



Original Research Article

Regional assessment of the vulnerability of biotopes to landscape change



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ABSTRACT

To halt habitat loss, landscape planning and conservation management could benefit from a regional analysis of the spatially differing impacts caused by landscape changes. These impacts usually also differ according to the specific vulnerability of the affected biotopes, i.e., the characteristic assemblage of plants and animals on a particular site.

A vulnerability map of biotopes will determine those with a high potential to be adversely affected and a low capacity to recover. The identification of vulnerability hot spots will provide guidance for potential protection and maintenance interventions.

Following the interdisciplinary vulnerability concept, the analysis on a regional level ($\approx 30,000 \text{ km}^2$) was structured into biotope exposure, biotope sensitivity, and biotope adaptive capacity. It involved patch and group metrics to describe the vulnerability of terrestrial, (semi-) natural biotopes to landscape change.

For the 32 biotope groups that were distinguished within this study, a relative ranking of vulnerability level is provided. At the level of biotope patches, spatial clusters and thematic clusters were identified. The biotopes dependent on high water availability, such as wet meadow, riparian habitat, and peatland were found to be particularly vulnerable. Moreover, herbaceous perennials, shrubland, groves, orchard meadows, and several pristine forest types also scored high, while the majority of forest biotope patches were less vulnerable to landscape change.

The biotope vulnerability index applied on a regional scale provided a sound overview for conservation planning. Only a few biotope groups showed a homogenous vulnerability level across their associated patches, suggesting that management based on local contexts is needed for the majority of biotopes.

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1. Introduction

The planetary boundary of biosphere integrity has clearly been exceeded (Rockström et al., 2009; Steffen et al., 2015), and most international strategies to halt biodiversity losses have been far from successful (CBD, 2014). In terrestrial ecosystems, habitat loss and fragmentation due to landscape change are generally considered to be the main drivers of the extinction of terrestrial species (Collinge, 2001), although fragmentation *per se* has been overestimated as a biodiversity threat (Tschardt et al., 2012). Primarily in already highly transformed landscapes, nature conservation managers seek to judge threats to the remaining natural and semi-natural areas and could benefit from an objective prioritization of vulnerable sites. A

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vulnerability analysis of the concerned biotopes would tell which sites have the most need for protection or maintenance. The term *biotope* is almost synonymous with the more common term *habitat*. However, it emphasises that the biocoenosis is in the focus instead of a population. Plant species communities supplemented with some typical animal species are the major feature to distinguish biotope types from each other.

The assessment of the vulnerability of natural systems has emerged from several research fields – mainly conservation biology, climate change research, and ecological risk assessment (Weißhuhn et al., 2018). Derived from the general understanding of vulnerability across very different topics and disciplines as a potential for loss caused by external impacts (Adger, 2006; Füssel, 2007), biotope vulnerability should describe the potential for loss in the species community within its respective habitat. It has been widely agreed upon that vulnerability is a function of a system's exposure, sensitivity, and adaptive capacity (Turner et al., 2003; Füssel, 2007). Correspondingly, biotope exposure is defined by the (driver of) change in biotope configuration, biotope sensitivity describes the likelihood of a species community being harmed by this change, and biotope adaptive capacity entails the ability of the affected species community to respond and persist (Weißhuhn et al., 2018).

A major goal of species protection is to safeguard populations that are capable of evolving (e.g., Veith and Seitz, 1995; Agatz et al., 2012). However, conservation efforts are more effective when the arenas of biological activity are conserved rather than single species or even single populations (Beier and Brost, 2010). If a vulnerability analysis is to inform a pattern-oriented management strategy that is complementary to traditional species-oriented conservation (Fischer and Lindenmayer, 2007), it should include species assemblages and their habitats (De Lange et al., 2010; Ippolito et al., 2010) and provide spatially explicit scores. Further, cumulative ecological degradation has to be taken into account (Jackson et al., 2004). However, many conservation organizations often lack reference to the wider ecological context of individual sites or species (Freeman et al., 2011). Therefore, analysing the vulnerability of biotopes on a regional level appears to be an interesting solution.

The database for such an assessment seems to be available in biotope maps, which can be considered as inventories of nature with patches of a single biotope type as the smallest spatial unit. They are usually derived from stable correlations between spectral information acquired through remote sensing and ground truth field data from biotope cartographers. For example, in Germany, all the state environmental authorities have developed biotope maps, and some of them are already comprehensive (e.g. Altena et al., 2018). Throughout the European Union, large areas of biotopes have been mapped with a high level of detail (e.g., Alexandridis et al., 2009; Frélichová et al., 2014; Bell et al., 2015; Viciani et al., 2016). These biotope maps provide information on water balance, nutrient availability, common animal species, and several conservational aspects and thus report more biological detail than, for example, a typical land cover or land use map.

Biotopes are commonly mapped as vector data, which limits the available geospatial analytical tools. In particular, the use of distance-related and neighbourhood metrics is scarce, and processing time grows rapidly with patch number and buffer size (Lang and Tiede, 2003). However, to cover a wider landscape context for each biotope and to analyse biotope maps on an extent that is useful for conservation management, a large number of patches and large buffers are to be analysed. This calls for measures on a high level of abstraction to feed into a biotope vulnerability index. Such a set of computationally effective, largely uncorrelated indicators has been suggested recently (Weißhuhn, 2019) to calculate spatially explicit vulnerability scores for biotopes on a landscape level.

Based on this work, the objective of the current study is to apply a biotope vulnerability analysis at the regional level using the federal state of Brandenburg (Germany) as an example. This involves i) calculating a number of patch and group metrics customized to analyse biotope maps, ii) transforming those metrics into a vulnerability map, which will then be analysed in terms of its vulnerability patterns, and iii) discussing the implications of detected vulnerability clusters and the analytical limitations of the vulnerability index.

2. Methods

2.1. Study area and geodata processing

The application of the biotope vulnerability analysis on a regional level, covering almost 30,000 km² of the federal state Brandenburg (Fig. 1), was based on open-access, spatially gapless geodata from the Landesamt für Umwelt Brandenburg (2013). The biotopes were mapped in 2009 with a spatial resolution of 0.5 m for the spectral information (colour infrared) and a thematic resolution of approximately 2500 biotope types, which are delimited with respect to the plant species community and land use. Each biotope type is coded as an 8-digit number. The mapping key is specific to the biotopes of the state and does not apply to the national or broader levels.

To reach a useful scale for a regional vulnerability assessment, the high amount of detail was mainly aggregated on the level of biotope groups (Weißhuhn, 2019), leading to 38 different biotope groups (see Table 1). In the case of urban areas, special biotopes, and arable lands, the information extractable from biotope maps is generally limited due to very high anthropogenic influences on the composition of the species community. In the case of aquatic habitats, the species community is generally difficult to map via remote sensing. Biotope vulnerability analysis related to landscape changes seems to not apply here or would otherwise need very different indicators and different data on species occurrence. These biotopes were only used for neighbourhood analysis, and no vulnerability index scores are reported. All interior borders of adjacent patches within the same biotope group were then dissolved, reducing the number of patches to 486,690, of which 74% belonged to terrestrial, (semi-) natural patches.

