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Integrating remote sensing and ecological modelling to assess the potential impact of *Brachypodium genuense* on grasslands habitat conservation.

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Abstract: Remote sensing (RS) has been widely adopted as a tool to investigate several biotic and abiotic factors, directly and indirectly, related to biodiversity conservation. European grasslands are one of the most biodiverse habitats in Europe. Most of these habitats are subject to priority conservation measure, and they are threatened by several human induced process. The broad expansions of few dominant species are widely reported as drivers of biodiversity loss. In this context, using Sentinel-2 (S2) images, we investigate the distribution of one of the most spreading species: *Brachypodium genuense*. We performed a binary Random Forest (RF) classification of *B. genuense* using a RS image and field sampled presence/absence points. Then, we integrate the occurrences obtained from RS classification into niche models to identify the topographic drivers of *B. genuense* distribution. Lastly, the impact of *B. genuense* distribution in the N2k habitats was assessed by overlay analysis. The RF classification process detected *B. genuense*'s cover with an overall accuracy of 91.18%. The integration of RS and topographic niche models shows that the most relevant topographic variables that influence the distribution of *B. genuense* are slope, elevation, solar radiation and Topographic Wet Index (TWI) in order of importance. The overlay analysis shows that 74.04% of the *B. genuense* identified in the study area falls on the semi-natural dry grasslands. The study highlights the importance of the RS classification and the topographic niche models as an integrated approach for mapping a broad-expansion species such as *B. genuense*. The coupled techniques presented in this work should be applicable to other plant communities with remotely recognizable characteristics for more effective management of N2k habitats.

Keywords: Habitat grasslands monitoring; *Brachypodium genuense*; vegetation dynamics; Campo Imperatore plateau; Sentinel-2; Machine learning; Multispectral classification; Topographic niche models; Natura 2000.

1. Introduction

European grasslands, especially those on limestone substrates, are one of Europe's richest ecosystems in terms of floristic richness and endemic species [1]. Indeed, most of these communities are considered priority habitats of community interest under the European Community Habitats Directive (92/43/EEC) [2].

The vegetation dynamics driven by land use change in Mediterranean mountains cause consequent drastic reduction in biodiversity [3]. The land use change, in these areas, is mainly related to the abandonment of traditional human activities that have favored the maintenance of the grasslands over previous centuries [4]. This land use change (abandonment of the traditional practices) had and is still having negative effect on several habitats including semi-natural grasslands [5]. Even though the semi-natural grasslands are actually in the priority conservation status across Europe, negative changes are expected not only on vegetation [6], but also for many animal species strongly connected to these habitats (e.g. Brunetti, *et al.* [7],Console, *et al.* [8]).

In this context, remote sensing (RS) has been widely adopted as tool to investigate several biotic and abiotic factors directly and indirectly related to biodiversity conservation [9,10].

In the last decade, satellite data showed great versatility in environmental studies such as fires disturbances [11], floods [12], droughts [13], spread of invasive alien species [14,15], and several other human induced pressures [16-18].

From this perspective, the RS has demonstrated to be a practical and economic tool for studying vegetation cover both on local and global scale [19,20], also proving a quantification of the biotic characteristics of grassland habitats [21,22].

Among the several information provided by RS, multispectral data, such as Landsat and Sentinel-2 MSI (S2) images, have proven suitable for detecting grassland disturbances and monitoring changes in these ecosystems [23-27]. Moreover, the higher spatial and temporal resolution of S2 compared to Landsat makes S2 a better tool (in some cases) for vegetation studies [28].

Integrate RS data with species distribution model (SDMs) is a key tool to investigate the realized niche of several species. Species distribution models are numerical tools that combine observations of species occurrence or abundance with environmental estimates [29]. They are used to gain ecological and evolutionary insights and to predict distributions across landscapes [30,31]. Species occurrences are often biased by sampling effort. Indeed frequently, researchers sample easily accessible areas (i.e. near major roads or towns), leading to geographic clusters of localities [32,33]. To overcome this bias, RS data can provide an accurate distribution with a high number of occurrences to calibrate the models.

In this study we focused on Apennine grassland communities colonized by *Brachypodium genuense* and/or *B. rupestre* [34,35]. *B. genuense* is a spreading competitor species in the earliest stages of the colonization of the grasslands, that are widely diffused in the Apennine chain [36]. We focused on this species because its invasive behavior causes a change in community structure, species composition and a loss of biodiversity [37,38]. Therefore, controlling the spread of *B. genuense* is a key issue for the conservation of biodiversity and the maintenance or restoration of the value of mountain pastures [39,40].

The proposed integration of RS data and topographic niche models was tested on the Campo Imperatore upland plain (Abruzzo, Italy), in the south-eastern sector of the Gran Sasso and Monti of Laga National Park. This area, where the target species is widely diffused, is characterized by a remarkable floristic and vegetational biodiversity [41,42].

