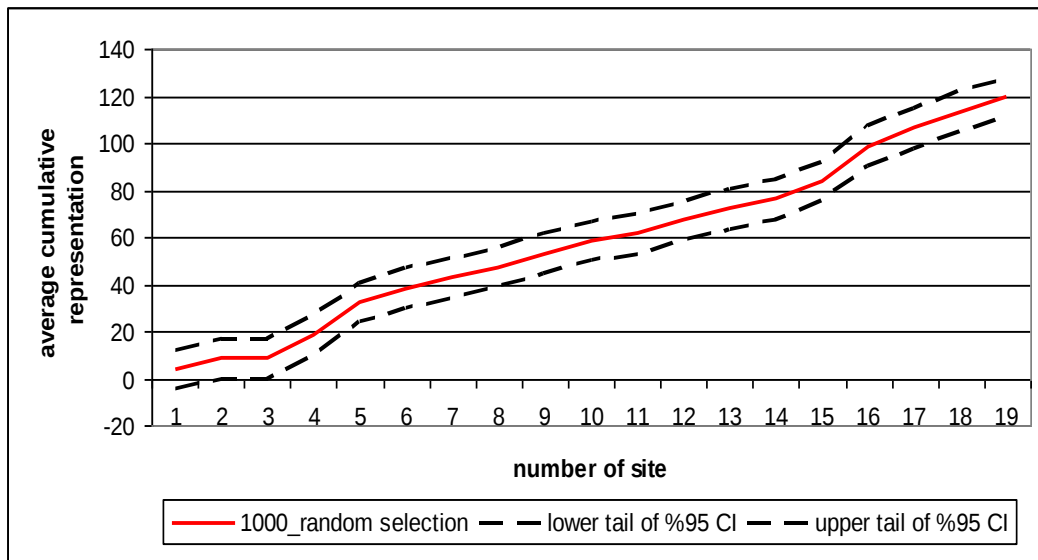


Figure 3.10 Graph showing average cumulative representation of null model

3.2 Environmental Diversity Analysis

3.2.1 Detecting Collinear Environmental Variables

As Expressed before in methodology part, multicollinearity among environmental variables might lead to inaccurate results for the rest of the analyses. Then, these variables were determined by applying both a global correlation analysis and calculating variance influence factors. Firstly, correlation analysis was performed to investigate pairwise correlations of variables and environmental variables that have pairwise correlation higher than 0.65 (>0.65) and lower than -0.65 (<-0.65) were decided to remove among variables (correlation table can be seen in Appendix F). There were 4 such variables indicating higher or lower correlation than determined correlation values with other environmental variables. These are annual temperature, annual precipitation, annual relative humidity and slope. Before eliminating these variables among environmental variables list, VIF's for each environmental variables was calculated and variables demonstrating VIF values higher than 10 were dropped from variables list as well.

Table 3.6 Table showing VIF's for each environmental variables

Variables	VIF	Variables	VIF
Dem	2.4	Prec-cm	8.0
Ruggedness	8.5	Prec-hm	3.6
Slope	193.0	Prec-sea	5.5
East-aspect	1.8	Annual-prec	480.2
North-aspect	1.8	An-rel-hum	188.0
Annual-tmp	123.2	Rel-hum-cm	6.5
Max-tmp-hm	148.6	Rel-hum-hm	3.1
Min-tmp-hm	112.0	Solar-rad-hm	2.2
Tmp-an-rng	8.3	Solar-rad-cm	6.3
Diurnal-rng	9.0	River-int	1.2
Isothermality	3.2	Soil-het	1.8
Lakeshoreline	1.3	VIF; 1.3<VIF<480.2	

Above table indicates the VIF values of each environmental variable and as can be seen from this table, variables demonstrating higher or lower correlation than determined correlation values have quite higher VIF values too (Table 3.6). Another remarkable situation that can be observed from the table is that two more environmental variables were added among the eliminated environmental variables. These variables are maximum temperature of hottest month with its 148.6 VIF value and minimum temperature of coldest month variable with 112.0 VIF. That is, in total six environmental variables were dropped among the environmental variables and 17 variables remained in order to use in subsequent part. Below table demonstrate VIF values of remaining environmental variables (Table3.7).

Table 3.7 Table showing VIF values for remaining variables

Variables	VIF	Variables	VIF
Dem	2.2	Prec-sea	4.0
Ruggedness	5.3	Rel-hum-cm	6.3
East-aspect	1.7	Rel-hum-hm	2.6
North-aspect	1.7	Solar-rad-hm	1.2
Tmp-an-rng	4.6	Solar-rad-cm	2.7
Diurnal-rng	6.3	River-int	1.1
Isothermality	1.4	Soil-het	1.7
Prec-cm	7.6	Lakeshoreline	1.2
Prec-hm	2.5	VIF; 1.3<VIF<6.3	

3.2.2 Determining Significant Environmental Variables for Each Taxon

For this part, GWR that is a spatial statistical model was used. One of abilities of GWR model, it provides to detect local variables demonstrating significant spatial variation as specified before in methodology chapter. Using this property of the GWR model, significant local environmental variables were determined for each taxon. Results of GWR analysis for taxa can be seen below in table 3.8.

As far as, it is assumed, there is a positive relationship between environmental factors and species occurrences and environmental variables very much influence

distribution of species. Therefore, detecting environmental variables that have significant spatial variation for a taxon is too important since it means high species variation as well. Determining such variables provides both to identify environmental variables that have positive relations with related taxon and to figure out redundant variables for a taxon since if a variable is not indicate significant spatial variation for a taxon, then it doesn't have any effect on variation pattern of species of this taxon. Therefore, these variables can be called as the redundant environmental variables for related taxon and can be eliminated for the rest of the analyses.

Table 3.8 Table demonstrates significant environmental variables for each taxon

Taxonomic Groups	
Environmental Variables	End-and non_end threatened plant
	Annual temperature range/ an_temp_rng (0***)
	Diurnal range/drn_rng (0***)
	Isothermality/isotm (0***)
	Relative humidity of hottest month/rl_hmd_hm (0***)
	Relative humidity of coldest month/rl_hmd_cm (0***)
	Solar radiation of hottest month/ rdt_hm (0***)
	Solar radiation of coldest month/ rdt_cm (0.02*)
Environmental Variables	Reptile and Amphibian
	Annual temperature range/ an_temp_rng (0***)
	Diurnal range/drn_rng (0***)
	Isothermality/isotm (0***)
	Precipitation of coldest month/pr_cm (0***)
	Precipitation seasonality/pr_sea (0***)
	Relative humidity of hottest month/rl_hmd_hm (0***)
	Relative humidity of coldest month/rl_hmd_cm (0***)
	Solar radiation of hottest month/ rdt_hm (0***)
	Solar radiation of coldest month/ rdt_cm (0***)
	Lake shore line /shr_ln (0.02*)
Environmental Variables	Butterfly
	Annual temperature range/ an_temp_rng (0***)
	Diurnal range/drn_rng (0***)
	Precipitation seasonality/pr_sea (0***)
	Relative humidity of hottest month/rl_hmd_hm (0***)
	Relative humidity of coldest month/rl_hmd_cm (0.05*)
	Solar radiation of coldest month/ rdt_cm (0***)

Table 3.8 Table demonstrates significant environmental variables for each taxon

Taxonomic Groups	
Environmental Variables	Breeding Bird
	Digital Elevation model/dem (0***)
	Annual temperature range/ an_temp_rng (0***)
	Diurnal range/drn_rng (0***)
	Isothermality/isotm (0***)
	Precipitation seasonality/pr_sea (0.01*)
	Relative humidity of hottest month/rl_hmd_hm (0***)
	Relative humidity of coldest month/rl_hmd_cm (0***)
	Solar radiation of hottest month/ rdt_hm (0.01*)
Environmental Variables	Ecological Community
	Ruggedness/rgd (0***)
	Annual temperature range/ an_temp_rng (0***)
	Isothermality/isotm (0***)
	Precipitation of coldest month/pr_cm (0***)
	Precipitation of hottest month/pr_hm (0***)
	Relative humidity of coldest month/rl_hmd_cm (0.02*)
	Solar radiation of coldest month/ rdt_cm (0***)
	Lake shore line /shr_In (0.02*)
Environmental Variables	Large Mammal
	Eastern aspect/e_asp (0***)
	Annual temperature/ an_temp (0.02**)
	Diurnal range/drn_rng (0***)
	Isothermality/isotm (0***)
	Precipitation of coldest month/pr_cm (0***)
	Precipitation of hottest month/pr_hm (0.01*)
	Precipitation seasonality/pr_sea (0***)
	Relative humidity of hottest month/rl_hmd_hm (0***)
	Relative humidity of coldest month/rl_hmd_cm (0***)
	Solar radiation of hottest month/ rdt_hm (0***)
	Solar radiation of coldest month/ rdt_cm (0***)
	Lake shore line /shr_In (0***)

At the beginning of the analyses part, there were 23 environmental variables (table 2.6). But after application of a global correlation analysis and calculation of VIF values, 6 of them were removed from the variable list since these are collinear environmental variables. Afterwards, GWR was performed and results of it

indicated that northern aspect, river intensity and soil heterogeneity among the remaining 17 environmental variables don't indicate any significant spatial variation for none of the 6 biological taxa. This means that they don't provide any contribution for their distributions. Then, these 3 environmental variables were eliminated from the variable list as well. Shortly, during the data exploration procedures, 9 of the 23 environmental variables were dropped and the rest of analyses were followed with the remaining 14 environmental variables (Table 3.9).

Table 3.9 Results of Environmental Variable Exploration

All environmental variables	Variables eliminated after correlation	Variables eliminated after VIF	Stationary Variables	Remaining Variables used as environmental surrogates
Dem Ruggedness Slope North-aspect East-aspect Annual-tmp Max-tmp-hm Min-tmp-cm Tmp-an-rng Diurnal-rng Isothermality Prec-cm Prec-hm Prec-sea Annual-prec An-rel-hum Rel-hum-hm Rel-hum-cm Sol-rad-hm Sol-rad-cm River-int Soil-het Lakeshoreline	Annual-tmp Annual-prec An-rel-hum Slope Correlation;<-0.65 or>0.65	Max-tmp-hm Min-tmp-cm VIF> 10	North-aspect River-int Soil-het According to 95% and 99% significance	Dem Ruggedness East-aspect Tmp-an-rng Diurnal-rng Isothermality Prec-cm Prec-hm Prec-sea Rel-hum-hm Rel-hum-cm Sol-rad-hm Sol-rad-cm Lakeshoreline
Note: abbreviations can be seen in table 2.6				

3.2.3 Examining Variation Pattern of Environmental Surrogates and Calculating Dissimilarity matrix of These Surrogates

As indicated in methodology part, in order to investigate variation pattern of remaining 14 environmental variables, PCA was used. By this means, variation pattern of each of 336 grid cells was revealed. In other words, variation pattern of the study area for 14 environmental variables was measured grid by grid

Table that is below exhibits result of PCA (Table 3.10). As can be seen from this table, although there have been 14 PCA axes in total, only first five axes were used to explain results since remaining 9 PCA axes have very low Eigen values and % variations smaller than 1%. This means that, these axes can only explain very small amount of variation of the data. That is to say, ignoring these PCA axes don't lead to serious information loss about data. Therefore, these components of the PCA were removed and only first five axes were used in order to produce dissimilarity matrix.

As it can be observed from table 3.10, while first axis has the highest Eigen value (11.22) and highest % variation (70.58), the remaining axes have much smaller eigen and % variation values. PCA Eigen and % variation values are used to express amount of variation on each PCA axis. This means that first axis explains 70.58 % of variation in the entire data whereas others explain almost all remaining variation. And in total 98.00 % of variation of all data is clarified with first five PCA axes.

Moreover, there are one more table exhibiting component loadings of 14 environmental surrogates according to first five PCA axes (Table 3.11). These loading values provide to know which environmental surrogates contribute which PCA axes. As the table indicates, axis1 is highly positively related with all environmental surrogates except lake shore line (0.11) while other axes have weak positive and negative correlations with all environmental surrogates. This means that first component can summarize almost all the data. This situation can clarify the reason why axis 1 explains most of the variation of the data.

Table 3.10 Table demonstrates results of PCA for first five axes

	PCA1	PCA2	PCA3	PCA4	PCA5
Eigen value	11.22	4.04	2.37	0.92	0.58
% variation of axes	70.58	14.16	7.96	3.56	1.74
Cumulative % variation	70.58	84.74	93.7	96.26	98.00

Table 3.11 Table shows results of PCA loadings for first five axes

Environmental surrogates	PCA1	PCA2	PCA3	PCA4	PCA5
Dem	0.94	0.042	-0.30	0.16	-0.09
Ruggedness	0.79	-0.34	-0.41	0.41	0.10
East-aspect	0.87	0.06	-0.11	0.11	0.93
Tmp-an-rng	0.96	-0.036	0.08	-0.38	-0.08
Diurnal-rng	0.99	-0.032	-0.01	-0.04	-0.07
Isothermality	0.96	-0.02	0.34	-0.09	-0.082
Prec-cm	0.73	0.42	0.53	-0.38	0.09
Prec-hm	0.88	-0.22	0.23	-0.30	-0.10
Prec-sea	0.96	0.024	0.35	-0.03	-0.12
Rel-hum-hm	0.98	0.14	0.08	-0.13	-0.11
Rel-hum-cm	0.99	0.24	0.01	-0.002	-0.09
Sol-rad-hm	0.96	0.54	0.16	-0.27	-0.14
Sol-rad-cm	0.98	0.20	0.04	-0.18	-0.08
Lakeshoreline	0.11	0.88	-0.43	-0.15	-0.09

There are also some other noticeable things about component loadings. Although axis 1 is prominent with its high loadings for almost all data, this can only give a general idea about geographical variation of axes scores of environmental surrogates. This means, by looking at map of axis1 (map PCA-1), it can only be differentiated that north- west part of the study area indicate high variation in terms of almost all environmental surrogates. In other words, this cannot give any idea about geographical distributions of variation patterns of environmental surrogates one by one or as groups (Figure 3.11, PCA 1). However, when the table 3.11 is examined, it can be realized that axis 2 positively related with rel-hum-hm (0.14),

rel-hum-cm (0.24), sol-rad-hm (0.54), sol-rad-cm (0.20) and lakeshoreline (0.88) (see Table 2.6 for abbreviations). All these 5 environmental surrogates are related with humidity, radiation and lake, then it can be said that axis 2 summarize and explain variation pattern of these environmental surrogates. Additionally, when PCA-2 map is investigated, it can be recognized that variation scores are high around north-east part of the area for these four topographic environmental surrogates (Figure 3.11, PCA 2). This part and around it is too close to the lake Çıldır and Aktaş. Then, this means that this region exhibits high variation in terms of these environmental surrogates.