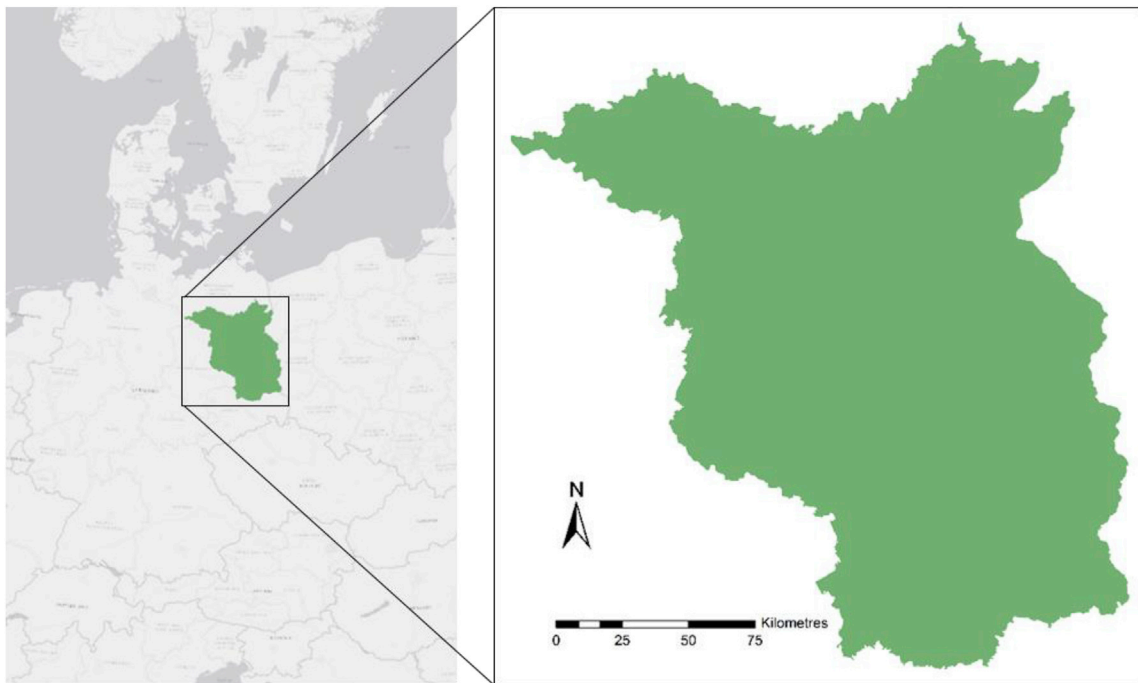


Fig. 1. Perimeter of the federal state Brandenburg (the area of the city of Berlin within it is not clipped out here). The Brandenburg biotopes belong to a postglacial landscape situated in northeast Germany, Central Europe. The background map (left) was obtained from ESRI's "World Light Grey Canvas Base" with copyright from OpenStreetMap contributors and the GIS user community.

The main software used to organize, display and edit the biotope data was *ArcGIS Desktop 10.6*, supplemented by the freeware add-ins *Patch Analyst* (Rempel et al., 2012) and *V-LATE* (Tiede, 2012). Furthermore, to run intersection analyses on large tables faster and in a more stable manner than in *ArcGIS*, two alternative tools in *FME Desktop* (Safe Software, 2017) were used, namely, "PointOnAreaOverlayer" and "AreaOnAreaOverlayer". The polygon data in vector format were projected with the coordinate system ETRS_1989_UTM_Zone_33N.

2.2. Vulnerability mapping

For this study, the indicator set suggested in Weißhuhn (2019) for analysing biotope vulnerability was used. It proved to be both synoptic and to avoid multicollinearity by being constrained to a small selection of indicators, as recommended by Riitters et al. (1995) and Lausch and Herzog (2002). The seven indicators cover all three vulnerability elements, with one indicator for biotope exposure and three indicators each for biotope sensitivity and biotope adaptive capacity (for details and in order to replicate the results, see Online Resource 1).

Biotope exposure to landscape change was measured by the *mesh size* of each biotope group, whereby small values indicate a high level of fragmentation (Jaeger, 2000). The size and shape of a patch (referred as patch size & fractal dimension, cf. McGarigal and Marks, 1995) and the conservation priority of the biotope group to which the patch belongs (*endangerment*) can be used to estimate biotope sensitivity. Small patches with complex shapes and assigned legal protection status would be assessed as the most sensitive to (further) habitat losses. The adaptive capacity of a patch is reflected by the number of surrounding patches belonging to the same biotope group, the amount of pristine or near-natural area in its neighbourhood, and its assignment to one of three dispersal classes as defined by its biotope group. Species communities with high average dispersal ability within biotope patches in a pristine neighbourhood with plenty of migratory options from and to similar patches would obtain a high score.

Applied on the dataset, these seven spatially explicit indicators did not exhibit a relevant amount of correlation (see Online Resource 2). Furthermore, a Kaiser-Meyer-Olkin criterion¹ of 0.56 suggests that the dataset is not meaningfully influenced by a hidden factor (Kaiser, 1970), i.e., the collinearity seems neglectable.

¹ Calculated using the "psych" package in R (Revelle, 2018).

Table 1

List of all 38 biotope groups and their percent coverage in the study area. The English names and the truncated biotope codes are based on the original mapping code and the German descriptions from the Brandenburg biotope map ([Landesamt für Umwelt Brandenburg, 2013](#)). The six biotope groups that were not evaluated in terms of vulnerability are displayed in grey, as they do not refer to terrestrial, (semi-) natural biotopes. Altogether, the evaluated biotope groups accounted for 74% of all patches and cover 58% of the study area.

Biotope code	Translated name	Coverage [%]
01	stream	0.44
02	standing water	2.32
022	riparian vegetation	<0.01
031	bare soil	0.22
032	ruderal vegetation	2.10
045	reeds	0.24
046	peatland	0.41
047	peatland forest	1.01
0510	wet meadow	2.59
0511	fresh meadow	4.07
0512	dry grassland	0.38
0513	fallow grassland	1.78
0514	herbaceous perennials	0.11
0515	intensive grassland	6.01
0516	lawn	0.15
06	heather	0.45
0710	shrubland	0.16
0711	grove	0.34
0712	forest edge	0.01
0713	hedges, avenue and individual trees	<0.01
0717	orchard meadow	0.08
0720	orchard	0.12
0811	pristine alder-ash forest	0.21
0812	pristine alluvial forest	0.06
0815	pristine maple-ash forest	<0.01
0825	pristine coniferous forest	0.15
0826	cleared woodland	0.57
0828	pioneer forest	0.47
0829	pristine deciduous forest	0.28
083	deciduous forest	4.00
084	coniferous forest	20.01
085	deciduous-coniferous mixed forest	2.74
086	coniferous-deciduous mixed forest	7.59
0913	arable land	32.22
0914	fallow, game forage field	2.02
10	urban green	1.42
11	special biotope	0.29
12	built-up area	4.99

Following the vulnerability index generation procedure described in [Weißhuhn \(2019\)](#), three sub-indexes according to the three vulnerability elements and variance weights² for each contributing indicator were calculated. The final index has no absolute interpretation but a relative meaning. Its scores range between 0 and 1. The vulnerability index is displayed in five classes, which are stratified according to their statistical distribution (quintiles).

2.3. Vulnerability cluster analysis

To detect distinct groups within the vulnerability scores, two kinds of cluster analyses were chosen. First, an analysis of spatial clusters (hot spot analysis) was conducted to find patterns in the spatial distribution of high and low vulnerability scores. Second, thematic clusters were searched in the distribution of scores within and across the biotope groups. Clustering generally involves partitioning data into groups (clusters) such that the observations within one cluster are more similar to one another than those in different clusters. Any detected (*a priori* unknown) patterns may be interpreted as identifying specified clusters based on the similarity to the clusters' features ([Halkidi et al., 2001](#)).

