

## CORINE for large-scale monitoring of PAs in Europe

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### Abstract

CORINE Land Cover Change provides official European land cover monitoring. Here, we investigate how CORINE can be used for large-scale monitoring of Protected Areas (PAs) in Europe. Main processes observed include changes from and to 'forest and semi-natural vegetation'. Rates of change differ significantly between PAs and their direct vicinity, as well as between protection statuses of PAs. Comparison with alternative data will show that shortcomings due to the spatial and categorical resolution of CORINE might be overcome for European-wide PA monitoring.

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### Keywords

large-scale monitoring, protected areas, land cover, CORINE

### Introduction

Protected Areas (PAs) are recognized to play a crucial role in safeguarding European biodiversity, and are therefore also directly addressed in international conservation obligations through the Convention of Biodiversity, namely the Aichi Targets. Large-scale monitoring of PAs, including not only NATURE2000 sites, but also the numerous nationally designated PAs, has not yet been well established within the EU (EEA, 2012), although a number of existing Pan-European datasets could make a start for such a monitoring.

Land cover change is among the most obvious transitions that ecosystems can go through and that often indicates the overall state of the ecosystem. CORINE land cover monitoring has been established in the late 1980s and has been iterated several times since then. It covers all Europe, including all PAs. CORINE has not specifically been designed for the monitoring across PAs, and even less so for the monitoring of single PAs. Still, it remains one of the most promising data sets for large-scale land cover monitoring of PAs across Europe over the past almost 30 years, and there is a strong potential to learn from this monitoring for future, possibly more adapted monitoring of PAs based on recently more and more available remote sensing data.

In this contribution, we aim at identifying (1) large-scale patterns of land cover change in PAs based on CORINE data and (2) main drivers for land cover change in PAs across Europe.

### Data and Methods

#### CORINE Land Cover Change data

CORINE land cover change (LCC) has been published for the four survey periods in 1990, 2000, 2006 and 2012. In addition to the well-known wall-to-wall European land cover data, also CORINE LCC focuses specifically on the monitoring of change. These data cover all 44 CORINE land cover classes, and use a Minimum Mapping Unit of 5 ha with a width of at least 100 m. The technique of mapping changes first has been applied by most countries since 2006, and for previous survey periods these data have been reconstructed. Hence, the land cover change data are available between all survey periods, i.e. for 90-00, 00-06, and 06-12.

To analyse land cover changes, the 44 CORINE land cover classes have been grouped in major land cover flows (LCF) according to Feranec et al. (2010). These LCFs include a total six flows, with LCF4 representing changes towards forest and natural ecosystems and LCF5 representing all changes with loss of forest and natural ecosystems.

#### Common Database on Designated Areas

The Common Database on Designated Areas (CDDA) is the official source of PA information from European countries to World Database of Protected Areas. It contains various types of nationally designated PAs and provides the IUCN category of each PA. In December 2016, CDDA contains 101,712 PAs, with 97% of them including also spatially explicit information on their extent. Data gaps still exist for Austria, Estonia, Hungary, Ireland, Montenegro, Romania and Turkey. Greenland had to be excluded because of missing CORINE land cover data. After all a total of 97,705 nationally designated PAs covering a total of 276 Mio ha, including 105 Mio ha on land, were included in the analysis.

## Driving factors of land cover change

Variables tested to explain observed land cover change in PAs include data on the level of the individual PA, NUTS3, NUTS2, national and higher levels.

### GIS analysis

All observed CORINE LCC were assigned to one of the six LCFs. Then all spatially explicit PAs boundaries of the CDDA were intersected by CORINE LCC. A 1km-buffer was calculated for each PA, and again intersected with the CORINE LCC. Areas of PAs, PA buffers as well as areas of each observed change within PAs were calculated. The annual fraction of change was derived by normalising observed change by PA size and the number of years between surveys. For this first analysis only land cover change was included that was completely contained within a PA, with a consequent reduction of analysed PAs by about 19 % of the PA with observed change.

### Descriptive analysis and tests of observed changes

Annual fractions of change for all LCFs are plotted for each change period to identify most important processes. Using Kruskal-Wallis tests, significant differences in annual fractions of change were tested for (1) PAs, buffers around PAs and across European were tested and for (2) different IUCN categories for the last period 06-12.

### Explaining land cover change

Quantile regression analysis was used to identify main drivers of CORINE LCC within European PAs. In the analysis we use drivers of different spatial resolution, namely from the level of the individual PA, NUTS3, NUTS2, NUTS1, and pan-European scale.

## **Results**

The presented results are only preliminary and will be further analysed and confirmed until the symposium in November 2017.