Furthermore, when loadings of component 3 and 4 are overviewed, it is seen that while axis 3 has positive correlations with isothermality (0.34), prec-hm (0.53), prec-cm (0.23) and prec-sea (0.35) axis 4 indicates weak positive correlations with dem (0.16), ruggedness (0.41) and east-aspect (0.11) (Table 3.11; see Table 2.6 for abbreviations). That is to say, axis 3 mostly summarizes and explains precipitation related variables whereas axis 4 clarifies topography related environmental surrogates. Also, when the maps for component 3 and 4 are investigated, it is clearly seen that PCA 3 has high score values in south, south-east and east part while PCA 4 has high score values north and north-east parts for the study area.. Shortly, precipitation related variables demonstrates high variation axis scores around south and east whilst topographic features exhibits high variation axis scores around in north and north-east.

After, investigating geographic distributions of variation patterns of significant environmental surrogates through the study area, a distance matrix were produced using score values of first five components. This matrix is a 336*336 data matrix and includes pairwise similarities for each grid pairs. Since it is a huge matrix, it cannot be presented inside the thesis.

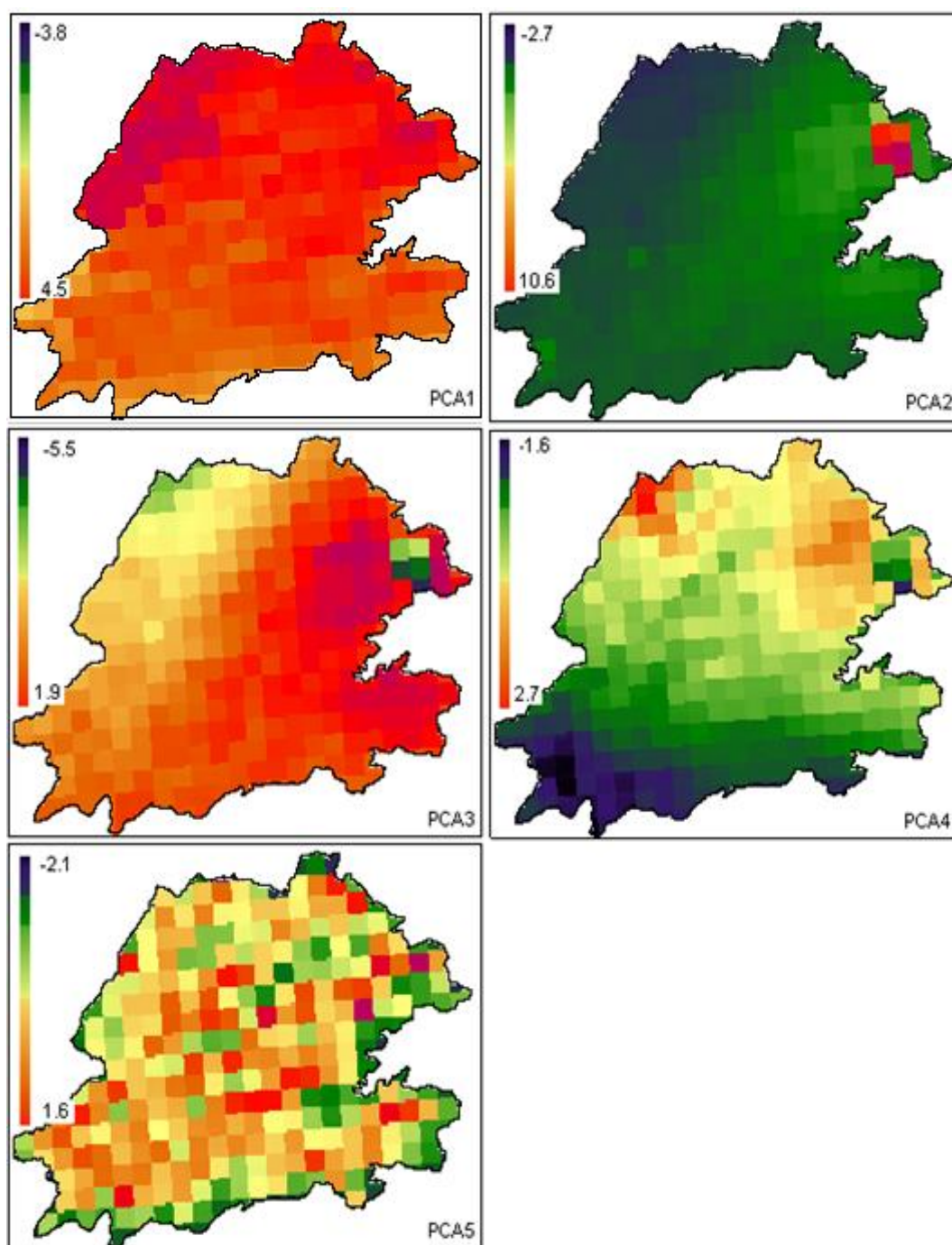


Figure 3.11 Maps showing geographic distributions of PCA axes scores of environmental surrogates

3.2.4 Efficacy of P Median Model for Representing Biodiversity of Lesser Caucasus Region

As expressed in methodology part, p-median model was used to detect environmental diversity (ED) areas. These ED areas were identified in order to test biodiversity representation of them and to evaluate efficiency of environmental surrogates in conservation area planning. Result of the p median model can be seen below in Figure 3. 12. As is seen, this map exhibits locations and distributions of environmental diversity (ED) areas. And as it is recognized, ED areas mostly located in North West part of the study area which is around Kaçkar mountain ranges and Çoruh valley (highlighted with red circle) (Figure 3. 12).

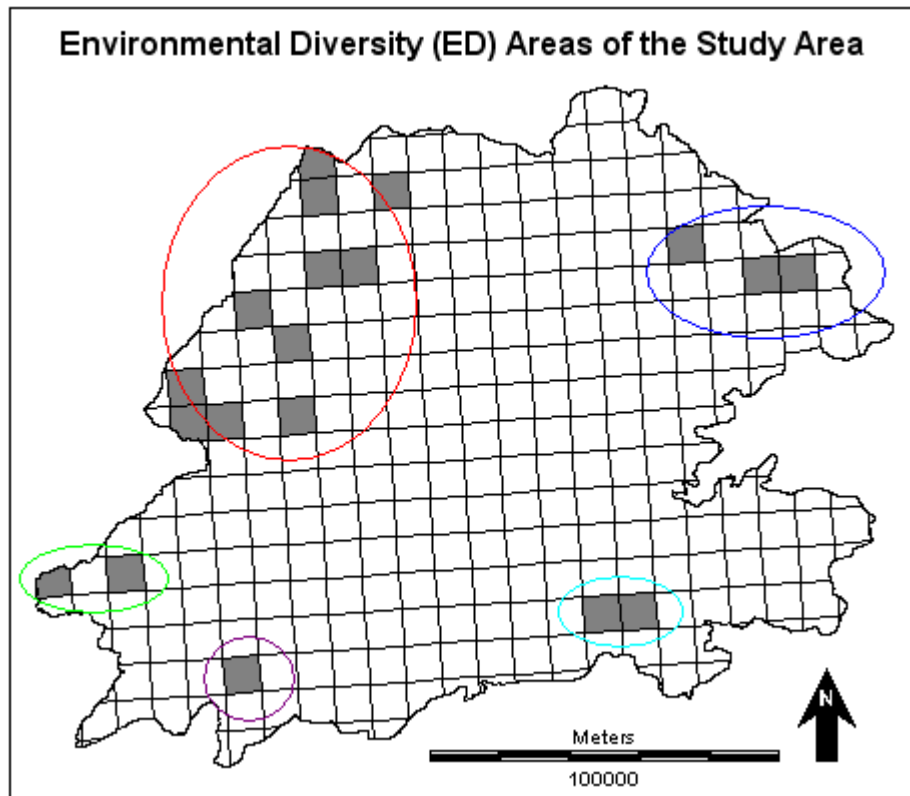


Figure 3.12 Map showing distributions and locations of environmental diversity (ED) areas

There are also some other sites that are in south west (green circle) and north east (blue circle) parts of the area (Figure 3.12). These sites are substantially meaningful in respect to their locations since these are very much congruent with

some of the complementarity based priority biodiversity protected areas. Furthermore, there are three more sites in south-west and south-east parts of the study area detected as ED areas (circled with purple and light blue, Figure 3.12). Among them, areas that are marked with light blue circle are very meaningful in respect to demonstrate congruence with some biodiversity complementarity sites.

After presenting result of p median model visually with a map, four different measurements were applied in order to assess their surrogate efficiency and biodiversity representation. Firstly, visual comparison was done between complementarity based priority biodiversity protected areas and p median based ED areas. And then Jaccard coefficient was calculated to implement more formal comparison between them. Below maps indicate distributions of both biodiversity protected areas and ED areas. These are presented together in order to do easy comparison during visual comparison and further assessments (Figure 3.13).

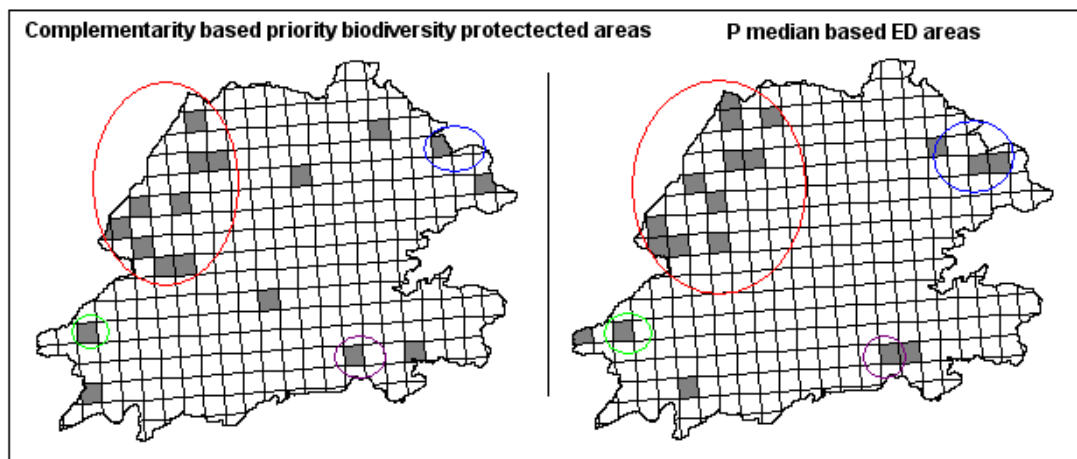


Figure 3.13 Maps showing distributions and locations of both P median based environmental diversity (ED) areas and complementarity based priority biodiversity protected areas

As is seen from these maps, both approaches tend to select their sites mostly around north west part of the study area that is near to Kaçkar mountain ranges and Çoruh valley. And, it is known that this part of the area is very attractive with its precious biodiversity features. Also, there are two more overlapped sites in south west and south east parts (green and purple circles). The area that is in the south west is very remarkable with its butterfly composition while the other site marked with purple is around Sarıkamış Allahuekber mountains national park and featured with its scots pine forest and these forest host many species. There is also another

part in north east part of the study signed with blue colour. Even though sites in that part of the area do not indicate any overlap, these are substantive due to occupy around Lake Çıldır and Aktaş. These both lakes are important wetlands for the area in respect to host many colonies of birds. Although, this general appearance that exhibits congruence among detected sites of both approaches is very hopeful, looking result of Jaccard coefficient is substantially useful to reach a certain conclusion about locational harmony between these two approaches. Below table demonstrates result of Jaccard coefficient between complementarity based site selection and p median model. And as is seen, coefficient indicating percentage overlap between these two approaches is 36.36 (Table 3.12). That is, overlap is not high as expected. Even if high overlap between biodiversity sites and environmental diversity sites means efficiency of environmental surrogates in respect to represent biodiversity of the area, by looking at this low congruence, it early to say that there is poor environmental surrogate efficiency for representing biodiversity.

Table 3.12 Table shows results of Jaccard Coefficient between complementarity based site selection and P median model

Site selection based on	Biodiversity surrogates	Environmental surrogates
Biodiversity surrogates		36.36
Environmental surrogates		

Another measurement that was applied is percent representation. It was used to compare results of complementarity based priority biodiversity areas, p median based ED areas and random null model. Percent representation values were calculated separately for three of these and a graph was plotted to indicate results (Figure 3.14). Although percent representation value is a quite simple calculation, it is very effective to measure representation of each taxon for each approach. In this way, efficiencies of approaches can be evaluated in terms of biodiversity representation.