A hot spot is an area where patches with a high vulnerability level are surrounded by patches that also have high vulnerability scores, while a cold spot is represented by a number of patches of particularly low vulnerability scores within an area of largely low vulnerabilities. The analysis of multiple hot spots could shed light on particular underlying biotope groups that repeatedly occur in a vulnerable biotope complex. The ArcGIS tool "OptimizedHotSpotAnalysis" was used, with a number

² Variance weights are based on a principal component (PC) analysis and the corresponding PC loadings from the indicators. For details and in order to replicate the results, see Online Resource 3.

of outlier locations of 6202 (1.7% of the total number of patches), a fixed distance band of 811 m (rounded) based on the average distance to 30 nearest neighbours, and a result of 94,531 statistically significant output features based on a false discovery rate correction (cf. [Caldas de Castro and Singer, 2006](#)).

A thematic cluster may reveal similarity in vulnerability scores between biotope groups as well as between individual sites within one biotope group. To be aware of the influence of the applied cluster algorithm, a partitional and a hierarchical analysis were performed, and the resulting clusters compared. Every clustering task requires the analysis of a certain assumption regarding the dissimilarity between the cases. As the biotope vulnerability dataset consisted of a numeric variable (vulnerability score) and a categorical variable (biotope group), the dissimilarity was calculated according to the *gower* method ([Gower, 1971](#)) using the *R* package “cluster” ([Maechler et al., 2018](#)). The hierarchical clustering involved a simple agglomerative process, i.e., each patch at the beginning was assigned to its own cluster, and then, at each stage, the two most similar clusters were joined iteratively based on the unweighted pair group method with arithmetic mean (UPGMA). The calculation was implemented using *R* and the *R* package “fpc” ([Hennig, 2018](#)). In contrast to the hierarchical analysis, the data were also clustered with the *k-means* method, i.e., the patches were partitioned to a number of groups with the aim to minimize the overall distance between the centre of the group and its group members. Again, the mix of numerical and categorical variables is problematic. One solution is *k*-prototyping, i.e., the computation of cluster prototypes consisting of cluster means for numeric variables (as in *k-means*) and cluster modes for categorical variables ([Huang, 1998](#)). This calculation was implemented using the *R* package “clustMixType” ([Szepeannek, 2018](#)).

The crucial point in both approaches is that the number of clusters must be set *a priori*. Therefore, the algorithms should be run for different numbers of clusters to find meaningful clustering. In the past, very different criteria have been used to judge the appropriate number of clusters. This clustering built on four different internal criteria to attain more confidence. The *elbow method* is a very basic but robust criterion because it directly measures the sum of the within-cluster dissimilarities. A bend in the curve of decreasing within-cluster dissimilarity with increasing number of clusters suggests the appropriate number. The silhouette coefficient compares the average distance to elements in its assigned cluster with the average distance to elements in other clusters ([Rousseeuw, 1987](#)). The Dunn criterion helps to identify dense and well-separated clusters. It is the ratio of the minimum separation distance between two clusters to the maximum diameter found in the clusters ([Dunn, 1974](#)). As the Dunn criterion is based on two edge values and is potentially skewed by outliers, the Dunn2 criterion was also applied, which uses a minimum average value of separation and a maximum average cluster diameter ([Hennig, 2018](#)).

Unfortunately, especially for the distance matrix but also for the random initializations associated with *k*-prototyping, computational effort increases substantially with the size of the input dataset. Therefore, a random sample for the cluster analysis was drawn utilizing the *R* package “splitstackshape” ([Mahto, 2018](#)). The sample size of 5464 patches was chosen as a compromise between data representation and computational effort (cf. [Schönbrodt and Perugini, 2013](#)). The correlations between the indicators and the share of patches for all the biotope groups were mimicked precisely, but at least one patch of each biotope group was included (for details see Online Resource 4). Data visualization was conducted in *R* with the packages “ggplot2” ([Wickham, 2016](#)) and “factoextra” ([Kassambara and Mundt, 2017](#)).

3. Results

3.1. Vulnerability map

Based on the seven indicators and their transformation into index scores, a biotope vulnerability index was calculated for the study area at a regional level ($\approx 30,000 \text{ km}^2$). Among all the biotope patches in Brandenburg, those *not* referring to terrestrial, (semi-) natural biotope groups were excluded from the index calculation and therefore, the index was based on 362,217 patches (cf. Methods section). The patch-wise scores are displayed on a categorical scale of 5 levels (i.e., low, slightly low, medium, slightly high, and high) according to the statistical distribution (quintiles) of the scores, which underlines their relative meaning (see [Fig. 2](#)). This means that each of the five vulnerability levels accounts for the same number of patches, although a first glance at the vulnerability map may suggest otherwise, as the blue area dominates, indicating the patches with low vulnerability. This is due to the size effect, as larger biotope patches, generally speaking, have been less exposed to fragmentation, are less sensitive to landscape changes and, to a lesser extent, have a higher chance to have similar neighbouring biotopes for population exchange. A reduced exposure and sensitivity score, as well as an increased adaptive capacity score, would in turn result in a lower vulnerability score. The detailed inspection of the map revealed that red- and orange-coloured patches often follow the river courses and borders of lakes, indicating the special susceptibility of the underlying biotopes. Further, in those parts of the study region with large areas of arable land or built-up area, which together make up 88% of the not evaluated parts of the map (displayed in grey), biotopes also tend to show higher vulnerability. In contrast, streets are repeatedly bordered by blue patches, which represent rows of avenue trees or other edge strip vegetation.

3.2. Cluster analysis I (spatial hot spot analysis)

The search for vulnerability hot spots aimed at sharpening the vulnerability map with regard to its guiding function for prioritizing conservation efforts. The hot spots reflected all major areas of high vulnerability evident in the vulnerability map and further emphasized agglomerations of small vulnerable patches within areas of otherwise low vulnerability. The particular vulnerability of water-related biotopes was confirmed. Additionally, large cold spots and a high density of cold