### Observed land cover changes in PAs

Out of the almost 95,000 PA available with their geographic boundaries, 3394 were affected by land cover change according to CORINE LCC. Changes within PAs are dominated by LCFs 4 and 5 (gain and loss of 'forest and natural vegetation') in all three CORINE LCC periods, although the identified rates of change vary considerably between the three periods (Fig. 1). Rates for LCFs 4 and 5 also dominate land cover change outside PAs and across Europe. Across all periods rates of change in close vicinity of PAs and across Europe are similar, with rates being particularly high for the period 06-12.

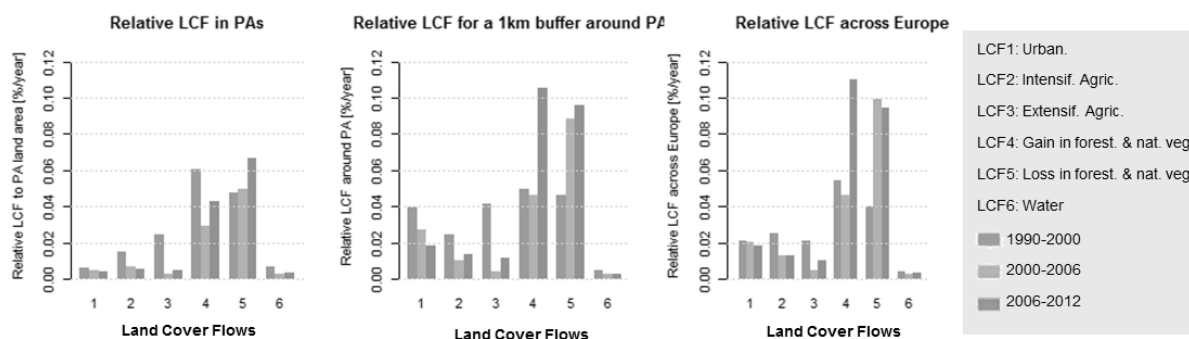


Figure 1: Mean rates of LCC for all six different LCFs within PAs, in a 1km buffer around PAs and across Europe for the periods 90-00, 00-06 and 06-12.

The two dominating LCFs vary considerably between IUCN categories (Fig. 2A) with absolute change adding up tremendously in particular for the large extent of areas protected on IUCN level V. Rates of changes normalized by the area covered by different levels of protection, however, are not exceptional for the IUCN categories V and VI, which both explicitly allow for human intervention to sustain the region and biodiversity (Fig. 2B). Gain of forest and natural vegetation is more similarly distributed between IUCN categories than loss, which is particularly low for IUCN categories Ia and Ib. Kruskal-Wallis and Dunn's test confirm significant difference in land cover change between IUCN categories, as well as within and outside PAs.

### Driving factors of land cover changes

First median regression models of potential driving factors indicate patterns to explain rates of change for LCF4 and LCF5. Significant contribution to explain both rates of land cover change include the elevation, IUCN categories, population density at NUTS 3 level, the national environmental tax as the share of GDP and latitude position of the PA. Significant explanation, thus, include factors from local, NUTS 3 and national level.

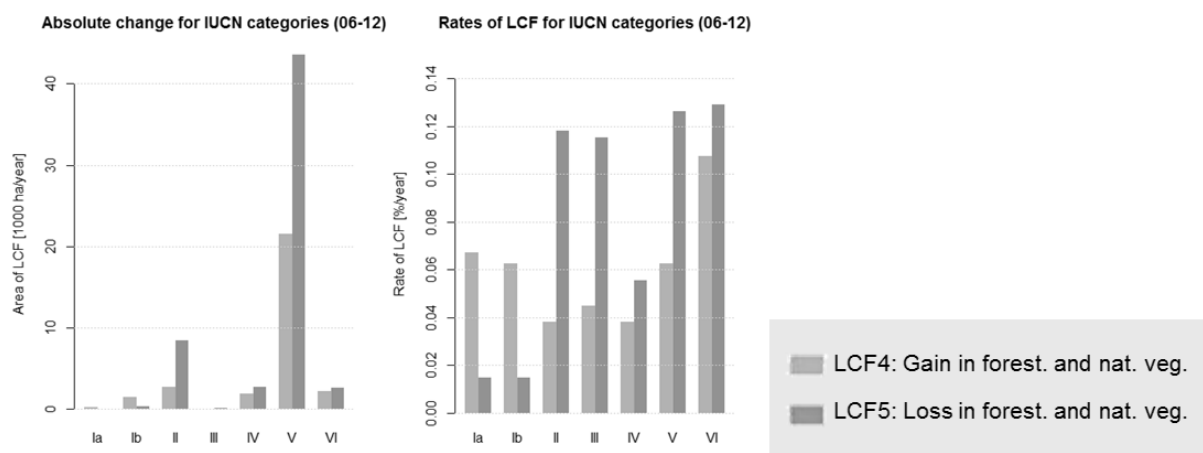


Figure 2: Rates of LCC for LCFs 4 and LCF5 (loss and gain of forest and natural vegetation) across IUCN categories for 06-12.