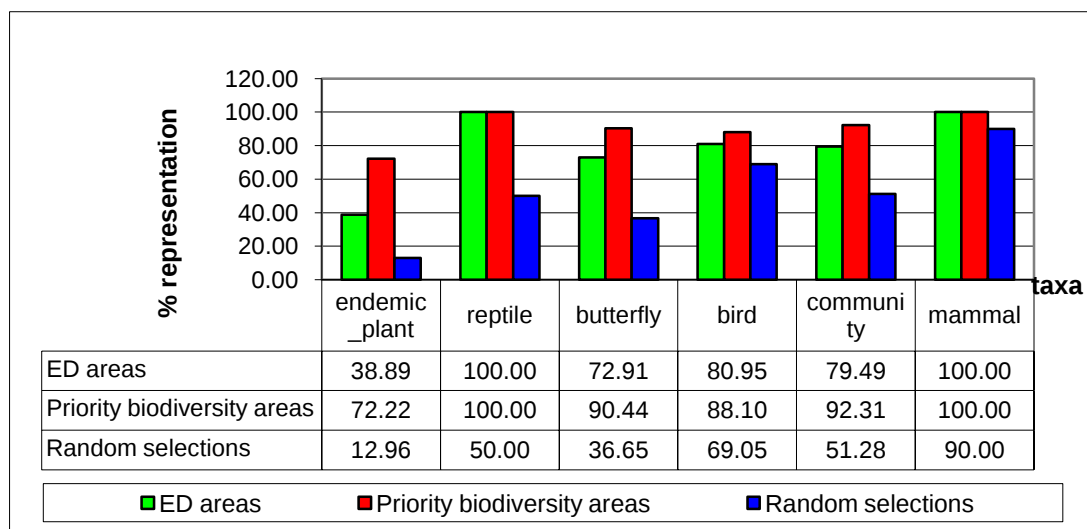


Figure 3.14 Graph showing percent representations of each approach

As can be observed from the graph, random null model is the worst one among others in terms of its percent representation values. That is to say, its biodiversity representation is very poor. And the priority biodiversity sites have highest representation values for all taxa whereas ED areas have smaller percent representations than the priority biodiversity areas. This means that ED areas remain less representative for biodiversity of the area. Especially, ED areas are very poor for representing endemic and non endemic highly threatened plant species. Their representation value for plant taxa is 38.89 %. However, representation values of ED areas for other taxa that are reptile, butterfly, bird, community and mammal are not worse. Particularly, representation for reptile and mammal are great since representation values of ED areas for these taxa are 100%. This means that these taxa can be represented with their all species. And for butterfly, bird and community, ED areas indicate fairly well representations.

Their representation values are 72.91 %, 80.95 % and 79.49 % respectively. Although, ED areas have not bad representations for most of taxa, these are not as good as priority biodiversity areas for representing biodiversity of the area

Furthermore, cumulative representations were calculated for complementarity based priority biodiversity areas, p median based ED areas and random selections. And then accumulation curves for each of these three approaches were plotted (Figure 3.15). These curves demonstrate total number of species represented within detected sites of each approach. That is, this graph exhibits efficiency of each approach in terms of biodiversity representation. Also, it provides to test whether efficiency of approaches is a chance or not. When investigating this graph, it is clearly distinguished that both priority biodiversity areas and ED areas have cumulative representation values higher than random selections. That is, these are more efficient than random selections and at the same time, their efficiency in respect to biodiversity representation is not a chance. As is seen in previous measurement that is percent representation, once again priority biodiversity areas are more successful than ED areas since they have higher cumulative representation values. This means that these sites include more species than ED sites and this provide more effective conservation for the study area.

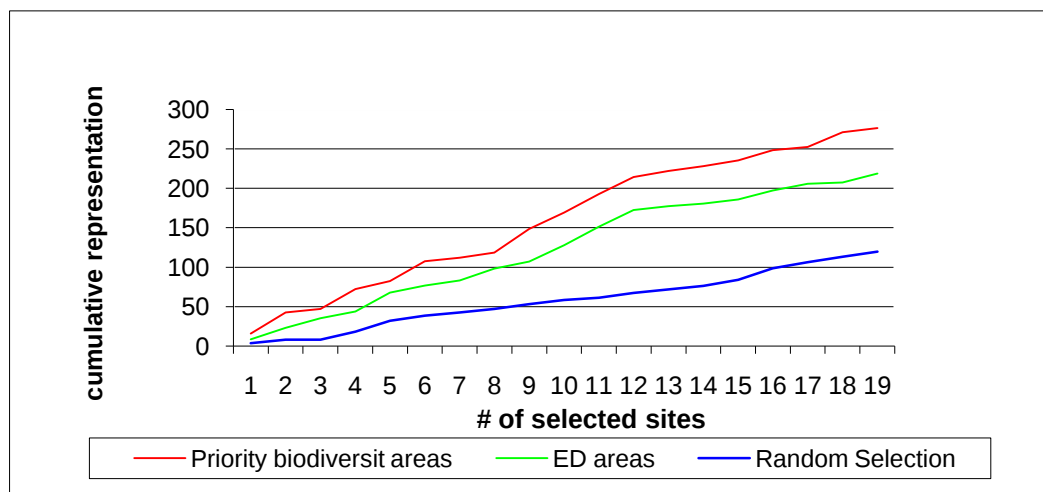


Figure 3.15 Graph showing cumulative representations of each approach

Although priority biodiversity areas, in other words sites selected with biodiversity surrogates are more successful than ED areas detected with environmental surrogates for representing biodiversity of the area, the pleasing situation is that cumulative representation of ED areas are too close to the cumulative representation values of priority biodiversity areas. And other important thing is that efficiency of ED areas with regard to biodiversity representation is not coincidental since their cumulative representation values higher than cumulative representation values of random selection. All these are too crucial due to prove efficiency of environmental surrogates for representing biodiversity.

Fourth measurement is complementarity score. It was calculated for each of three approaches in order to investigate their complementarity. Also, percent complementarity was calculated to do more reasonable comparisons. Results of complementarity calculations can be seen below in table 3.13 (Table 3.13). As this table demonstrates, priority biodiversity areas have the highest complementarity score and percent complementarity that are 4.505 and 75.07 while ED areas have the second highest values for complementarity score (4.109) and percent complementarity (68.48%). And random selection remains as the worst one among them once again with its lowest complementarity score (2.696) and percent complementarity (44.93%).

Table 3.13 Table shows both complementarity scores and their percent values for complementarity based priority biodiversity areas, p median based ED areas and random selection

	Priority biodiversity areas	Ed areas	Random selection
Avg-Complementarity score	4.505	4.109	2.696
% Complementarity score	75.07	68.48	44.93

All these mean that priority biodiversity areas are more successful than ED areas and random selection in regard to biodiversity complementarity. Complementarity is one of the significant aspects of the conservation area planning. Actually, it expresses variability of the protected areas network in terms species composition. That is, the greater the complementarity score, the greater the species composition of the protected areas network. And this provide more effective biodiversity conservation for an area since in this case, protected areas network includes different species of the area and can represent wide variety of biodiversity of the area.

Last measurement is a little bit different from the others because up to now, effectiveness of ED areas and random selection has been measured with biodiversity representations. And comparisons among three approaches have been performed using different measures related to the biodiversity. However in that part, variation scores of PCA axis 1 and axis 2 were used to compare differences among three approaches. In other words this time, comparison among complementarity based priority biodiversity areas, P median based ED areas and random selection were implemented in respect to environmental variation, not biodiversity representation. Below graph indicates results of variation scores for each of three approaches (Figure 3.16).

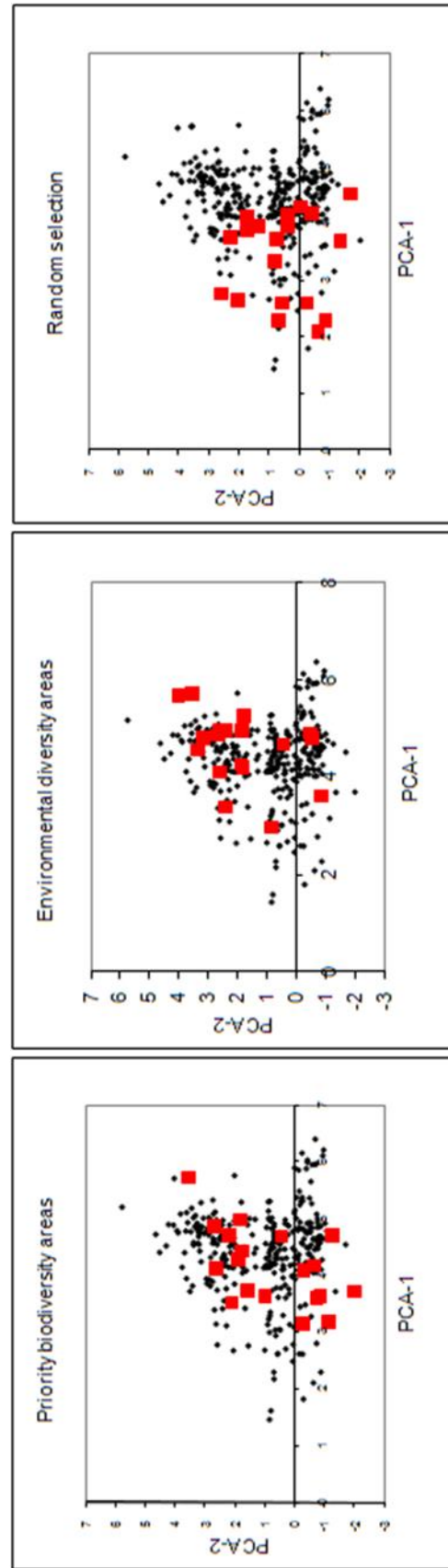


Figure 3.16 Graph showing environmental variation scores of PCA-1&2 for priority biodiversity areas, ED areas and random selection

In this graph, X axis represents variation score of component 1 while Y axis represents variation score of component 2. And points on graphs indicate detected areas of related approaches together with their variation scores. That is, when investigating these graphs, environmental variations of areas of each approach can be differentiated. As is recognized from Figure 3.16, environmental variation scores of both priority biodiversity areas and ED areas are almost resemble since their points occupy more or less same parts of the graphs. Especially, sites that are on the above parts of the graphs very much look like each other in terms of their environmental variation scores. However, random selection distributes very different parts of the area. They are generally scatters between 0 and 4 units of PCA-2 while priority protected areas and ED areas disperse around 4 on PCA-2. This means that environmental variation scores of random selection according to PCA-1 and PCA-2 are not same with environmental variation scores of priority biodiversity areas and ED areas. Also, their environmental variation scores are not as high as environmental variation scores of other approaches. That is to say, both priority biodiversity areas and ED areas have high environmental variation while environmental variation of random null model remains less according to them.

Lastly, it can be said that four different measurements were used to evaluate performance of ED areas. One of them among these measurements is related with the environmental variations while others are related with the biodiversity representation. Also, in order to reveal success of ED areas detected using environmental surrogates, comparisons were applied with priority biodiversity areas selected with biodiversity surrogates and random null model. And as all results of these measurements exhibit both priority biodiversity areas and ED areas are always more successful than random null model in terms of biodiversity representations. This means that their efficiency to represent biodiversity is not incidental. And the other prominent thing about results is that although priority biodiversity areas and ED areas are very much resemble with their environmental variation scores and demonstrate near representation results for biodiversity, priority biodiversity areas are more efficient than ED areas in respect to biodiversity representation. That is to say, even if environmental diversity used to detect ED areas are effective as surrogate for representing biodiversity of the study area, these are not as good as biological taxa used to select priority biodiversity areas in terms of biodiversity representation of the area. This less efficiency of environmental surrogates for representing biodiversity may be due to the deficiency of environmental diversity data or unsuitability of p median algorithm

used to detect ED areas. Nevertheless, efficiency of environmental diversity as surrogate for representing biodiversity is very encouraging in order to improve results and use them in conservation area planning. For increasing biodiversity representation potential of environmental diversity surrogates, methodologies that were applied to produce environmental surrogate surface may be revised and p median algorithm used to determine ED sites may be improved. Other important point that can lead to the inefficiency of ED areas for representing biodiversity may be resolution of the UTM grids. As it is known, resolution of UTM grids is 10*10 square km. This means that each study unit is 100 square km and this size of grids can be too large in order to properly reflect topographic features of them, especially for grids located in diverse topographic parts of the area. This situation mostly affects north west parts of the area where high mountain ranges and deep valleys occupy the area together. In that part of the area, topographic features such as elevation, slope, aspect and ruggedness and in parallel these; climatic features can change rapidly within very narrow parts. That is, in this case, it may not be highly possible to capture every aspect of environmental diversity such a large grid size. And all of these can cause to decrease biodiversity representation efficiency of environmental surrogates. Due to these defects, using just environmental diversity as surrogate in conservation area planning of lesser Caucasus region may not be a good idea. Therefore, using environmental surrogates in combination with biodiversity surrogates or using only biodiversity as surrogate in order to determine priority protected areas for lesser Caucasus region seems more wisely as long as not improving biodiversity representation efficiency of environmental surrogates.

CHAPTER 4

CONCLUSION

As emphasized in previous parts, this thesis that aims to investigate cross taxon congruence and efficiency of environmental diversity for representing biodiversity is the first example of such a study for Turkey. Both questions that tried to solve and evaluated during the thesis is too valuable for biodiversity conservation since they can provide useful contributions for biodiversity conservation studies.

In the first part of thesis, cross taxon congruence among different taxonomic groups were examined. This means that each taxon was evaluated in respect to its biodiversity representation efficiency. This would provide to figure out which taxonomic group can be a good surrogate in order to represent biodiversity of an area. Results of the thesis indicated that endemic and non endemic highly threatened plant species, butterfly species and ecological communities separately can represent biodiversity of an area well enough so each of these taxa can be suggested as surrogate for conservation area planning to represent biodiversity. However, remaining taxa that are bird, amphibian and reptile and large mammals cannot indicate high biodiversity representation. This means that these are not good surrogates to use them in conservation area planning. Another prominent thing among results, In order to protect ecological communities and butterfly species in protected area network, ecological communities, butterfly and endemic and non endemic highly threatened plants can be used as surrogate. But, to cover endemic and non endemic highly threatened plants in selected sites, only plant taxon should be used as surrogate since otherwise, plant taxon cannot be represented within protected areas. This indicates that to protect such a highly threatened and endemic species, their own taxa should be used as surrogate while designing protected area network (Figure 4.1).

In the second part of thesis, efficiency of environmental diversity in respect to biodiversity representation was evaluated. As results of this part demonstrated, even though environmental surrogates can represent biodiversity of an area well, these are not as good as biodiversity surrogates. Then, if there is reliable and complete biodiversity data set, using this biological data as surrogate can be recommended instead of using environmental surrogates. However, if there is not appropriate biological data to use them in conservation area planning and suitable conditions like enough resource, enough time to carry out detailed field studies, then using environmental diversity as surrogate can be an alternative choice. An important point that would be useful to be remembered is that using environmental surrogate together with highly threatened and endemic species like endemic and non endemic highly threatened plant species can not only increase representation of related taxon but also increase representation of other taxa. Therefore, it can be wise to incorporate such taxonomic groups among environmental surrogates in order to increase biodiversity representation of protected areas network (Figure 4.1).