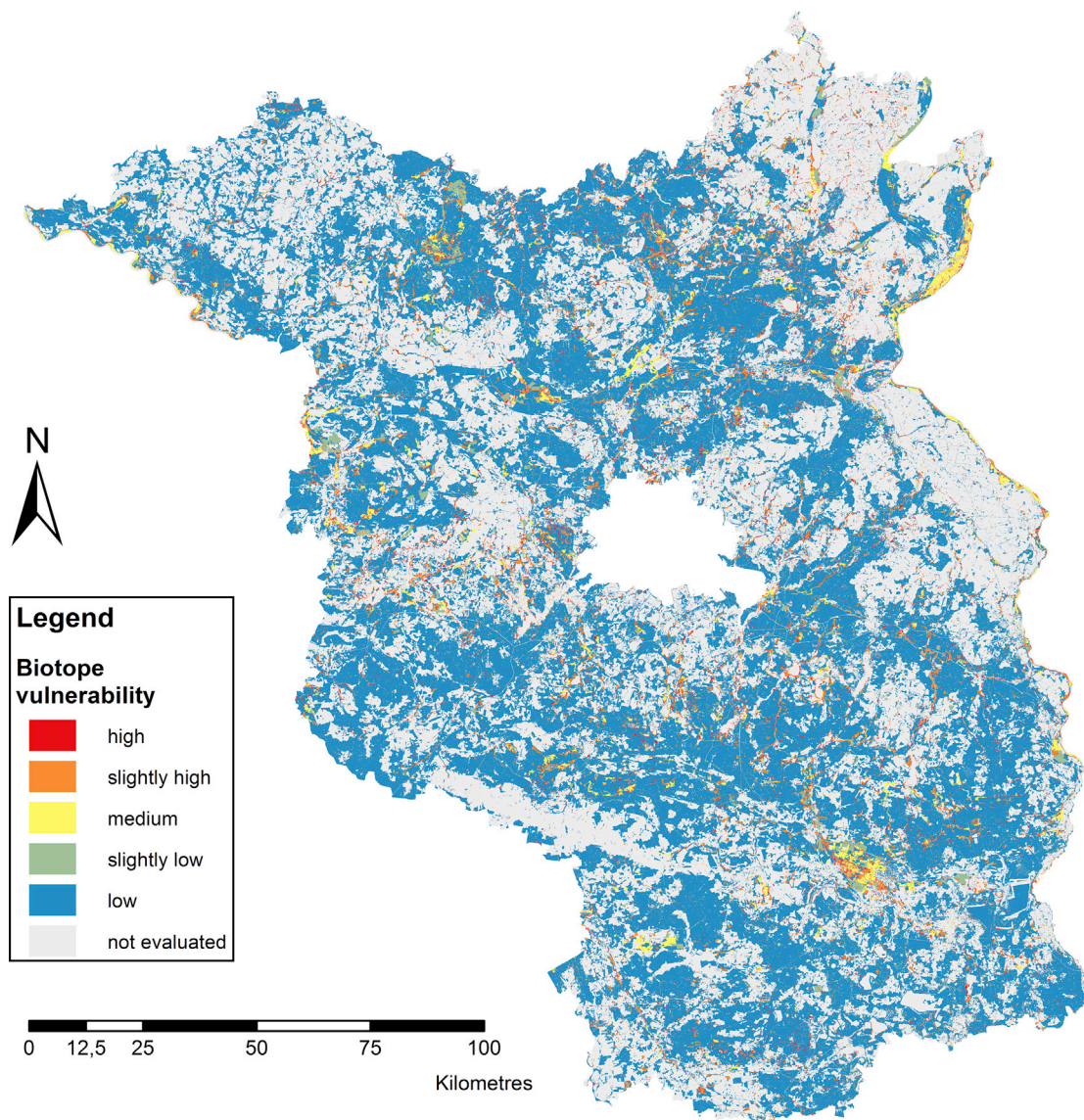


Fig. 2. Biotope vulnerability map of Brandenburg (Germany) showing a five-scaled index indicating patches with low to high vulnerability. The relative score is given for all terrestrial, (semi-) natural biotope patches. Non-evaluated patches included built-up areas, arable land and all aquatic biotopes.

spots potentially point to areas of low concern (cf. Fig. 3). To depict what kind of biotope group commonly underlies the spatial clusters with high or low vulnerability scores, an arbitrary but illustrative zoom-in is provided. In Fig. 4, three hot spots and two cold spots have been marked on both a hot spot map and a map of aggregated biotope groups. Cluster A shows a typical arrangement of highly vulnerable patches around a village. It is a small hot spot consisting of meadow, shrubland and grove surrounded by arable land and separated by settlement. Clusters B₁ and B₂ are hot spots of vulnerable meadows, reeds and peatland surrounded by intensive grassland and other meadows. Cluster C is a cold spot of forested area that encloses patches of heather, ruderal vegetation, and settlement. Cluster D is a cold spot of a forest-meadow mosaic surrounded by arable land and other meadows and forests of insignificant vulnerability clustering.

3.3. Cluster analysis II (biotope groups)

In addition to the spatial prioritization of conservation efforts, biotope groups whose sites repeatedly scored high in biotope vulnerability were also of interest. Furthermore, the identification of similarities in the vulnerability distributions between biotope groups potentially yields a reduction in necessary management options.

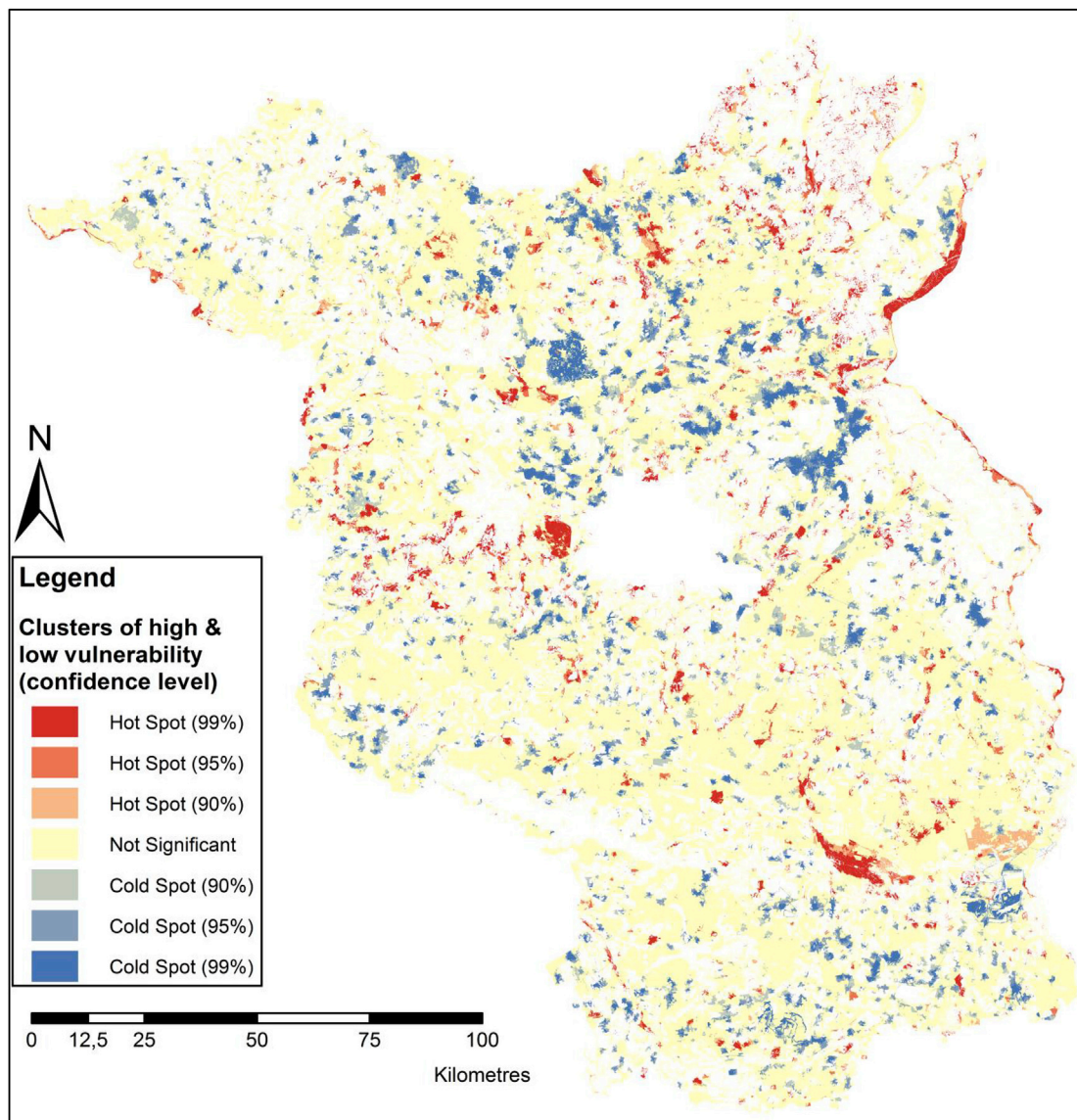


Fig. 3. Map of vulnerability hot spots in Brandenburg (Germany). Red areas indicate patches with high vulnerability scores in the neighbourhood of other patches with high scores, while blue areas indicate patches with low vulnerability scores in the neighbourhood of other low-scoring patches. The colour intensity increases with the likelihood of not detecting a grouping as a result of randomness. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