Scale	Variable	LCF4				LCF5			
		Value	Std. Error	t value	Pr(> t )	Value	Std. Error	t value	Pr(> t )
	(Intercept)	-0,0707	0,3245	-0,2178	0,8276	0,7042	0,3036	2,3193	<b>0,0204</b>
PA specific	Elevation (m)	0,0004	0,0001	-4,7652	<b>0,0000</b>	0,0003	0,0001	-5,3686	<b>0,0000</b>
	Slope (%)	0,0025	0,0018	1,4195	0,1558	0,0051	0,0019	2,6203	<b>0,0088</b>
	Marine fraction (%)	0,0146	0,0460	0,3163	0,7518	0,0037	0,0026	1,4165	0,1567
	Land area (ha)	0,0000	0,0030	-0,0161	0,9872	0,0000	0,0001	0,1923	0,8475
	Site area (ha)	0,0000	0,0030	0,0152	0,9879	0,0000	0,0001	-0,2148	0,8299
	Ann. rate of LCF4/5 (%/a)	3,0631	1,2173	2,5163	<b>0,0119</b>	1,6652	1,5762	1,0564	0,2908
	IUCNCATlb	-0,6177	0,1232	-5,0155	<b>0,0000</b>	-1,0524	0,1165	9,0300	<b>0,0000</b>
	IUCNCATII	-0,8092	0,1007	-8,0364	<b>0,0000</b>	-0,5253	0,0913	-5,7540	<b>0,0000</b>
	IUCNCATIII	0,0201	0,1527	0,1316	0,8953	0,1984	0,1049	1,8906	0,0588
	IUCNCATIV	0,0648	0,0649	-0,9979	0,3184	0,2200	0,0643	-3,4185	<b>0,0006</b>
IUCNCATUA	-0,6183	0,0873	-7,0831	<b>0,0000</b>	-0,3581	0,0869	-4,1215	<b>0,0000</b>	
IUCNCATV	-0,6959	0,0670	-10,3917	<b>0,0000</b>	-0,5242	0,0701	-7,4725	<b>0,0000</b>	
IUCNCATVI	-0,1084	0,1714	-0,6327	0,5270	-0,3496	0,1537	-2,2746	<b>0,0230</b>	
NUTS 3 level	Population density	0,0001	0,0000	2,0814	<b>0,0375</b>	0,0003	0,0001	2,1169	<b>0,0343</b>
	Migration rate	0,0040	0,0052	0,7739	0,4390	0,0079	0,0033	2,3731	<b>0,0177</b>
NUTS 2 level	Population density	0,0002	0,0001	1,1163	0,2644	0,0000	0,0002	-0,0415	0,9669
	Migration rate	-0,0113	0,0066	-1,7152	0,0864	-0,0057	0,0052	-1,0907	0,2755
National level and higher	Environ.. Tax (% GDP)	-0,2761	0,0468	-5,8986	<b>0,0000</b>	-0,1578	0,0443	-3,5627	<b>0,0004</b>
	Latitude (°)	-0,0231	0,0045	-5,1237	<b>0,0000</b>	-0,0463	0,0047	-9,8619	<b>0,0000</b>
	Longitude (°)	0,0175	0,0037	4,6827	<b>0,0000</b>	0,0049	0,0026	1,8829	0,0598

Table 1: Summary of Median Regression Models for LCF5 and LCF4. Significant factors are indicated in bold for each model.

## Discussion and outlook

CORINE LCC, as the one available pan-European land cover change monitoring programme, indicates dynamics in land cover within PAs that differ substantially from their direct surrounding and overall Europe. Dominating land cover changes are gains and losses of forest and natural vegetation. The observed changes are mainly from and to 'forest and natural vegetation', and confirm that development and changes in agriculture are minor within PA.

ICUN category and elevation above sea level and also regional parameter from the NUTS 3 and national level and higher are significant PA specific factors to explain rates of change. The analysis, hence, shows that drivers for land cover change within European PAs can be identified at different scales.

Following up on these first results, we will assign land cover change to human intervention or natural processes, conduct more systematic testing of individual drivers and use hierarchical modelling for single groups of PAs. For Pan-European land cover monitoring system of PAs, higher temporal and spatial resolution and better indication of natural disturbances and ecosystem degradation would be a powerful asset. Comparison with alternative data might give an indication about the robustness of CORINE and shortcomings due to the spatial and categorical resolution.