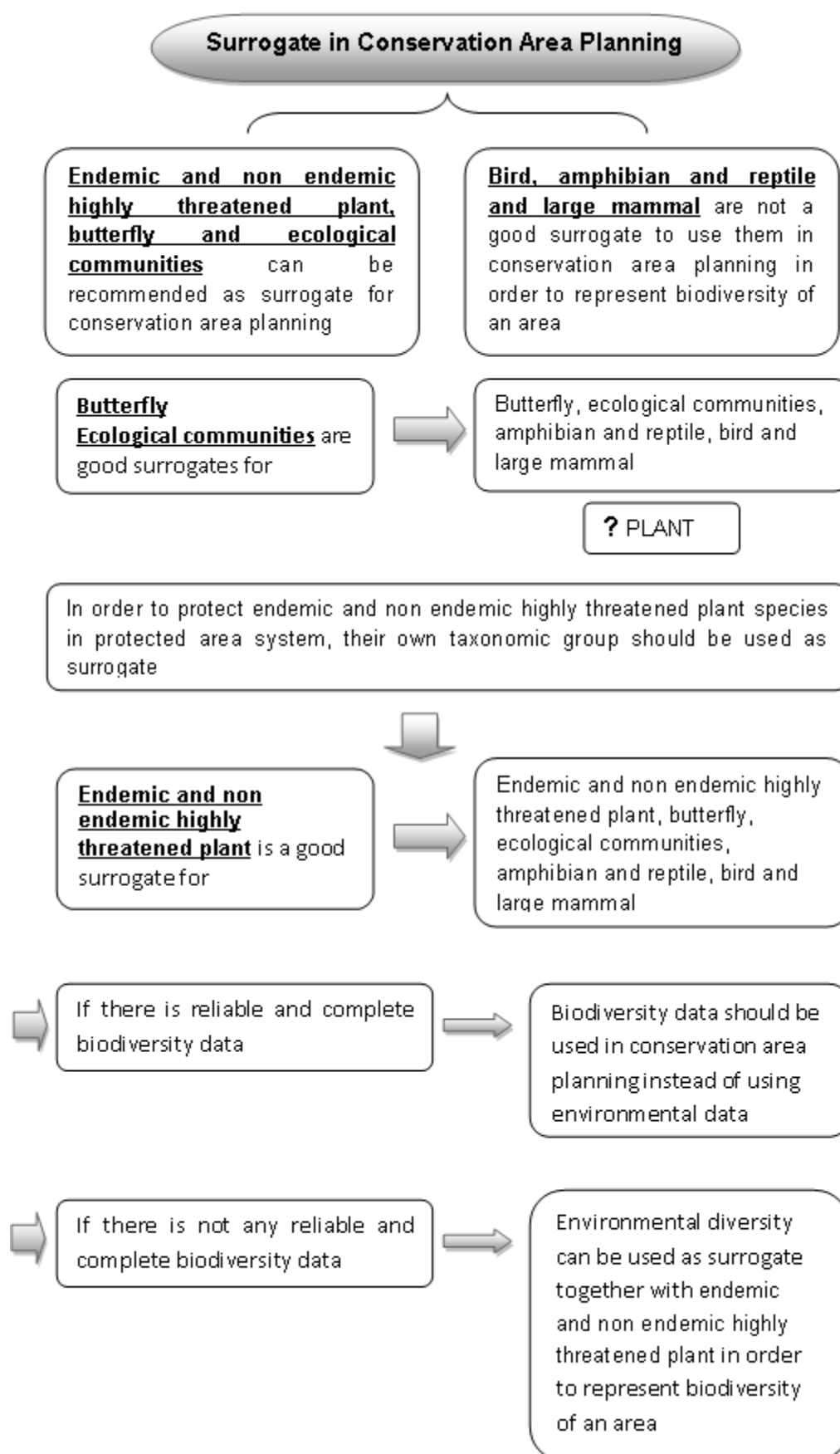


Figure 4.1 Schematic presentation of conclusion of the Thesis

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Appendix A

SPECIES OF THE LESSER CAUCASUS REGION

Table A.1: Endemic and non endemic highly threatened plants of the lesser caucasus ecoregion

No	Species name	Species id
1	<i>Allium pseudoalbidum</i>	1101
2	<i>Anthemis calcarea</i> var. <i>calcarea</i>	1102
3	<i>Anthemis calcarea</i> var. <i>discoidea</i>	1103
4	<i>Asperula virgata</i>	1104
5	<i>Astragalus eliasianus</i>	1105
6	<i>Astragalus tatlii</i>	1106
7	<i>Barbarea lutea</i>	1107
8	<i>Campanula choruhensis</i>	1108
9	<i>Campanula troegerae</i>	1109
10	<i>Centaurea armena</i>	1110
11	<i>Centaurea leptophylla</i>	1111
12	<i>Centaurea straminicephala</i>	1112
13	<i>Centaurea taochia</i>	1113
14	<i>Cephalaria anatolica</i>	1114
15	<i>Chaerophyllum karsianum</i>	1115
16	<i>Cirsium davisianum</i>	1116
17	<i>Cirsium eliasianum</i>	1117
18	<i>Clypeola raddeana</i>	1118
19	<i>Crocus biflorus</i> spp. <i>artvinensis</i>	1119
20	<i>Crocus biflorus</i> spp. <i>fibroannulatus</i>	1120
21	<i>Delphinium munzianum</i>	1121
22	<i>Drosera rotundifolia</i>	1122
23	<i>Elymus sosnowskyi</i>	1123
24	<i>Galanthus caucasicus</i>	1124
25	<i>Galanthus krasnovii</i>	1125
26	<i>Galium tortumense</i>	1126
27	<i>Geranium platypetalum</i> var. <i>albipetalum</i>	1127

Table A.1 (continued)

No	Species name	Species id
28	<i>Helichrysum artvinense</i>	1128
29	<i>Heracleum sphondylium</i> spp. <i>artvinense</i>	1129
30	<i>Hieracium diaphanoidiceps</i>	1130
31	<i>Hieracium foliosissimum</i>	1131
32	<i>Hieracium radiatellum</i>	1132
33	<i>Hieracium tamderense</i>	1133
34	<i>Hypericum fissurale</i>	1134
35	<i>Hypericum marginatum</i>	1135
36	<i>Iris caucasica</i> spp. <i>caucasica</i>	1136
37	<i>Knautia montana</i>	1137
38	<i>Lamium tschrochense</i>	1138
39	<i>Lamium vreemanii</i>	1139
40	<i>Lathyrus woronovii</i>	1140
41	<i>Morina persica</i> var. <i>decussatifolia</i>	1141
42	<i>Onosma arcuatum</i>	1142
43	<i>Onosma circinnatum</i>	1143
44	<i>Orobanche armena</i>	1144
45	<i>Paracaryum leptophyllum</i>	1145
46	<i>Reseda armena</i> var. <i>scabridula</i>	1146
47	<i>Rhodothamnus sessilifolius</i>	1147
48	<i>Scutellaria orientalis</i> ssp. <i>tortumensis</i>	1148
49	<i>Sempervivum brevipetalum</i>	1149
50	<i>Stachys choruhensis</i>	1150
51	<i>Symphytum savvalense</i>	1151
52	<i>Verbascum decursivum</i>	1152
53	<i>Verbascum gracilescens</i>	1153
54	<i>Viola yuzufeliensis</i>	1154

Table A.2: Globally important amphibian and reptile species of the lesser caucasus ecoregion

No	Species name	Species id
1	<i>Vipera barani</i>	2001
2	<i>Vipera wagneri</i>	2002
3	<i>Vipera kaznakovi</i>	2003
4	<i>Vipera (ursinii) eriwanensis</i>	2004
5	<i>Lacerta clarkorum</i>	2005
6	<i>Mertensiella caucasica</i>	2006

Table A.3: Butterfly species of the lesser caucasus ecoregion

No	Species Name	Species id
1	<i>Aglais utricae</i> subspec. <i>turcica</i>	3001
2	<i>Anthocharis damone</i> subspec. <i>eunomia</i>	3002
3	<i>Anthocharis gruneri</i> subspec. <i>armeniaca</i>	3003
4	<i>Aporia crataegi</i> subspec. <i>crataegi</i>	3004
5	<i>Arethusana arethusana</i>	3005
6	<i>Argynnis adippe</i> subspec. <i>adippe</i>	3006
7	<i>Argynnis aglaja</i> subspec. <i>aglaja</i>	3007
8	<i>Argynnis niobe</i> subspec. <i>orientalis</i>	3008
9	<i>Argynnis pandora</i> subspec. <i>pandora</i>	3009
10	<i>Argynnis paphia</i> subspec. <i>paphia</i>	3010
11	<i>Boloria caucasica</i>	3011
12	<i>Boloria euphrosyne</i> subspec. <i>euphrosyne</i>	3012
13	<i>Boloria graeca</i> subspec. <i>karina</i>	3013
14	<i>Brenthis daphne</i> subspec. <i>daphne</i>	3014
15	<i>Brenthis hecate</i> subspec. <i>hecate</i>	3015
16	<i>Brenthis ino</i> subspec. <i>schmitzi</i>	3016
17	<i>Brintesia circe</i>	3017
18	<i>Callophrys chalybeitincta</i>	3018
19	<i>Callophrys paulae</i>	3019
20	<i>Callophrys rubi</i>	3020
21	<i>Callophrys suaveola</i>	3021
22	<i>Carcharodus alceae</i>	3022
23	<i>Carcharodus flocciferus</i>	3023
24	<i>Carcharodus lavatherae</i>	3024
25	<i>Carcharodus orientalis</i>	3025
26	<i>Carcharodus stauderi</i>	3026
27	<i>Celastrina argiolus</i> subspec. <i>argiolus</i>	3027
28	<i>Chazara bischoffii</i>	3028
29	<i>Chazara briseis</i> subspec. <i>meridionalis</i>	3029
30	<i>Chazara persephone</i> subspec. <i>transiens</i>	3030
31	<i>Chilades trochylus</i> subspec. <i>trochylus</i>	3031
32	<i>Coenonympha arcania</i>	3032
33	<i>Coenonympha glycerion</i> subspec. <i>glycerion</i>	3033
34	<i>Coenonympha leander</i> subspec. <i>leander</i>	3034
35	<i>Coenonympha pamphilus</i>	3035
36	<i>Coenonympha symphyta</i>	3036
37	<i>Colias alfacariensis</i>	3037
38	<i>Colias aurorina</i> subspec. <i>aurorina</i>	3038
39	<i>Colias chlorocoma</i>	3039
40	<i>Colias crocea</i>	3040
41	<i>Colias hyale</i>	3041
42	<i>Colias thisoa</i> subspec. <i>thisoa</i>	3042
43	<i>Cupido argiades</i> subspec. <i>argiades</i>	3043

Table A.3 (continued)

No	Species Name	Species id
44	Cupido mimimus subspec.minimus	3044
45	Cupido osiris	3045
46	Eogenes alcides	3046
47	Erebia aethiops subspec.melusina	3047
48	Erebia graucasica subspec.transcaucasica	3048
49	Erebia hewitsonii	3049
50	Erebia medusa subspec.euphrasia	3050
51	Erebia melancholica	3051
52	Erynnis marloyi	3052
53	Erynnis tages	3053
54	Esperarge climene subspec.valentinae	3054
55	Euchloe ausonia subspec.taurica	3055
56	Euchloe penia	3056
57	Euphydryas aurinia subspec.bulgarica	3057
58	Glaucopsyche alcon subspec.monticola	3058
59	Glaucopsyche alexis subspec.alexis	3059
60	Glaucopsyche arion subspec.arion	3060
61	Glaucopsyche iolas subspec.lessei	3061
62	Glaucopsyche nausithous	3062
63	Gonepteryx farinosa subspec.farinosa	3063
64	Gonepteryx rhamni subspec. miljanowskii	3064
66	Hesperia comma	3066
67	Hipparchia fatua subspec.fatua	3067
68	Hipparchia parisatis	3068
69	Hipparchia pellucida subspec.pellucida	3069
70	Hipparchia statilinus	3070
71	Hipparchia syriaca subspec.syriaca	3071
72	Hyponphele lupina subspec.intermedia	3072
73	Inachis io subspec.io	3073
74	Iphiclides podalirius subspec. podalirius	3074
75	Issoria lathonia	3075
76	Krinia roxelana	3076
77	Lampides boeticus	3077
78	Lasiommata maera	3078
79	Lasiommata megera subspec.transcaspica	3079
80	Lasiommata petropolitana subspec.petropolitana	3080
81	Leptidea duponcheli subspec.lorkovici	3081
82	Leptidea sinapis subspec. sinapis	3082
83	Libythea celtis subspec.celtis	3083
84	Limenitis camilla subspec.camilla	3084
85	Limenitis reducta subspec.herculeana	3085
86	Lycaena alciphron subspec. melibaeus	3086

Table A.3 (continued)

No	Species Name	Species id
87	Lycaena asabinus	3087
88	Lycaena candens subspec. candens	3088
89	Lycaena ochimus subspec. ochimus	3089
90	Lycaena phlaeas subspec. phlaeas	3090
91	Lycaena thersamon	3091
92	Lycaena thetis subspec. thetis	3092
93	Lycaena tityrus subspec. tityrus	3093
94	Lycaena virgaureae subspec. virgaureae	3094
95	Maniola jurtina subspec. phormia	3095
96	Melanargia galathea subspec. satnia	3096
97	Melanargia larissa subspec. noacki	3097
98	Melanargia russiae subspec. russiae	3098
99	Melitaea arduinna	3099
100	Melitaea athalia subspec. athalia	3100
101	Melitaea aurelia subspec. ciscaucasica	3101
102	Melitaea caucasogenita	3102
103	Melitaea cinxia subspec. cinxia	3103
104	Melitaea diamina subspec. diamina	3104
105	Melitaea didyma subspec. didyma	3105
106	Melitaea interrupta subspec. interrupta	3106
107	Melitaea perseae subspec. perseae	3107
108	Melitaea phoebe subspec. phoebe	3108
109	Melitaea punica subspec. telona	3109
110	Melitaea trivia subspec. trivia	3110
111	Muschampia proteides	3111
112	Muschampia tessellum	3112
113	Neptis rivularis subspec. rivularis	3113
114	Nymphalis antiopa subspec. antiopa	3114
115	Nymphalis polychloros subspec. polychloros	3115
116	Nymphalis vaualbum subspec. vaualbum	3116
117	Nymphalis xanthomelas subspec. fervescens	3117
118	Ochlodes venatus	3118
119	Papilio alexanor subspec. orientalis	3119
120	Papilio machaon subspec. syriacus	3120
121	Pararge aegeria subspec. tircis	3121
122	Parnassius apollo subspec. graslini	3122
123	Parnassius apollo subspec. tirabzonus	3123
124	Parnassius mnemosyne caucasica	3124
125	Parnassius mnemosyne caucasica subspec. nubilosus	3125
126	Parnassius nordmanni thomai	3126
127	Pieris bowdeni	3127