According to each biotope group, the vulnerability distribution is depicted in Fig. 5. The boxplots show, as usual, the median as a black line, the boxes represent 50% of the input data for each group, while the whiskers represent data points beyond the lower and upper quartiles up to 1.5 times the range of the box (interquartile range). If data points lie beyond the whiskers, they are displayed as dots and often considered outliers. Additionally, the width of the box was drawn to be proportional to the square root of the number of observations in the groups, i.e., wider boxes in the diagram indicate a more frequent occurrence of the biotope group.

The maximum range within a biotope group was limited to 0.55 (compared to the overall range of 0.89), and the inter-quartile range was always below 0.13, with one exception of 0.17 in one of the two very rare biotope groups ("0815", $n = 10$). Therefore, an important part of the variance seemed to derive from the different types of biotope groups (cf. Fig. 5).

The herbaceous perennials ("0514") was the biotope group with the highest vulnerability level, followed by several ecologically very different biotope groups with mean scores (and mostly also the lower quartile, i.e., the lower end of the box) above 0.5. These further biotope groups of major concern for conservation management, according to this study, included riparian vegetation ("022"), all three groups of peatland and reeds ("045", "046", "047"), shrubland ("0710"), groves ("0711"),

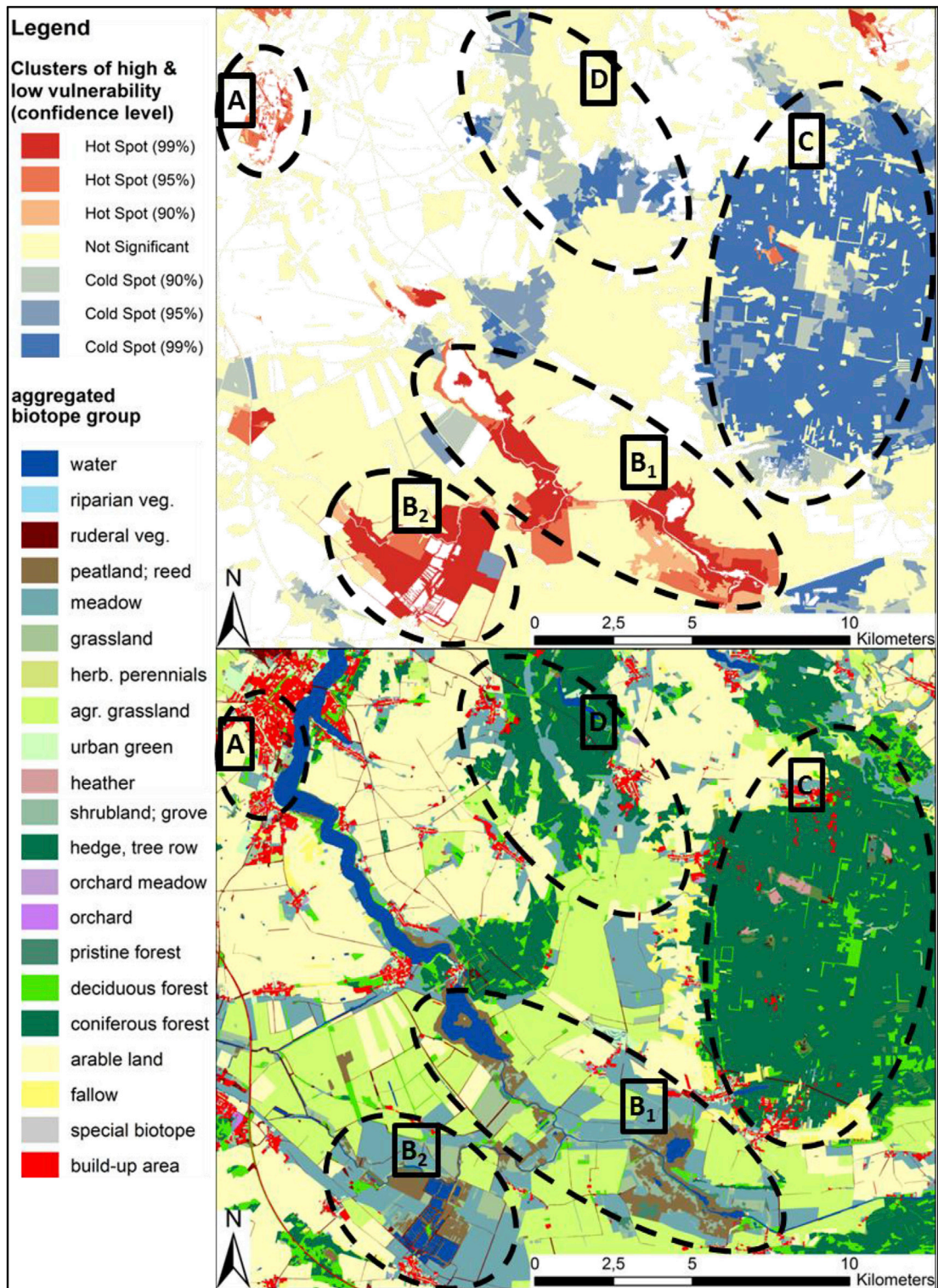


Fig. 4. Spatial clusters of biotope vulnerability hot spots (A, B₁, B₂) and cold spots (C, D) in an illustrative subarea ($\approx 50 \text{ km}^2$) of the study region. The upper map shows the confidence level of the patches as vulnerability hot spots or cold spots, while the lower map shows the underlying biotope groups.