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## Endemism below the species rank: Population genetics of the European Mudminnow (*Umbra krameri*)

Josef Wanzenböck

### Keywords

mitochondrial DNA, microsatellites, Structure

### Summary

Endemism is commonly handled on the level of species - an example is the theme topic of this session of the conference. However, biodiversity has an important sub-specific component, e.g. evolutionary significant units (ESUs) which are comprised of one or more populations. In fact, estimates of biodiversity loss due to population extinction are much higher compared to species loss (DICKMAN et al. 2007). Modern molecular genetic techniques shed new light on within-species diversity, starting with genetic variability of individuals, populations, ESUs and up to species (GEFFEN et al. 2007). Specifically population genetics and barcoding studies provide new information on the interplay of different levels of organization and contrast genetic with traditional, morphometric approaches (e.g. PALANDACIC et al. 2017). Here we provide an example of a population genetic study on the European mudminnow (*Umbra krameri*) analyzing the within-species genetic variability throughout the entire known range of occurrence (MARIC et al 2017). The aim of the study was to test if the populations within the specie's range are genetically uniform or if significant genetic structuring is present to warrant certain populations to be treated as unique and therefore endemic on a sub-specific level.

The European mudminnow (*Umbra krameri*) is a rare fish species with a relatively small total area of occurrence: It extends from Vienna in the west, through the Danube lowlands to the delta, including the Sava and Tisza River lowlands, and reaches the Dniester River in the east (WANZENBÖCK 1995). In Austria, the species occurs in only two habitats, one situated in the national park Donauauen (WANZENBÖCK & SPINDLER 1995). The species is specifically adapted to groundwater-fed waterbodies on the margins of floodplains and swamps and may serve as an indicator species of the ecological status of such critically endangered ecosystems (WANZENBÖCK 2004).

Mudminnows were sampled from 17 locations across the species natural distribution area (see Figure 1 in MARIC et al. 2017) and DNA extracted from fin clips. The mitochondrial protein-coding gene cytochrome b (1085 bp 3' - end) was PCR-amplified using GluF and ThrR primers and sequenced on an ABI Prism 3130xl machine. The genealogical relations between haplotypes were presented as a minimum spanning network (MSN) using the 95% statistical parsimony criterion in the TCS 1.2 program. Seven tetranucleotide microsatellite loci were amplified according to published protocols (WINKLER & WEISS 2009) and fragments analyzed on the ABI prism 3130xl machine. Software used to analyze the data included Gene-Mapper, Microchecker, Genetix 4.04, ADZE, SPAGeDI 1.3 and STRUCTURE (for details see MARIC et al. 2017).

The analysis of the mitochondrial cytochrome b gene revealed ten haplotypes. Their spatial distribution showed divergence of mudminnow populations according to the larger drainages: Populations in the Sava drainage showed exclusive haplotypes not found in the upper, middle or lower Danube (with one exception of the middle Danube close to the Sava mouth) or in the Tisza drainage. Similarly, populations in the Tisza drainage were composed of exclusive haplotypes not found anywhere else. The largest variety of haplotypes was found in the Danube delta (see Figure 1 in MARIC et al. 2017), however, most haplotypes dominating the populations in the upper and middle Danube were lacking in the delta.

Hierarchical STRUCTURE analysis of the microsatellite fragment length data revealed discrimination of a group consisting of populations in the upper and middle Danube, Drava, Mura and Lake Balaton from a group of populations of the lower Danube, Sava, Tisza and Dniester in a first division. Anyhow, already the second discrimination step allowed to distinguish populations of the Drava, Mura and Balaton area from populations of the middle and upper Danube, and within the latter group the population of Austria (Eckartsau) was clearly discernible from three other populations (see Figure 4 in MARIC et al. 2017). The third step of discrimination separated almost all the populations (with few exceptions).

In contrast to population genetic studies on a related species, the Olympic mudminnow (*Novumbra hubbsi*), which showed no genetic structure on the mitochondrial (mt) haplotype level, such structuring was clearly evident in the European mudminnow. Genetic structuring on the mt haplotype level coincided with the drainages of the Danube, Tisza and Sava i.e. the largest sub-drainages in the Danube system. Therefore, these three phyletic lineages could be considered potential evolutionary significant units (ESU). On the other hand, the uneven distribution of microsatellite polymorphism among the small sampled populations and high genetic structuring within each of the three phyletic lineages may not reflect a natural evolutionary process but rather random drift governed by recent habitat fragmentation as a result of human impact (e.g. damming).