Table A.3 (continued)

No	Species Name	Species id
128	<i>Pieris brassicae</i> subspec. <i>brassicae</i>	3128
129	<i>Pieris bryoniae</i> subspec. <i>turcica</i>	3129
130	<i>Pieris ergane</i> subspec. <i>detersa</i>	3130
131	<i>Pieris krueperi</i> subspec. <i>krueperi</i>	3131
132	<i>Pieris mannii</i> subspec. <i>hethaea</i>	3132
133	<i>Pieris napi</i> subspec. <i>pseudorapae</i>	3133
134	<i>Pieris rapae</i> subspec. <i>rapae</i>	3134
135	<i>Plebeius agestis</i>	3135
136	<i>Plebeius alcedo</i>	3136
137	<i>Plebeius anteros</i> subspec. <i>crasspunctus</i>	3137
138	<i>Plebeius argus</i> subspec. <i>aegidion</i>	3138
139	<i>Plebeius argyrognomon</i> subspec. <i>caspicus</i>	3139
140	<i>Plebeius artaxerxes</i> subspec. <i>sheljuzhkoi</i>	3140
141	<i>Plebeius eumedon</i> subspec. <i>eumedon</i>	3141
142	<i>Plebeius eumedon</i> subspec. <i>modestus</i>	3142
143	<i>Plebeius eurypilus</i> subspec. <i>eurypilus</i>	3143
144	<i>Plebeius idas</i> subspec. <i>baldur</i>	3144
145	<i>Plebeius isauricus</i> subspec. <i>latimargo</i>	3145
146	<i>Plebeius loewii</i> subspec. <i>loewii</i>	3146
147	<i>Plebeius pylaon</i> subspec. <i>sephirus</i>	3147
148	<i>Plebeius pyrenaicus</i> subspec. <i>dardanus</i>	3148
149	<i>Plebeius teberdinus</i> subspec. <i>nahizericus</i>	3149
150	<i>Polygonia c-album</i>	3150
151	<i>Polygonia egea</i>	3151
152	<i>Polyommatus admetus</i>	3152
153	<i>Polyommatus aedon</i> subspec. <i>myrrhinus</i>	3153
154	<i>Polyommatus alcestis</i> subspec. <i>alcestis</i>	3154
155	<i>Polyommatus altivagans</i> subspec. <i>altivagans</i>	3155
156	<i>Polyommatus amandus</i> subspec. <i>amandus</i>	3156
157	<i>Polyommatus antidolus</i> subspec. <i>antidolus</i>	3157
158	<i>Polyommatus aserbeidschanus</i>	3158
159	<i>Polyommatus bellargus</i>	3159
160	<i>Polyommatus carmon</i> subspec. <i>carmon</i>	3160
161	<i>Polyommatus coelestinus</i>	3161
162	<i>Polyommatus corydonius</i> subspec. <i>caucasicus</i>	3162
163	<i>Polyommatus cyaneus</i> subspec. <i>cyaneus</i>	3163
164	<i>Polyommatus damon</i> subspec. <i>kotshubeji</i>	3164
165	<i>Polyommatus daphnis</i> subspec. <i>versicolor</i>	3165
166	<i>Polyommatus diana</i>	3166
167	<i>Polyommatus dorylas</i> subspec. <i>armenus</i>	3167
168	<i>Polyommatus eriwanensis</i>	3168

Table A.3 (continued)

No	Species Name	Species id
169	<i>Polyommatus eros</i> subspec.yildizae	3169
170	<i>Polyommatus firdussii</i>	3170
171	<i>Polyommatus hopfferi</i>	3171
172	<i>Polyommatus huberti</i>	3172
173	<i>Polyommatus icarus</i>	3173
174	<i>Polyommatus iphigenia</i> subspec.iphigenia	3174
175	<i>Polyommatus menalcas</i>	3175
176	<i>Polyommatus merhaba</i>	3176
177	<i>Polyommatus mithridates</i>	3177
178	<i>Polyommatus ninae</i>	3178
179	<i>Polyommatus phyllis</i> subspec.vanensis	3179
180	<i>Polyommatus poseidon</i> subspec.poseidon	3180
181	<i>Polyommatus ripartii</i>	3181
182	<i>Polyommatus semiargus</i> subspec.bellis	3182
183	<i>Polyommatus tankeri</i>	3183
184	<i>Polyommatus thersites</i>	3184
185	<i>Polyommatus turcicus</i>	3185
186	<i>Polyommatus wagneri</i>	3186
187	<i>Pontia callidice</i> subspec.chrysidice	3187
188	<i>Pontia chloridice</i> subspec.chloridice	3188
189	<i>Pontia edusa</i>	3189
190	<i>Proterebia afra</i> subspec.afra	3190
191	<i>Pseudochazara anthelea</i> subspec.anthelea	3191
192	<i>Pseudochazara beroe</i> subspec.beroe	3192
193	<i>Pseudochazara geyeri</i>	3193
194	<i>Pseudochazara mamurra</i> subspec.mamurra	3194
195	<i>Pseudochazara mnischechii</i> subspec.caucasica	3195
196	<i>Pseudochazara pelopea</i> subspec.persica	3196
197	<i>Pseudochazara thelephassa</i>	3197
198	<i>Pseudophilotes bavius</i> subspec.egea	3198
199	<i>Pseudophilotes vicrama</i> subspec.schiffermuelleri	3199
200	<i>Pyrgus cinarae</i>	3200
201	<i>Pyrgus (carlinae) cirsii</i>	3201
202	<i>Pyrgus (malvae) melotis</i>	3202
203	<i>Pyrgus alveus</i> subspec.alveus	3203
204	<i>Pyrgus armoricanus</i>	3204
205	<i>Pyrgus serratulae</i>	3205
206	<i>Pyrgus sidae</i>	3206
207	<i>Satyrium abdominalis</i>	3207
208	<i>Satyrium acaciae</i>	3208

Table A.3 (continued)

209	Satyrium hyrcanicum subspec.cyri	3209
210	Satyrium ilicis subspec.ilicis	3210
211	Satyrium ledereri subspec.ledereri	3211
212	Satyrium myrtale subspec.armenum	3212
213	Satyrium spini	3213
214	Satyrium w-album	3214
215	Satyrus amasinus subspec.amasinus	3215
216	Satyrus favonius subspec.favonius	3216
217	Scolitantides orion subspec.orion	3217
218	Spialia orbifer	3218
219	Spialia phlomidis	3219
220	Tarucus balkanicus	3220
221	Thecla betulae	3221
222	Thymelicus acteon	3222
223	Thymelicus hyrax	3223
224	Thymelicus lineola	3224
225	Thymelicus novus	3225
226	Thymelicus sylvestris	3226
227	Tomares callimachus	3227
228	Tomares romanovi	3228
229	Turanana endymion subspec.endymion	3229
230	Vanessa atalanta subspec.atalanta	3230
231	Vanessa cardui	3231
232	Anthocharis cardamines subspec.mischpopulationen	3232
233	Colias caucasica subspec. Caucasica	3233
234	Favonius quercus subspec.quercus	3234
235	Melanargia larissa subspec.massageta	3235
236	Thaleropsis ionia	3236
237	Pyrgus alveus subspec. alveus alveus and iliensis	3237
238	Pyrgus alveus subspec. iliensis	3238

Table A.4: Breeding bird species of the lesser caucasus ecoregion

No	Species name	Species id
1	Pernis apivorus (Honey Buzzard)	4001
2	Accipiter (Hawk)	4002
3	Coturnix coturnix (Quail)	4003
4	Anser anser (Greylag Goose)	4004
5	Saxicola rubetra (Whinchat)	4005
6	Actitis hypoleucos (Common Sandpiper)	4006
7	Delichon urbica (Common House Martin)	4007
8	Coracias garrulus (Roller)	4008
9	Dryocopus martius (Black Woodpecker)	4009
10	Aegypius monachus (Cinereous Vulture)	4010
11	Milvus migrans (Black Kite)	4011
12	Alectoris chukar (Chukar Partridge)	4012
13	Acrocephalus schoenobaenus (Sedge Warbler)	4013
14	Gyps fulvus (Griffon Vulture)	4014
15	Buteo rufinus (Long-legged Buzzard)	4015
16	Tringa totanus (Common Redshank)	4016
17	Neopron percnopterus (Egyptian Vulture)	4017
18	Hieraaetus pennatus (Booted Eagle)	4018
19	Falco naumanni (Lesser Kestrel)	4019
20	Aquila pomarina (Lesser Spotted Eagle)	4020
21	Sitta krueperi (Krüper's Nuthatch)	4021
22	Riparia riparia (Sand Martin)	4022
23	Haematopodidae (Oystercatcher)	4023
24	Aquila heliaca (Eastern Imperial Eagle)	4024
25	Gypaetus barbatus (Bearded Vulture)	4025
26	Motacilla citreola (Citrine Wagtail)	4026
27	Circus aeruginosus (Western Marsh Harrier)	4027
28	Columba palumbus (Common Wood Pigeon)	4028
29	Aythya fuligula (Tufted Duck)	4029
30	Circaetus gallicus (Short-toed Eagle)	4030
31	Pelecanus onocrotalus (Great White Pelican)	4031
32	Circus pygargus (Montagu's Harrier)	4032
33	Oxyura leucocephala (White-headed Duck)	4033
34	Crex crex (Corn Crane)	4034
35	Aythya nyroca (Ferruginous Duck)	4035
36	Ficedula semitorquata (Semi-collared Flycatcher)	4036
37	Tetrao mlokosiewiczi (Caucasian Grouse)	4037
38	Pelecanus crispus (Dalmatian Pelican)	4038

Table A.4 (continued)

No	Species name	Species id
39	Melanitta fusca (Velvet Scoter)	4039
40	Gruidae (Crane)	4040
41	Dendrocopos leucotos (White-backed Woodpecker)	4041
42	Podiceps grisegena (Red-necked Grebe)	4042

Table A.5: Ecological communities of the lesser caucasus ecoregion

No	Community name	Community id
1	Low mountain oak forest	5001
2	Alpine meadow	5002
3	High mountain step	5003
4	Mountain mixed oak hop-hornbeam forest	5004
5	High mountain mixed coniferous forest	5005
6	Mountain mixed oak juniper forest	5006
7	Low mountain mixed oak juniper forest	5007
8	High mountain populus forest	5008
9	Mountain populus forest	5009
10	Mountain oak forest	5010
11	Low mountain oak forest	5011
12	High mountain scotch pine forest	5012
13	Mountain oak juniper forest	5013
14	Alpine meadow	5014
15	Meadow	5015
16	Mountain oak forest	5016
17	Alpine meadow	5017
18	Meadow	5018
19	Low mountain mixed coniferous-broad leaved forest	5019
20	High mountain mixed broad leaved forest	5020
21	Mountain mixed broad leaved forest	5021
22	Low mountain mixed broad leaved forest	5022
23	High mountain mixed coniferous forest	5023
24	Mountain mixed coniferous forest	5024
25	Low mountain mixed coniferous forest	5025
26	High mountain populus forest	5026
27	Mountain populus forest	5027
28	Mountain oak forest	5028
29	Low mountain oak forest	5029
30	Shore oak forest	5030
31	High mountain scotch pine forest	5031
32	Mountain scotch pine forest	5032
33	Low mountain scotch pine forest	5033
34	High mountain beech forest	5034
35	Mountain beech forest	5035
36	Low mountain beech forest	5036
37	High mountain spruce forest	5037
38	Mountain spruce forest	5038
39	Low mountain spruce forest	5039

Table A.6: Ecological communities of the lesser caucasus ecoregion

No	Species name	Species id
1	Lynx lynx (lynx)	6001
2	Capra aegagrus (wild goat)	6002
3	Sus scrofa (wild boar)	6003
4	Canis aureus (jackal)	6004
5	Ursus arctos (grizzly bear)	6005
6	Lutra lutra (otter)	6006
7	Canis lupus (wolf)	6007
8	Cervidae (roe)	6008
9	Rupicapra rupicapra (ibex goat)	6009
10	Cervus elaphus (red deer)	6010

Appendix B

METEOROLOGY STATIONS

Table B.1: List of meteorology stations used to produce climate data layers

No	Name of Station	Province	Latitude	Longitude	Altitude
1	TRABZON	TRABZON	41	39.43	30
2	RIZE	RIZE	41.11	40.53	79
3	HOPA	ARTVIN	41.24	41.26	33
4	ARTVIN	ARTVIN	41.11	41.49	628.0
5	ERZINCAN	ERZINCAN	39.45	39.3	1218
6	ERZURUM	ERZURUM	39.57	41.1	1757
7	KARS	KARS	40.37	43.06	1775
8	AGRI	AGRI	39.43	43.03	1631.0
9	IGDIR	IGDIR	39.55	44.03	858
10	AKCAABAT	TRABZON	41.01	39.35	3.0
11	PAZAR	RIZE	41.11	40.53	79
12	ARDAHAN	ARDAHAN	41.07	42.43	1829.0
13	ARPACAY	KARS	40.51	43.2	1688.0
14	ISPIR	ERZURUM	40.29	41	1222
15	OLTU	ERZURUM	40.33	41.59	1321
16	BAYBURT	BAYBURT	40.15	40.14	1584
17	TORTUM	ERZURUM	40.18	41.33	1572
18	HORASAN	ERZURUM	40.03	42.1	1540
19	SARIKAMIS	KARS	40.2	42.34	2103
20	TERCAN	ERZINCAN	39.47	40.23	1425
21	MERZIFON	AMASYA	40 50	35 27	759
22	CORUM	CORUM	40 33	34 58	776
23	AMASYA	AMASYA	40 39	35 51	412
24	TOKAT	TOKAT	40 18	36 34	608
25	BAFRA	SAMSUN	41 33	35 35	20
26	TOSYA	KASTAMONU	41 01	34 02	820
27	OSMANCIK	ÇORUM	40 58	34 48	410
28	ZILE	TOKAT	40 18	35 53	700
29	SEBINKARAHISAR	GİRESUN	40 17	38 25	1300
30	TURHAL	TOKAT	40 54	36 05	500
31	SUSEHRI	SIVAS	40 09	38 04	1163
32	ZARA	SIVAS	39 54	37 45	1348