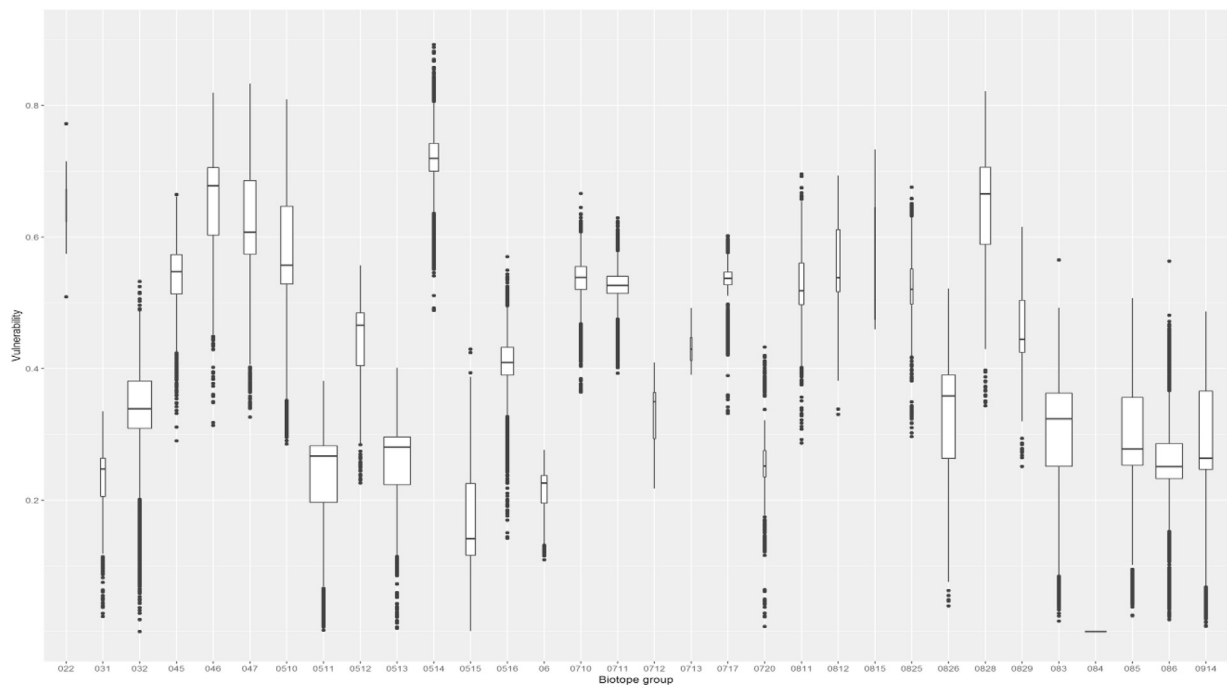


Fig. 5. Vulnerability score distribution of each of the 32 evaluated biotope groups displayed as boxplots with box width representing the number of underlying observations (patches). The overall number of patches was 362,217, and the overall vulnerability scores ranged from 0 to 0.89.

orchard meadows (“0717”), all the pristine deciduous forest with particular main tree species (“0811”, “0812”, “0815”), pristine coniferous forests (“0825”), and pioneer forests (“0828”). Remarkably, the pristine deciduous forest with a diversity of native main tree species (“0829”) scored lower than all the other pristine forest biotope groups but still considerably higher than the commercial forest biotope groups. Another interesting observation was that rarity did not automatically render biotope groups highly vulnerable. Neither a small overall number of patches nor a low overall amount of area reliably predicted high vulnerability scores. However, of the top ten biotope groups according to patch number, 8 scored low, and among the top ten biotope groups according to area, 9 scored relatively low. Indeed, a remarkable negative correlation with vulnerability scores was observed. The correlation coefficient (Kendall’s tau) was -0.35 for a pairing with the number of patches per biotope group and -0.51 for a pairing with the occupied area per biotope group (both p-values were numerically equal to zero).

The most striking distribution of vulnerability scores was that for the biotope group of coniferous forests (“084”). All patches that were evaluated to have zero vulnerability occurred in this group, and the group exhibited zero scores only. This sharp distinction from the other biotope groups also reappeared in the cluster analysis (cf. Figs. 6–8). This result can be explained by the far greatest share of area (20.01%) that this biotope group covers in Brandenburg. Its exposure and sensitivity is low, while its adaptive capacity is high. Other biotope groups with homogenous scores, i.e., having a range below 0.2 (outliers excluded), were riparian vegetation (“022”), herbaceous perennials (“0514”), lawn (“0516”), and the biotope groups of non-forest woods, such as shrubs, hedges, and orchards (“0710”, “0711”, “0712”, “0713”, “0717”, “0720”). The individual patch traits seemed to be of minor importance for those biotope groups, which would suggest the existence of a generalizable interpretation for each of their vulnerability scores. Furthermore, these biotope groups with a particularly small range of scores were often represented by only a small number of patches (i.e., compact boxplots tend to have slim boxes, cf. Fig. 5). All the other biotope groups showed a rather large range of vulnerability scores, suggesting more differentiation among the patches.

For the cluster analysis, a sample from the full dataset was used (cf. Methods section).

The hierarchical clustering of the random sample ($n = 5464$) identified 3 different clusters, while the partitional clustering identified 4 different clusters. The four applied criteria to decide on the appropriate number of clusters (cf. Methods section) were largely concordant for the hierarchical clustering, while the decision for the k-prototyping was a compromise between the contradicting criteria (cf. Online Resource 5).

The cluster dendrogram derived from hierarchical clustering (Fig. 6) shows that one cluster (blue) was formed right at the beginning and then separated from the rest throughout the whole iterative process. Patches from the other biotope groups were stepwise merged into two further clusters (yellow, red). A large jump in merged cluster dissimilarity occurred at a number of 32 clusters (1 blue, 13 green, 18 red). Apparently, these clusters reflect the 32 biotope groups. It turned out that the early-formed cluster (blue) consisted of all and only patches of the biotope group of coniferous forest (“084”). Furthermore,

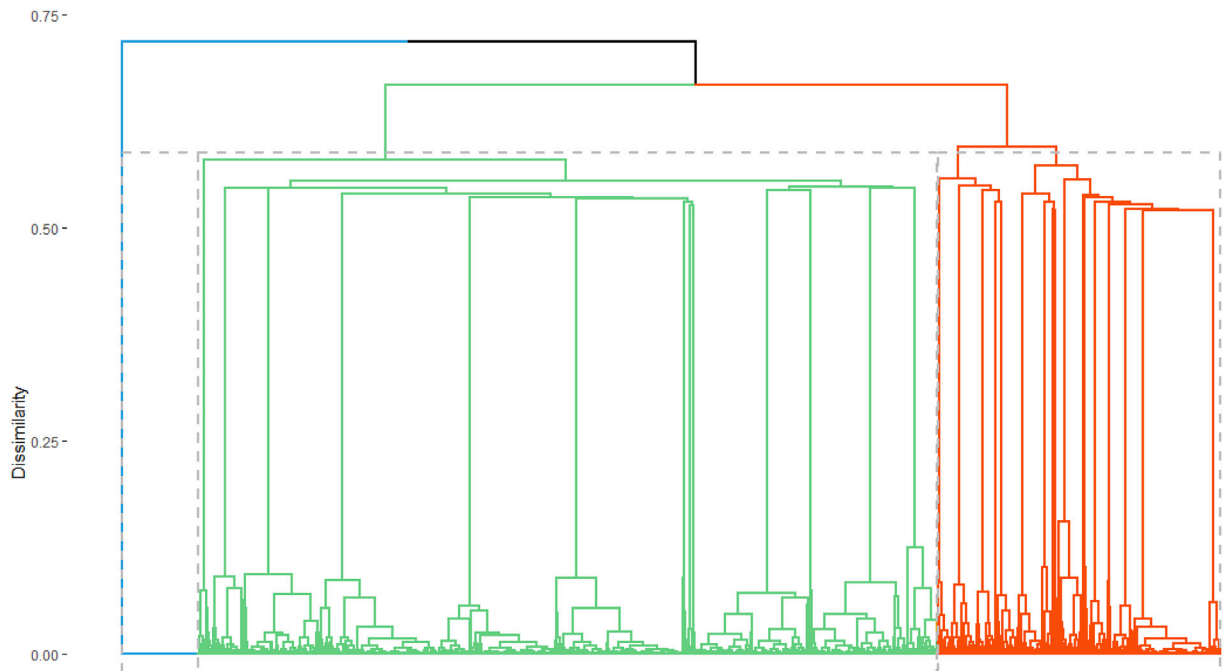


Fig. 6. Cluster dendrogram illustrating the results of the hierarchical clustering with three clusters represented by the blue, green, and red branches, respectively. The dissimilarity was based on the variables *vulnerability score* (numerical) and *biotope group* (categorical). (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

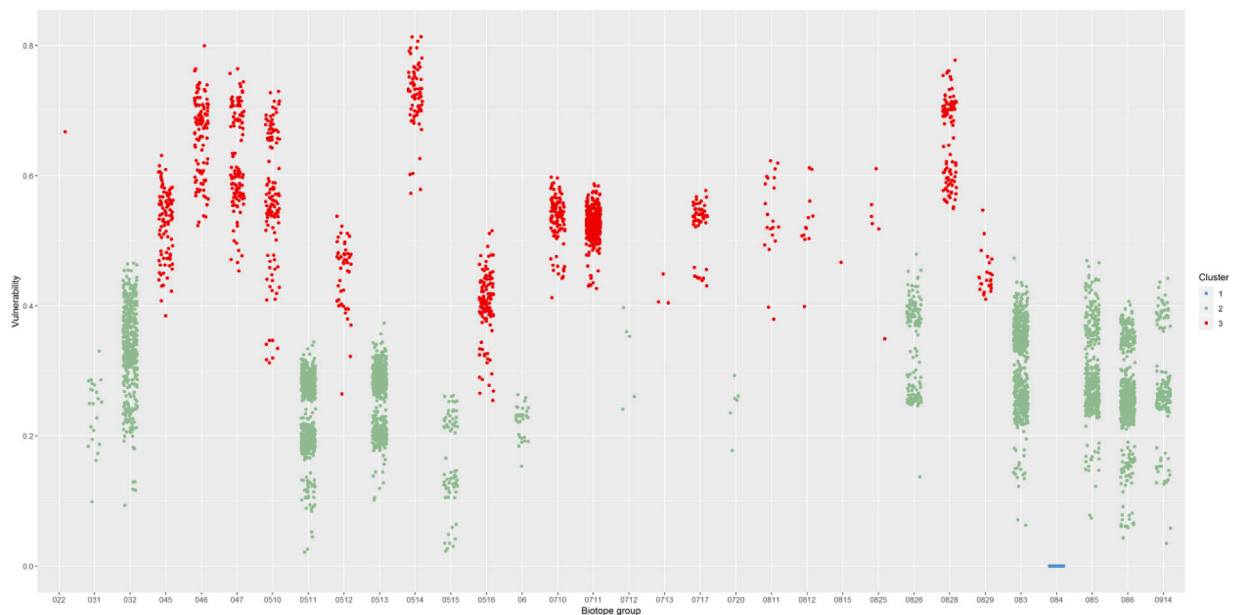


Fig. 7. Distribution of the patches from each of the biotope groups (x-axis) in terms of their vulnerability score (y-axis) and their allocation to one of three clusters (different colours) derived from hierarchical clustering. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

the algorithm distributed all patches of one biotope group homogenously into one of the clusters, i.e., no biotope group was spread across several clusters. Thus, the categorical variable seemed to dominate the process. The allocation to the clusters is depicted in Fig. 7. The biotope groups in the three clusters were classified as “high vulnerability” (red), “low vulnerability” (green), and “not vulnerable” (blue).

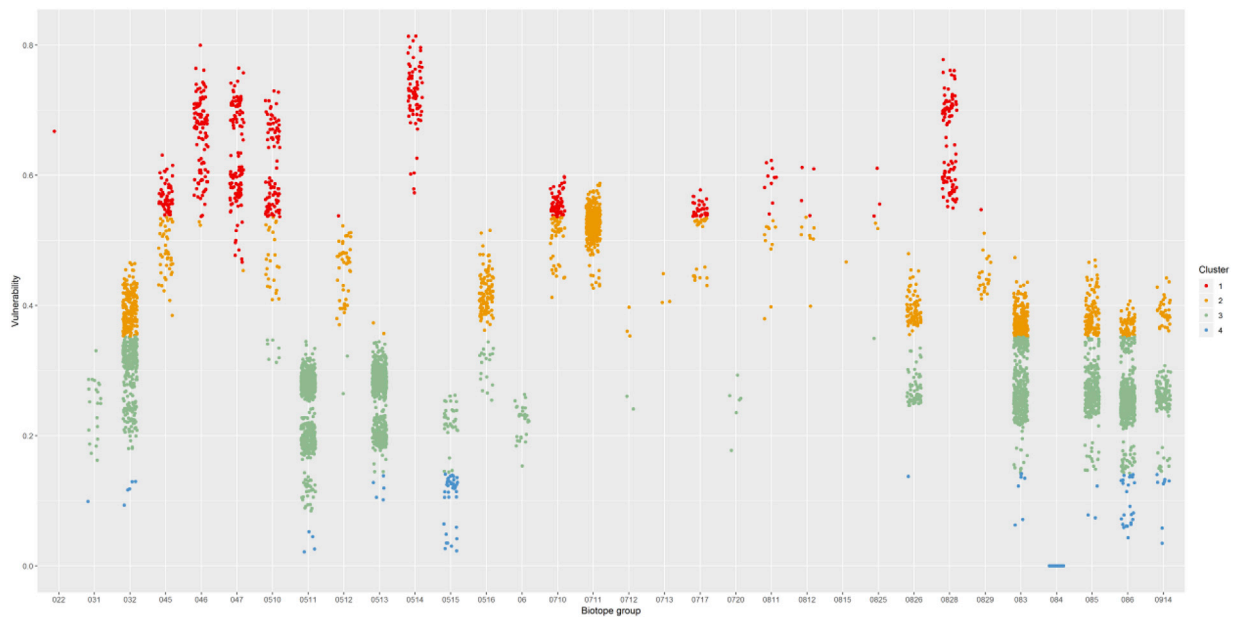


Fig. 8. Distribution of the patches from each of the biotope groups (x-axis) in terms of their vulnerability score (y-axis) and their allocation to one of four clusters (different colours) derived from k-prototyping. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

The partitional clustering with k-prototypes showed a more differentiated patch allocation to four different clusters (cf. Fig. 8). Of the 32 biotope groups, 13 had patches allocated to two clusters, and ten had patches distributed to three clusters. While the groups belonging to two clusters partly showed priority to one of them, the biotope groups belonging to three clusters did not show priority to one of them, which makes the assessment of their vulnerability difficult and would demand differentiated management. Every cluster included at least one biotope group entirely. The cluster of highly vulnerable biotope patches (red) had three groups fully allocated to it (“022”, “0514”, “0828”), and another two were almost fully allocated to it (“046”, “047”). The cluster of biotope patches with slightly high vulnerability (orange) made up all patches in three groups, of which two were very small (“0711”, “0713”, “0815”), and dominated in another two (“0512”, “0829”). The patch cluster of slightly low vulnerability (green) only had one small biotope group entirely allocated to it (“0720”) and dominated in three other groups (“031”, “0511”, “0513”). Similar to the results from hierarchical clustering, the biotope group of coniferous forests (“084”) was entirely allocated to the cluster of low vulnerability (blue), but now patches from ten other biotope groups were also included. Nevertheless, this cluster reached no dominance in these other groups. Thus, more biotope groups could be clearly evaluated to have high vulnerability (many concerns) than low vulnerability (few concerns). Moreover, many biotope groups occur to some extent in rather robust patches if they are otherwise vulnerable and the other way around.