Table B.1 (continued)

No	Name of Station	Province	Latitude	Longitude	Altitude
33	SINOP	SINOP	42 02	35 10	32
34	SAMSUN	SAMSUN	41 51	36 15	4
35	ORDU	ORDU	40 59	37 54	4
36	SIVAS	SIVAS	39 45	37 01	1285
37	DOGUBEYAZIT	AĞRI	39 33	44 05	1725
38	GUMUSHANE	GUMUSHANE	40.28	39.28	1219

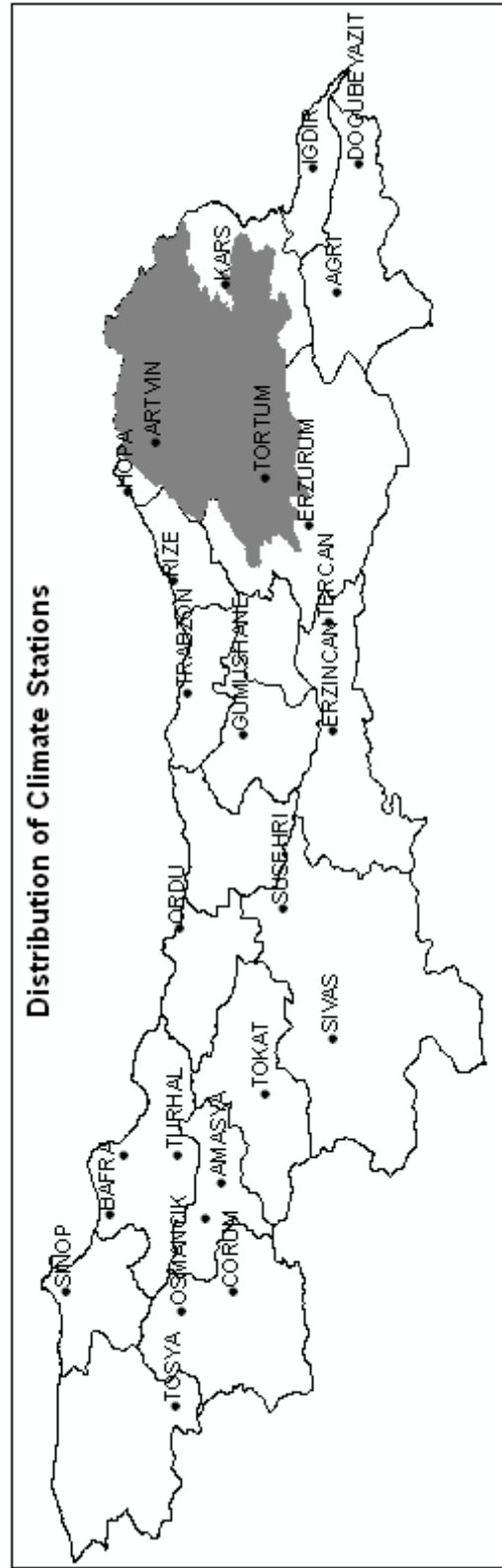


Figure B.1: Distribution of Climate Stations

Appendix C

PROTECTED AREAS OF THE LESSER CAUCASUS REGION

Table C.1: List for existing protected areas of the lesser Caucasus region

N o	Protected area name	Provi nce	Status	Are a	Declara tion
1	Camili-Gorgit	Artvin	Nature protected area	490, 5	1998
2	Camili-Efeler	Artvin	Nature protected area	145 3	1998
3	Hatila Vadisi	Artvin	National park	171 38	1994
4	Kaçkar Dağları	Rize	National park	515 50	1994
5	Sarıkamış- Allahuekber Dağları	Kars	National park	229 80	2004
6	Karagöl-Sahara	Artvin	National park	376 6	1994
7	Borkça-Karagöl	Artvin	Nature park	368	2002
8	Yusufeli çoruh Vadisi	Artvin	Wildlife protection and development areas	235 00	2002
9	Şavşat-Balıkli	Artvin	Wildlife protection and development areas	349 1	1981
1 0	Kars Sarıkamış Kağızman	Kars	Wildlife protection and development areas	208 00	1988
1 1	Posof	Ardah an	Wildlife protection and development areas	433 75	1981

Table C.1 (continued)

N o	Protected area name	Provi nce	Status	Are a	Declara tion
1 2	Kars Kuyucuk Gölü	Kars	Wildlife protection and development areas	245	1990
1 3	Erzurum Oltu	Erzuru m	Wildlife protection and development areas	504 4	1987
1 4	Erzurum Çat	Erzuru m	Wildlife protection and development areas	632 15	1981
1 5	Erzurum Ispir Vercenik Dağı	Erzuru m	Wildlife protection and development areas	631 30	1980
1 6	Pazaryolu	Erzuru m	Wildlife protection and development areas	203 26	1999
1 7	Rize çamlıhemşin Kaçkar	Rize	Wildlife protection and development areas	432 0	1973

Appendix D

RESULTS OF MARXAN FOR OPTIMUM NUMBER OF PRIORITY PROTECTED AREAS OF EACH COMBINATION SET

Table D.1: 20 solution sets of endemic and non-endemic highly threatened plants

Run no.	Score	Cost	Boundary Length	Penalty	Shortfall	Missing Values	Planning Units
1	6290.61	1740.64	605	3944.97	15	15	18
2	6266.84	1700.7	570	3996.14	15	15	18
3	6378.07	1724.17	555	4098.9	15	15	18
4	6195.12	1726.72	575	3893.4	15	15	18
5	6401.33	1723.5	575	4102.83	15	15	18
6	6399.1	1725.2	575	4098.9	15	15	18
7	6380.81	1723.5	555	4102.31	15	15	18
8	6129.52	1713.37	575	3841.15	15	15	18
9	6290.16	1704.77	600	3985.39	15	15	18
10	6227.68	1725.87	605	3896.81	15	15	18
11	6234.16	1725.02	605	3904.14	15	15	18
12	6269.31	1703.92	580	3985.39	15	15	18
13	6206	1716.78	555	3934.22	15	15	18
14	6206.69	1724.36	585	3897.33	15	15	18
15	6228.56	1715.93	575	3937.63	15	15	18
16	6356.35	1730.69	545	4080.66	15	15	18
17	6232.72	1703.92	540	3988.8	15	15	18
18	6339.87	1731.55	535	4073.32	15	15	18
19	6215.87	1723.32	585	3907.55	15	15	18
20	6252.49	1715.93	595	3941.56	15	15	18

Table D.2: 20 solution sets of globally important amphibian and reptile

Run no.	Score	Cost	Boundary Length	Penalty	Shortfall	Missing Values	Planning Units
1	141.94	101.94	40	0	0	0	2
2	140.49	102.49	38	0	0	0	2
3	159.59	109.59	50	0	0	0	2
4	142.5	114.5	28	0	0	0	2
5	154.57	114.57	40	0	0	0	2
6	155.6	116.6	39	0	0	0	2
7	161.6	121.6	40	0	0	0	2
8	156.58	126.58	30	0	0	0	2
9	171.63	126.63	45	0	0	0	2
10	157.61	128.61	29	0	0	0	2
11	156.14	131.14	25	0	0	0	2
12	173.64	138.64	35	0	0	0	2
13	196.08	141.08	55	0	0	0	2
14	194.64	141.64	53	0	0	0	2
15	218.48	163.48	55	0	0	0	2
16	250.86	180.86	70	0	0	0	2
17	2272.08	1722.08	550	0	0	0	19
18	2297.2	1729.2	568	0	0	0	21
19	2331.3	1729.3	602	0	0	0	20
20	2294.56	1718.56	576	0	0	0	19

Table D.3: 20 solution sets of butterfly

Run no.	Score	Cost	Boundary Length	Penalty	Shortfall	Missing Values	Planning Units
1	2943.06	1686.17	515	741.89	16	16	19
2	2951.51	1694.33	517	740.18	16	16	19
3	2934.57	1687.68	505	741.89	16	16	19
4	2938.96	1691.78	507	740.18	16	16	19
5	2953.04	1694.15	517	741.89	16	16	19
6	2834.54	1687.02	451	696.52	16	16	19
7	2883.06	1686.17	455	741.89	16	16	19
8	2912.15	1715.26	455	741.89	16	16	19
9	2940.67	1691.78	507	741.89	16	16	19
10	2942.2	1687.02	515	740.18	16	16	19
11	2952.37	1693.48	517	741.89	16	16	19
12	2903.05	1687.87	475	740.18	16	16	19

Table D.3 (continued)

Run no.	Score	Cost	Boundary Length	Penalty	Shortfall	Missing Values	Planning Units
13	2903.91	1687.02	475	741.89	16	16	19
14	2919.82	1690.93	487	741.89	16	16	19
15	2921.52	1690.93	487	743.59	16	16	19
16	2923.05	1687.87	495	740.18	16	16	19
17	2901.52	1692.63	467	741.89	16	16	19
18	2882.37	1691.78	447	743.59	16	16	19
19	2883.91	1687.02	455	741.89	16	16	19
20	2901.52	1692.63	467	741.89	16	16	19

Table D.4: 20 solution sets of breeding bird

Run no.	Score	Cost	Boundary Length	Penalty	Shortfall	Missing Values	Planning Units
1	650.76	473.76	177	0	1	1	7
2	711.52	538.52	173	0	1	1	7
3	725.8	524.8	201	0	1	1	7
4	792.71	587.71	205	0	1	1	7
5	783.61	570.61	213	0	1	1	7
6	791.86	586.86	205	0	1	1	7
7	799.54	544.76	185	69.78	2	2	22
8	744.59	541.59	203	0	1	1	6
9	782.76	569.76	213	0	1	1	7
10	633.68	470.68	163	0	1	1	6
11	642.78	487.78	155	0	1	1	7
12	711.52	538.52	173	0	1	1	7
13	782.94	569.94	213	0	1	1	7
14	736.62	555.62	181	0	1	1	7
15	729.1	544.1	185	0	1	1	7
16	729.76	544.76	185	0	1	1	7
17	737.73	530.73	207	0	1	1	6
18	711.52	538.52	173	0	1	1	7
19	720.66	527.66	193	0	1	1	7
20	725.46	534.12	191	0	1	1	6

Table D.5: 20 solution sets of ecological communities

Run no.	Score	Cost	Boundary Length	Penalty	Shortfall	Missing Values	Planning Units
1	969.24	730.24	239	0	0	0	9
2	927.99	730.99	197	0	0	0	9
3	985.49	738.49	247	0	0	0	9
4	962.29	748.29	214	0	0	0	9
5	1047.72	767.72	280	0	0	0	9
6	1038.57	768.57	270	0	0	0	9
7	915.79	713.79	202	0	0	0	9
8	955.79	713.79	242	0	0	0	9
9	990.09	731.09	259	0	0	0	9
10	1033.03	776.03	257	0	0	0	10
11	1053.03	776.03	277	0	0	0	10
12	1075	782	293	0	0	0	9
13	947.13	730.13	217	0	0	0	9
14	989.24	730.24	259	0	0	0	9
15	1055.16	772.16	283	0	0	0	10
16	1056.68	773.68	283	0	0	0	10
17	1043.07	767.07	276	0	0	0	9
18	969.46	728.46	241	0	0	0	9
19	1029.47	769.47	260	0	0	0	9
20	1039.43	769.43	270	0	0	0	9

Table D.6: 20 solution sets of mammal

Run no.	Score	Cost	Boundary Length	Penalty	Shortfall	Missing Values	Planning Units
1	471.68	200.38	70	0	0	0	2
2	4047.32	1726.33	587	0	0	0	2
3	365.85	157.6	50	0	0	0	2
4	355.31	158.41	38	0	0	0	2
5	456.1	198.67	58	0	0	0	2
6	311.62	140.11	31	0	0	0	2
7	457.81	199.53	58	0	0	0	2
8	480.11	199.53	80	0	0	0	2
9	454.78	198.01	58	0	0	0	2
10	4066.72	1741.6	576	0	0	0	2
11	351.65	156.58	38	0	0	0	2
12	341.85	156.74	28	0	0	0	2
13	458.52	198.87	60	0	0	0	2

Table D.6 (continued)

Run no.	Score	Cost	Boundary Length	Penalty	Shortfall	Missing Values	Planning Units
14	301.98	143.9	14	0	0	0	2
15	345.77	158.7	28	0	0	0	2
16	379.31	159.26	60	0	0	0	2
17	369.77	159.56	50	0	0	0	2
18	357.35	161.96	33	0	0	0	2
19	369.32	167.44	34	0	0	0	2
20	437.53	182.8	71	0	0	0	2

Table D.7: 20 solution sets of butterfly, ecological community combination

Run no.	Score	Cost	Boundary Length	Penalty	Shortfall	Missing Values	Planning Units
1	4094.41	1707.7	497	1889.71	18.9	21	20
2	4207.33	1713.52	543	1950.81	20.6	22	19
3	4225.75	1708.89	531	1985.86	20.9	23	18
4	4510.33	1722.89	520	2267.44	21.2	24	20
5	4294.64	1714.64	553	2027	19.9	22	19
6	4285.61	1713.61	510	2062	19.2	22	20
7	4282.27	1712.46	480	2089.81	19.5	23	20
8	4342.78	1712.46	520	2110.32	20.9	23	20
9	4076.85	1706.14	481	1889.71	18.9	21	19
10	4354.28	1713.12	516	2125.16	20.9	23	19
11	4351.77	1714.83	499	2137.94	19.2	22	20
12	4378.64	1719.56	491	2168.08	20.6	22	20
13	4432.68	1713.97	529	2189.71	19.6	21	20
14	4263.44	1705.25	506	2052.19	20.9	23	19
15	4263.66	1695.58	505	2063.08	20.5	24	19
16	4461.66	1738.07	529	2194.59	22.2	25	20
17	4485.9	1729.43	531	2225.47	19.5	23	19
18	4290.97	1727.1	502	2061.87	20.9	23	20
19	4481.11	1713.91	497	2270.2	20.9	23	20
20	4521.27	1709.28	415	2396.27	20.9	23	20