4. Discussion

4.1. Vulnerability map

The high level of spatial and thematic abstraction of the vulnerability index, which seems necessary for supporting a regional conservation management plan, comes at a price. The biotope vulnerability index could give the same score for two locations where different drivers are at work. Thus, it may be beneficial to either provide quantifications of each biotope exposure, sensitivity and adaptive capacity score for the determination of variation in vulnerability levels (Inostroza et al., 2016) or to use the original indicators to underpin ecological planning and management decisions (Abson et al., 2012). Even the seven underlying metrics do not account for the more complex habitat and resource requirements that many species have. Particular species may need larger habitat fragments (Rösch et al., 2013) or may require more movement among distinct habitats during their lifetime to survive (Tscharntke et al., 2012). Moreover, the interpretation of a landscape consisting of a mosaic of patches is conceptually simple and intuitive but subsumes all internal heterogeneity, although most ecological attributes are inherently continuous in their spatial variation (McGarigal et al., 2009). For a meaningful analysis, 38 biotope groups were aggregated from the more than 2000 different biotope types in the raw biotope dataset. This thematic aggregation influences the size of the biotope group and, in many cases, the size and shape of the biotope patches. The applied aggregation across species and space, i.e., considering species communities within homogenous patches of habitat, surely

underestimates the complexity of ecological processes and the differences among individual species. Nevertheless, it seems rather impossible to analyse every single species within a given landscape (Fischer and Lindenmayer, 2007).

Another limitation of the developed biotope vulnerability index is its static approach, which is based on a current snapshot of the landscape. Although the current distribution of biotopes is a result of past landscape development, the method did not account for the processes of landscape change, either past or present, or for the effect of future landscape configuration. Time lags regarding extinction debts or immigration credits of species communities (Jackson and Sax, 2010; Kolk et al., 2017) were not included.

An artefact in the vulnerability distribution was expected, as all patches close to the border of the study area exhibit a bias towards lower values for all indicators based on neighbourhoods, i.e., surrounding natural area (125 m range) and surrounding patches of the same biotope group (10 km range). Hence, these areas close to the border, especially in corners, should exhibit falsely lower scores for adaptive capacity and in turn higher scores for vulnerability. However, this effect was not observed. This results seems to have occurred because many patches in the interior of the study area are so isolated (in the sense of habitat islands according to MacArthur and Wilson, 1967) that they did not differ significantly in terms of the metrics on neighbourhood. The remaining weak difference may be overridden by the other indicators.

An advantage of this vulnerability index is that it does not rely on artificial subjective weighting factors, which are necessary, for example, in the repeatedly applied analytical hierarchy process (e.g., Chang and Chao, 2012; Hou et al., 2015). The variance weights slightly favoured the sensitivity indicators over the adaptive capacity and exposure indicators. The variance contributions of the indicators did not differ much, which generally limits the influence of the weights. The weight for the lowest contribution to variance of *near natural area* amounted to 79% of the variance weight calculated for *fractal dimension*, which provided the largest contribution to variance. Comparing the final biotope vulnerability index values to the same index values calculated without index weights reveals slightly reduced numbers, as expected by the weights, which ranged from 0.938 to 1. The largest difference amounts to a reduction below 2.5% in cases of very high vulnerability scores. However, in very few cases, the index score was even slightly increased (always less than 1.2%) by the index weights in cases of high adaptive capacity and relatively small contributions of the sensitivity or exposure indicators.

4.2. Cluster analysis

Generally, the additional insights from the hot spot analysis compared to the detailed inspection of the vulnerability map seem to be limited. However, the small vulnerable areas were better visualized and agglomerations of medium vulnerable biotopes, which may be overlooked as point of concern, became more visible.

Further, the analysis of cold spots may provide guidance towards principles of robustness or resilience. With additional information on the habitat requirements of the different species communities, this can be translated into management principles regarding the biotope group-specific minimum area and biotope group-specific optimal spatial arrangement of patches. At this point, the concepts of green infrastructure and biotope networks must be mentioned, which are inherent in the European conservation sites under the label of “NATURA 2000” and especially elaborated in the German nature conservation community (e.g. Jedicke, 1994; Altena et al., 2018).

For the cluster analysis according to the biotope groups it turned out that several conclusions can be drawn beyond those deriving directly from analysing the score distribution among the biotope groups. The clusters allow to better distinguish biotope groups that can be considered of a similar vulnerability configuration and this difference can be quantified. Further, a decision can be made whether a generally rather vulnerable biotope group has ‘refuge patches’ or otherwise is vulnerable as a whole.

Clusters found by k-prototyping better handled the categorical variable, as expected. Nevertheless, k-prototyping mainly builds upon the k-means algorithm and is therefore prone to noise and outliers and cannot detect the non-convex shapes of clusters (Halkidi et al., 2001). Furthermore, the decision to use four clusters was less confident than the decision to use three clusters for the hierarchical clustering. In general, the definition of the number of clusters *a priori* remains a constraint in both approaches but could be amended by the use of different internal evaluation criteria. A strict external validation criterion, i.e., a test of whether the vulnerability level was correctly assigned to a biotope patch was not applicable, as a true vulnerability level is not available. Nevertheless, the thematic vulnerability clusters do not seriously contradict the vulnerability map or the analysis of spatial clusters. Thus, the insights from the thematic clusters can be taken into account to describe inherent similarities in the vulnerability within and between biotope groups.

5. Conclusion

Finally, with consideration of the discussed limitations, the prioritization of conservation effort for the study region can be inferred from the results. The vulnerability score distribution and the analysis of the different spatial and thematic clusters suggest the following:

- i) A handful of ecologically very different biotope groups are likely to be highly vulnerable to further landscape change and have no refuge patches of low vulnerability. They would need the most attention of conservation management.

- ii) With the exception of a few patches, the biotopes dependent upon wet conditions, such as the wet meadow, riparian, or peatland biotopes, are generally in a vulnerable condition.
- iii) The majority of forest biotope patches are less vulnerable to landscape change, but a larger share of the pristine forest patches is concerned.
- iv) For more than half of the biotope groups, the vulnerability of their patches differs considerably, and a general level of concern cannot be substantiated.

These statements provide an overview of biotopes for which a closer look seems fruitful to identify the causes of severe vulnerability and develop mitigation measures not only at the level of habitat or species community but also at the population, species, or ecosystem level. Any implementation of results into conservation interventions should be substantiated by more specific information on the concerned species and on the local context. A conservation strategy could be oriented to the major source of a biotope's vulnerability, which is either the exposure to landscape change, the sensitivity to the consequences of change, or the lack of adaptive capacity to cope with that change. Accordingly, the aims of conservation management interventions may address the drivers of habitat loss in one case, while in another area, the biotope networks need to be restored to reconnect populations. The important point is that interventions in a particular protected piece of land are not necessarily the most useful to safeguard its biodiversity in the long run, but its neighbourhood and other patches of a similar biotope type in the same landscape should also be considered. With a few adjustments, the partly automated method may be transferred to other biotope maps and could therefore inform conservation or planning agencies in other regions as well.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.gecco.2019.e00771>.

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