Table D.8: 20 solution sets of breeding bird, ecological community combination

Run no.	Score	Cost	Boundary Length	Penalty	Shortfall	Missing Values	Planning Units
1	1408.35	1023.35	385	0	1	1	11
2	1391.76	1016.76	375	0	1	1	12
3	1354.12	995.12	359	0	1	1	11
4	1292.55	967.55	325	0	1	1	11
5	2377.42	1731.36	567	79.06	2	2	19
6	1458.82	1086.82	372	0	1	1	13
7	1455.21	1072.21	383	0	1	1	12
8	1441.66	1066.66	375	0	1	1	13
9	2787.77	1730.31	640	417.46	2.6	4	19
10	1465.09	1071.09	394	0	1	1	13
11	1485.29	1032.51	383	69.78	2	2	12
12	1345.8	925.02	351	69.78	2	2	10
13	3167.31	1727.56	593	846.75	4.2	7	19
14	1390.81	1015.81	375	0	1	1	12
15	2349.22	1721.44	558	69.78	2	2	19
16	1322.4	969.4	353	0	1	1	11
17	2325.24	1727.24	598	0	1	1	19
18	1333.96	970.96	363	0	1	1	11
19	1407.98	1018.98	389	0	1	1	12
20	2734.78	1737.78	567	430	2.6	4	19

Table D.9: 20 solution sets of endemic and non-endemic highly threatened plant, ecological community combination

Run no.	Score	Cost	Boundary Length	Penalty	Shortfall	Missing Values	Planning Units
1	7714.56	1742.9	624	5347.66	18.2	21	19
2	7711.73	1709.71	605	5397.02	18.2	21	19
3	7488.6	1712.08	585	5191.52	17.5	21	19
4	7523.25	1720.1	569	5234.15	17.2	20	19
5	7525.13	1706.88	558	5260.25	17.2	20	19
6	7539.7	1724.46	567	5248.24	17.9	20	19
7	7556.47	1738.02	582	5236.45	18.2	21	19
8	7333.62	1716.05	585	5032.57	17.2	20	19
9	7581.33	1743.59	607	5230.74	17.2	20	19
10	7337.88	1716.9	585	5035.98	17.2	20	19

Table D.9 (continued)

Run no.	Score	Cost	Boundary Length	Penalty	Shortfall	Missing Values	Planning Units
11	7591.48	1737.19	612	5242.29	17.8	22	19
12	7543.46	1713.58	548	5281.88	17.5	21	18
13	7626.91	1714.41	595	5317.5	18.5	22	18
14	7480.58	1719.11	595	5166.47	17.9	20	19
15	7529.84	1720.1	579	5230.74	17.9	20	19
16	7623.69	1717.75	575	5330.94	18.2	21	19
17	7608.53	1726.96	591	5290.57	17.8	22	19
18	7650.02	1714.52	594	5341.5	17.2	20	19
19	7714.89	1724.47	595	5395.42	18.2	21	19
20	7591.48	1737.19	612	5242.29	17.8	22	19

Table D.10: 20 solution sets of butterfly, endemic and non-endemic highly threatened plant combination

Run no.	Score	Cost	Boundary Length	Penalty	Shortfall	Missing Values	Planning Units
1	12165.29	1736.56	589	9839.73	48	48	18
2	11737.25	1701.94	562	9473.31	49	49	18
3	12115.55	1740.25	593	9782.3	51	51	19
4	12143.08	1738.94	595	9809.14	49	49	18
5	11896.03	1755.73	570	9570.3	49	49	18
6	12098.7	1727.13	542	9829.57	48	48	19
7	11913.21	1735.71	559	9618.5	48	48	18
8	11926.46	1729.62	559	9637.84	48	48	19
9	11992.42	1738.64	625	9628.78	49	49	18
10	12015.33	1736	581	9698.33	50	50	19
11	12069.59	1739.97	605	9724.62	49	49	18
12	12088.03	1738.45	615	9734.58	48	48	18
13	12072.87	1728.59	599	9745.28	48	48	19
14	12109.98	1739.06	598	9772.92	48	48	19
15	12076.11	1730.47	609	9736.64	48	48	19
16	12120.26	1717	522	9881.26	48	48	19
17	11555.23	1731.14	609	9215.09	47	47	19
18	12141.47	1714	539	9888.47	50	50	19
19	12160.56	1726.02	536	9898.54	49	49	18
20	12099.46	1727.98	528	9843.48	49	49	19

Table D.11: 20 solution sets of globally important amphibian and reptile, breeding bird, butterfly and large mammal combination

Run no.	Score	Cost	Boundary Length	Penalty	Shortfall	Missing Values	Planning Units
1	3510.1	1706.14	525	1278.96	21	21	20
2	3459.44	1705.48	475	1278.96	20	20	19
3	3485.95	1685.87	494	1306.08	21	21	18
4	3567.27	1708.31	487	1371.96	21	21	19
5	3630.71	1707.46	507	1416.25	21	21	19
6	3539.32	1690.83	515	1333.49	21	21	19
7	3657.77	1717.32	494	1446.45	21	21	20
8	3573.5	1700.71	541	1331.79	21	21	19
9	3530.3	1649.05	465	1416.25	21	21	19
10	3578.31	1693.74	504	1380.57	21	21	18
11	3587.27	1708.31	507	1371.96	21	21	19
12	3589.4	1707.82	509	1372.58	22	22	18
13	3669.19	1703.51	530	1435.68	22	22	19
14	3464.54	1699.58	486	1278.96	20	20	19
15	3570.25	1706.96	489	1374.29	22	22	18
16	3575.21	1711.64	483	1380.57	21	21	19
17	3557.76	1708.31	496	1353.45	20	20	19
18	3630.53	1687.55	535	1407.98	21	21	19
19	3651.93	1720.66	549	1382.27	21	21	19
20	3682.66	1702.29	535	1445.37	21	21	19

Table D.12: 20 solution sets of endemic and non-endemic highly threatened plant, globally important amphibian and reptile, butterfly, breeding bird, ecological communities and large mammal combination

Run no.	Score	Cost	Boundary Length	Penalty	Shortfall	Missing Values	Planning Units
1	15048.67	1737.99	19	582	12728.68	65.2	68
2	14696.07	1700.83	19	531	12464.24	68.8	63
3	15867.65	1720.03	19	610	13537.62	65.8	70
4	15016.51	1710.49	19	595	12711.02	58.8	65
5	15672.26	1730.78	18	607	13334.48	61.5	73
6	15860.49	1725.62	19	597	13537.87	62.8	72
7	15201.03	1756.83	19	605	12839.29	57.5	67
8	15078.3	1723.92	18	591	12763.38	58.5	70
9	15643.75	1718.26	19	587	13338.49	61.8	67
10	15317.4	1743.78	19	611	12962.62	58.5	71

Table D.12 (continued)

Run no.	Score	Cost	Boundary Length	Penalty	Shortfall	Missing Values	Planning Units
11	15722.6	1763.22	19	672	13287.38	63.5	67
12	14881.64	1734.71	19	568	12578.93	56.8	72
13	15674.04	1746.92	19	593	13334.12	65.8	68
14	15690.04	1724.78	18	598	13367.26	67.5	71
15	14958.66	1765.38	19	546	12647.28	65.6	68
16	15783.66	1738.27	19	578	13467.39	67.6	70
17	15263.59	1729.32	19	567	12967.27	58.8	71
18	16164.34	1730.78	19	611	13822.56	65.5	67
19	15183.05	1727.43	19	598	12857.62	67.2	72
20	15564.25	1711.68	18	568	13284.57	65.8	71

Appendix E

RESULTS OF MARXAN FOR EQUAL NUMBER OF PRIORITY PROTECTED AREAS OF EACH COMBINATION SET

Table E.1: 20 solution sets of endemic and non-endemic highly threatened plants

Run no.	Score	Cost	Boundary Length	Penalty	Shortfall	Missing Values	Planning Units
1	7236.46	1740.08	575	4921.38	18	18	18
2	7372.57	1730.05	599	5043.52	18	18	19
3	6918.4	1756.78	608	4553.62	17	17	19
4	7430.48	1726.05	605	5099.43	15	15	18
5	7086.62	1751.98	640	4694.64	18	18	18
6	7192.45	1767.47	638	4786.98	17	17	18
7	7261.81	1792.21	670	4799.6	16	15	19
8	7056.39	1728.5	645	4682.89	17	18	19
9	7167.2	1730.72	628	4808.48	18	18	18
10	7254.65	1690.67	637	4926.98	16	17	19
11	7123.93	1704.32	607	4812.61	17	16	19
12	7087.4	1680.45	658	4748.95	16	17	19
13	7126.38	1766.3	675	4685.08	17	17	19
14	7265.9	1718.43	640	4907.47	18	18	18
15	7235.6	1805.67	685	4744.93	18	16	19
16	7094.67	1792.09	685	4617.58	16	15	19
17	7172.95	1815.04	670	4687.91	17	15	19
18	7234.5	1705.93	609	4919.57	15	18	19
19	7160.59	1816.73	620	4723.86	16	18	18
20	7029.4	1705.69	649	4674.71	17	18	18

Table E.2: 20 solution sets of globally important amphibian and reptile

Run no.	Score	Cost	Boundary Length	Penalty	Shortfall	Missing Values	Planning Units
1	143.94	101.94	40	0	0	0	2
2	143.94	101.94	40	0	0	0	2
3	156.13	119.13	35	0	0	0	2
4	143.94	101.94	40	0	0	0	2
5	2270.42	1723.42	528	0	0	0	19
6	2244.56	1709.56	535	0	0	0	19
7	2310.36	1745.36	565	0	0	0	19
8	2210.37	1690.37	520	0	0	0	19
9	2350.39	1780.39	570	0	0	0	19
10	2327.29	1720.29	607	0	0	0	19
11	2285.9	1695.9	590	0	0	0	19
12	2329.3	1756.3	573	0	0	0	19
13	2353.2	1805.2	548	0	0	0	19
14	2254.87	1704.87	550	0	0	0	18
15	2345.67	1805.67	540	0	0	0	19
16	2269.47	1690.47	579	0	0	0	19
17	2293.2	1748.2	545	0	0	0	18
18	2381.58	1816.58	565	0	0	0	19
19	2261.61	1714.61	547	0	0	0	19
20	2319.69	1776.69	543	0	0	0	19

Table E.3: 20 solution sets of butterfly

Run no.	Score	Cost	Boundary Length	Penalty	Shortfall	Missing Values	Planning Units
1	3736.08	1730.35	490	1515.73	20	20	19
2	3290.64	1723.73	531	1035.91	18	18	19
3	4317.29	1739.69	541	2036.6	21	21	20
4	3132.35	1710.17	541	881.18	16	16	20
5	3260.27	1710.8	531	1018.47	17	17	20
6	3085.74	1709.83	479	896.91	17	17	19
7	2938.96	1691.78	507	740.18	16	16	19
8	3774.08	1730.19	531	1512.89	20	20	20
9	3143.17	1715.26	531	896.91	17	17	19
10	3358.92	1722.84	536	1100.08	18	18	20
11	2923.05	1687.87	495	740.18	16	16	19
12	4119.57	1728.11	568	1823.46	21	21	20

Table E.3 (continued)

Run no.	Score	Cost	Boundary Length	Penalty	Shortfall	Missing Values	Planning Units
13	3736.08	1730.35	490	1515.73	20	20	19
14	3290.64	1723.73	531	1035.91	18	18	19
15	4317.29	1739.69	541	2036.6	21	21	20
16	3132.35	1710.17	541	881.18	16	16	20
17	3260.27	1710.8	531	1018.47	17	17	20
18	3085.74	1709.83	479	896.91	17	17	19
19	2938.96	1691.78	507	740.18	16	16	19
20	3774.08	1730.19	531	1512.89	20	20	20

Table E.4: 20 solution sets of breeding bird

Run no.	Score	Cost	Boundary Length	Penalty	Shortfall	Missing Values	Planning Units
1	729.76	544.76	185	0	1	1	7
2	724.52	470.68	163	90.84	2	2	6
3	737.73	530.73	207	0	1	1	7
4	736.62	555.62	181	0	1	1	7
5	711.52	538.52	173	0	1	1	7
6	2464.11	1736.23	568	159.88	3	3	20
7	800.68	573.68	227	0	1	1	7
8	782.94	569.94	213	0	1	1	7
26	2959.55	1743.53	641	575.02	6	6	19
9	711.52	538.52	173	0	1	1	7
10	737.73	530.73	207	0	1	1	7
11	720.66	527.66	193	0	1	1	7
12	736.62	555.62	181	0	1	1	7
13	782.76	569.76	213	0	1	1	7
14	783.61	570.61	213	0	1	1	7
15	720.66	527.66	193	0	1	1	7
16	2291.66	1727.66	564	0	1	1	19
17	791.86	586.86	205	0	1	1	7
18	737.73	530.73	207	0	1	1	7
19	725.8	524.8	201	0	1	1	6
20	724.52	470.68	163	90.84	2	2	6

Table E.5: 20 solution sets of ecological community

Run no.	Score	Cost	Boundary Length	Penalty	Shortfall	Missing Values	Planning Units
1	1072.84	815.84	257	0	0	0	10
2	1053.56	782.56	271	0	0	0	9
3	1075	782	293	0	0	0	9
4	989.24	730.24	259	0	0	0	9
5	1038.57	768.57	270	0	0	0	9
6	955.79	713.79	242	0	0	0	9
7	1127.51	832.51	295	0	0	0	10
8	2873.96	1728.36	608	537.6	0.9	3	19
9	1068.04	800.04	268	0	0	0	9
10	989.24	730.24	259	0	0	0	9
11	1069.49	787.49	282	0	0	0	10
12	2482.64	1735.8	545	201.84	0.3	1	19
13	2613.88	1726.46	592	295.42	0.6	2	20
14	1153.43	845.43	308	0	0	0	10
15	915.79	713.79	202	0	0	0	9
16	1060.03	802.03	258	0	0	0	10
17	2859.49	1730.7	589	539.79	0.9	3	20
18	1043.07	767.07	276	0	0	0	9
19	962.29	748.29	214	0	0	0	9
20	1036.99	783.99	253	0	0	0	10

Table E.6: 20 solution sets of mammal

Run no.	Score	Cost	Boundary Length	Penalty	Shortfall	Missing Values	Planning Units
1	171.11	140.11	31	0	0	0	2
2	207.6	157.6	50	0	0	0	2
3	171.11	140.11	31	0	0	0	2
4	253.8	182.8	71	0	0	0	3
5	207.6	157.6	50	0	0	0	2
6	171.11	140.11	31	0	0	0	2
7	157.9	143.9	14	0	0	0	2
8	2373.84	1741.84	632	0	0	0	18
9	171.11	140.11	31	0	0	0	2
10	184.74	156.74	28	0	0	0	2
11	207.6	157.6	50	0	0	0	2
12	2538.69	1747.93	590	200.76	1	1	19

Table E.6 (continued)

Run no.	Score	Cost	Boundary Length	Penalty	Shortfall	Missing Values	Planning Units
13	2317.6	1741.6	576	0	0	0	20
14	171.11	140.11	31	0	0	0	2
15	157.9	143.9	14	0	0	0	2
16	2536.45	1729.69	606	200.76	1	1	19
17	270.38	200.38	70	0	0	0	2
18	157.9	143.9	14	0	0	0	2
19	2313.33	1726.33	587	0	0	0	19
20	171.11	140.11	31	0	0	0	2

Table E.7: 20 solution sets of butterfly, ecological community combination

Run no.	Score	Cost	Boundary Length	Penalty	Shortfall	Missing Values	Planning Units
1	4541.91	1736.14	532	3983.71	26.2	29	20
2	2405.61	1707.7	497	1889.71	18.9	21	19
3	3674.75	1737.42	553	3097.15	24.6	26	20
4	2788.1	1713.91	497	2270.2	20.9	23	20
5	3009.16	1714.83	542	2444.26	22.9	25	19
6	3829.77	1718.21	569	3234.87	25.9	28	19
7	5061.11	1739.36	614	4419.31	27.8	32	20
8	3649.57	1719.98	539	3088.07	22.5	26	20
9	3726.94	1723.5	548	3155.44	23.5	27	20
10	3359.5	1737.15	566	2770.9	22.6	24	19
11	3705.44	1735.03	511	3171.64	22.8	27	20
12	3916.37	1744.04	535	3357.87	23.5	27	20
13	3529.07	1736.56	505	2999.87	24.2	27	20
14	2738.31	1713.97	529	2189.71	19.6	21	20
15	3241.71	1719.77	603	2616.11	22.6	24	19
16	4011.24	1737.17	531	3454.74	25.5	29	20
17	2927.59	1711.64	540	2366.39	21.2	24	19
18	3747.55	1734.07	559	3163.35	25.2	28	21
19	4069.79	1729.59	556	3487.29	26.5	30	20
20	2745.79	1738.07	529	2194.59	22.2	25	20

Table E.8: 20 solution sets of breeding bird, ecological community combination

Run no.	Score	Cost	Boundary Length	Penalty	Shortfall	Missing Values	Planning Units
1	1409.35	1023.35	385	0	1	1	11
2	1392.76	1016.76	375	0	1	1	12
3	1355.12	995.12	359	0	1	1	11
4	2764.96	1728.09	606	428.27	2.6	4	19
5	1293.55	967.55	325	0	1	1	11
6	2379.42	1731.36	567	79.06	2	2	19
7	1459.82	1086.82	372	0	1	1	13
8	3317.66	1740.79	626	944.27	6.6	8	19
9	1456.21	1072.21	383	0	1	1	12
10	1442.66	1066.66	375	0	1	1	13
11	2790.37	1730.31	640	417.46	2.6	4	19
12	1466.09	1071.09	394	0	1	1	13
13	1487.29	1032.51	383	69.78	2	2	12
14	1347.8	925.02	351	69.78	2	2	10
15	3171.51	1727.56	593	846.75	4.2	7	19
16	1391.81	1015.81	375	0	1	1	12
17	2351.22	1721.44	558	69.78	2	2	19
18	1323.4	969.4	353	0	1	1	11
19	2326.24	1727.24	598	0	1	1	19
20	1334.96	970.96	363	0	1	1	11

Table E.9: 20 solution sets of endemic and non-endemic highly threatened plant, ecological community combination

Run no.	Score	Cost	Boundary Length	Penalty	Shortfall	Missing Values	Planning Units
1	8157.59	1737.34	593	5827.25	19.1	24	19
2	8102.87	1726.87	585	5791	19.2	22	20
3	7894.11	1726.87	592	5575.24	17.8	22	19
4	7707.97	1711.36	567	5429.61	18.8	23	18
5	7787.93	1716.78	575	5496.15	17.4	23	18
6	8154.62	1743.77	633	5777.85	19.2	22	18
7	8180.86	1731.28	582	5867.58	19.2	22	19
8	7872.01	1727.7	615	5529.31	18.5	22	19
9	8499.01	1730.01	602	6167	21	21	19
10	8161.77	1736.5	582	5843.27	19.5	23	19

Table E.9 (continued)

Run no.	Score	Cost	Boundary Length	Penalty	Shortfall	Missing Values	Planning Units
11	8019.16	1703.23	578	5737.93	18.8	23	18
12	8265.92	1739.82	461	6065.1	19.8	24	19
13	7623.69	1717.75	575	5330.94	18.2	21	19
14	8009.07	1725.78	571	5712.29	18.6	20	19
15	8271.27	1732.15	590	5949.12	18.8	23	19
16	7480.58	1719.11	595	5166.47	17.9	20	19
17	7333.62	1716.05	585	5032.57	17.2	20	19
18	8489.25	1731.74	582	6175.51	21.8	26	18
19	7539.7	1724.46	567	5248.24	17.9	20	19
20	7523.25	1720.1	569	5234.15	17.2	20	19

Table E.10: 20 solution sets of butterfly, endemic and non-endemic highly threatened plant combination

Run no.	Score	Cost	Boundary Length	Penalty	Shortfall	Missing Values	Planning Units
1	12120.87	1728.59	599	9745.28	48	48	19
2	13723.77	1734.73	588	11349.04	52	52	19
3	12289.9	1731.21	568	9940.69	50	50	19
4	11974.46	1729.62	559	9637.84	48	48	19
5	12954.14	1714.63	583	10607.51	49	49	19
6	12727.25	1726.33	584	10366.92	50	50	19
7	12381.04	1706.53	602	10022.51	50	50	18
8	12352.61	1734.63	615	9952.98	50	50	18
9	13190.55	1725.39	600	10814.16	51	51	18
10	12833.7	1736.78	556	10490.92	50	50	19
11	12041.42	1738.64	625	9628.78	49	49	18
12	12344	1704.55	596	9992.45	51	51	18
13	12599.25	1737.23	589	10225.02	48	48	18
14	12461.9	1720.29	548	10143.61	50	50	19
15	12286.8	1741.73	606	9890.07	49	49	19
16	12702.62	1698.35	586	10366.27	52	52	18
17	12531.88	1714.61	594	10175.27	48	48	19
18	12387.55	1735.07	591	10012.48	49	49	19
19	13391.57	1708.13	602	11026.44	55	55	18
20	11786.25	1701.94	562	9473.31	49	49	18

Table E.11: 20 solution sets of globally important amphibian and reptile, breeding bird, butterfly and large mammal combination

Run no.	Score	Cost	Boundary Length	Penalty	Shortfall	Missing Values	Planning Units
1	3859.01	1723.19	574	1561.82	23	23	19
2	4747.93	1741.33	494	2512.6	24	24	20
3	4017.04	1714.99	541	1761.05	23	23	19
4	3510.1	1706.14	525	1278.96	21	21	19
5	3860.3	1725.34	554	1580.96	22	22	19
6	3744.45	1714.4	549	1481.05	22	22	19
7	5021.95	1738.97	594	2688.98	28	28	19
8	3669.19	1703.51	530	1435.68	22	22	19
9	3732.06	1680.32	561	1490.74	22	22	19
10	3657.77	1717.32	494	1446.45	21	21	20
11	3739.12	1711.94	519	1508.18	23	23	19
12	3782.23	1715.64	577	1489.59	22	22	19
13	4046.03	1723.4	554	1768.63	23	23	19
14	3906.25	1708.58	591	1606.67	21	21	19
15	4188.56	1729.73	537	1921.83	25	25	19
16	4554.73	1725.84	566	2262.89	27	27	20
17	4355.53	1731.73	585	2038.8	25	25	19
18	4282.51	1732.08	557	1993.43	25	25	18
19	3630.53	1687.55	535	1407.98	21	21	19
20	3682.66	1702.29	535	1445.37	21	21	19

Table E.11: 20 solution sets of endemic and non-endemic highly threatened plant, globally important amphibian and reptile, butterfly, breeding bird, ecological communities and large mammal combination

Run no.	Score	Cost	Boundary Length	Penalty	Shortfall	Missing Values	Planning Units
1	15048.67	1737.99	19	582	12728.68	65.2	68
2	14696.07	1700.83	19	531	12464.24	68.8	63
3	15867.65	1720.03	19	610	13537.62	65.8	70
4	15016.51	1710.49	19	595	12711.02	58.8	65
5	15672.26	1730.78	18	607	13334.48	61.5	73
6	15860.49	1725.62	19	597	13537.87	62.8	72
7	15201.03	1756.83	19	605	12839.29	57.5	67
8	15078.3	1723.92	18	591	12763.38	58.5	70
9	15643.75	1718.26	19	587	13338.49	61.8	67
10	15317.4	1743.78	19	611	12962.62	58.5	71

Table E.12 (continued)

Run no.	Score	Cost	Boundary Length	Penalty	Shortfall	Missing Values	Planning Units
11	15722.6	1763.22	19	672	13287.38	63.5	67
12	14881.64	1734.71	19	568	12578.93	56.8	72
13	15674.04	1746.92	19	593	13334.12	65.8	68
14	15690.04	1724.78	18	598	13367.26	67.5	71
15	14958.66	1765.38	19	546	12647.28	65.6	68
16	15783.66	1738.27	19	578	13467.39	67.6	70
17	15263.59	1729.32	19	567	12967.27	58.8	71
18	16164.34	1730.78	19	611	13822.56	65.5	67
19	15183.05	1727.43	19	598	12857.62	67.2	72
20	15564.25	1711.68	18	568	13284.57	65.8	71

Appendix F

TableF.1 Correlation table

corelation_matrix	lakeshoreline	annual-prec	an-rel-hum	east-aspect	north-aspect	annual-tmp	max-tmp-hm	min-tmp-cm	dinurnal-mg	isothermality	dem	ruggedness	slope	prec-cm	prec-hm	prec-sea	rel-hum-cm	rel-hum-hm	river-int	soil-het	tmp-an-mg	solar-rad-hm	solar-rad-cm
annual-prec	-0.003																						
an-rel-hum	0.031	0.402																					
east-aspect	0.146	0.176	0.231																				
north-aspect	-0.091	0.049	0.23	0.367																			
annual-tmp	0.109	0.709	0.553	0.169	0																		
max-tmp-hm	0.03	0.337	0.968	0.255	0.27	0.428																	
min-tmp-cm	0.114	0.524	0.035	0.03	-0.154	0.835	-0.13																
dinurnal-mg	0.035	0.701	0.801	0.282	0.164	0.863	0.646	0.481															
isothermality	0.075	0.77	0.527	0.18	0.005	0.985	0.414	0.613	0.59														
dem	0.033	0.035	0.368	0.211	0.308	0.026	0.366	-0.186	0.129	-0.006													
ruggedness	-0.138	0.52	0.012	0.154	0.095	0.271	0.051	0.198	0.418	0.398	-0.181												
slope	-0.145	0.507	0.032	0.173	0.116	0.264	0.08	0.171	0.426	0.39	-0.155	0.995											
prec-cm	-0.074	0.94	0.219	0.097	-0.046	0.566	0.177	0.449	0.561	0.653	-0.163	0.62	0.603										
prec-hm	0.116	0.845	0.484	0.209	0.072	0.909	0.359	0.572	0.77	0.604	0.131	0.245	0.232	0.658									
prec-sea	0.255	-0.027	0.328	0.416	0.362	0.337	0.245	0.281	0.256	0.25	0.245	-0.32	-0.321	-0.245	0.367								
rel-hum-cm	0.058	0.156	0.933	0.175	0.219	0.331	0.62	-0.159	0.558	0.266	0.446	-0.276	-0.25	-0.041	0.284	0.37							
rel-hum-hm	0.016	0.643	0.911	0.249	0.177	0.775	0.537	0.335	0.643	0.581	0.233	0.279	0.289	0.488	0.598	0.279	0.515						
river-int	-0.034	0.091	0.04	0.019	-0.067	0.019	0.046	-0.028	0.08	0.047	-0.139	0.151	0.158	0.094	0.029	-0.001	0.007	0.079					
soil-het	0.079	0.19	0.237	0.474	0.348	0.215	0.245	0.085	0.332	0.235	0.092	0.182	0.19	0.09	0.257	0.388	0.141	0.298	0.112				
tmp-an-mg	-0.077	-0.249	0.461	0.105	0.26	-0.452	0.609	-0.65	0.008	-0.442	0.333	-0.132	-0.096	-0.269	-0.437	-0.101	0.592	0.155	0.045	0.055			
solar-rad-hm	0.086	-0.126	0.419	0.113	0.248	-0.187	0.453	-0.439	0.053	-0.265	0.566	-0.469	-0.444	-0.319	-0.028	0.335	0.64	0.118	-0.074	0.035	0.58		
solar-rad-cm	0.022	0.383	0.591	0.315	0.345	0.15	0.644	-0.247	0.433	0.172	0.545	0.186	0.214	0.202	0.31	0.188	0.562	0.509	0.066	0.287	0.522	0.593	

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1. Zeydanlı, U., Turak, A., Kaya, B., Domaç, A., Çakaroğulları, D. Kündük, H., Çekiç, O. "Boşluk Analizi Klavuzu". Biyoçeşitlilik İzleme Birimi, Anlara, Türiye, 2005.

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