The study also aims to provide a new approach to monitor these important grassland habitats in view of the future European '5th Habitat Report ex-Art. 17' on Natura 2000 (N2k) habitats planned for the year 2024 (2019-2024).

Our study based on S2 images, aims to achieve the following targets: i) Mapping the *Brachypodium genuense* (*B. genuense*) distribution using RS data. ii) Investigate the topographic drivers of the target species by the integration of RS data with ecological modelling. iii) Identify the N2k habitats (European Commission 2013) which are the most invaded by *B. genuense*.

2. Materials and Methods

2.1 Study Area

In this study we focused on Campo Imperatore upland plain falling within the Gran Sasso and Monti of Laga National Park (Figure 1) in the alpine biogeographical region [43]. The Campo Imperatore plateau ranges from 1300 to 2500 m a.s.l., it is at the foot of the main limestone mountains of the Gran Sasso group, that has been strongly shaped by glaciations and morphogenetic phenomena, mainly by karst, snow, wind and water. Under these conditions, particularly extensive geoforms have originated, such as the sinkhole fields, the shallow and deep incisions, and the swallow holes [44]. The bioclimatic classification according to Rivas-Martínez, *et al.* [45] indicates a temperate macroclimate, an oceanic bioclimate, and an upper supratemperate thermotype and an orotemperate thermotype [46].

Since the past, the main land use in this area has been breeding (intensive grazing sheep). Currently, pastoral activity is much milder with the replacement of sheep with cattle and horses left in the wild pastures. In the eastern sector beech woods and conifer stands are present.

The study area, despite its limited size (~ 9400 ha), is characterized by a noticeable flora [42] and vegetation [47] and represents an optimal area to test the techniques presented in the work. Furthermore, the area falls within a Special Protection Areas (SPAs) (Birds Directive, EU), and in a Sites of Community Interest (SCIs) (Habitat Directive, EU) and is one of the largest upland plains in Europe, the largest in the Italian Apennines [48].

2.2 Target species

Brachypodium genuense (DC.) Roem. et Schult. is a graminoid perennial herb species of the Poaceae family. Is an endemic taxon of the Italian peninsula and is widespread in grasslands over 1300–1400 m a.s.l.. This plant reaches a height of 0.4 - 0.7 m (maximum 1.2 m) with wintering buds at ground level. Its large dimensions, strong capacity of vegetative reproduction (with remarkable lateral spreading), growth from basal meristems, and high phytomass production, makes *B. genuense* a dominant species in dense grasslands [49]. Indeed, the genus *Brachypodium* has hairy leaves rich in siliceous crystals that discourages domestic herbivores to feed on them [50]. From a phenological perspective, *B. genuense* in central Apennine follows precise stages: the vegetative growth starts in May and reach full flowering in July (Green up). After fruiting and seed production in July–August (Maturity), in November all individuals are fully dried (Senescence) [37].

2.3 Remote sensing dataset and pre-processing

In this paper, the distribution of *B. genuense* is measured by using the multispectral images of S2 satellites (Copernicus Program) at 10 m per pixel. S2 launched in June 2015, provides open-source multispectral data with a spatial resolution of 10 to 60 m per pixel, 13 spectral bands with a temporal resolution of 5 days [51]. These characteristics make S2 data suitable to environmental monitoring on a horizontal scale, indeed, S2 data were used in several studies concerning grassland communities [49,52]. S2 carries a MultiSpectral Instrument (MSI) that measures the Earth's reflected radiance in 13 bands, from 443 to 2190 nm. The visible RGB, the NIR, Red-edges and SWIR bands resulting highly suitable for the classification of both grassland and tree coverings [53]. The analyzed images were accessed by ESA's Open Access portal (https://scihub.copernicus.eu), with a temporal range between late June ÷ late August 2019 (Appendix S1). This time interval was chosen to distinguish *B. genuense* from other plant communities based on its phenology. Indeed, in the study area, the target species reaches the senescence phase after the other broadly covered species (e.g. *Bromopsis erecta*). The satellite images to perform the classification analysis were chosen taking into account the phenological stages of the *B. genuense* species in the central Apennines [37]. The phenological phases considered were: beginning of vegetative growth (Green up - 20 June 2019), flowering and fruiting (Maturity - 25 July 2019), beginning of leaf yellowing and full drying (Senescence - September 28, 2019) [54].

The 'Level 1C' (TOA – Top of Atmosphere reflectance) was initially chosen to obtain greater temporal coverage (compared to 'Level 2A' not yet available at the time of data acquisition) and to better choice of the images with low cloud percentage. Furthermore, the images were pre-processed (to obtain the 'Level 2A') by performing the atmospheric correction [55] with Sen2Cor [56] tool of the free software SNAP – Sentinel-2 Toolbox [57] provided by ESA.

Sen2Cor atmospheric correction algorithm relies on the APDA (Atmospheric Precorrected Differential Absorption) algorithm [58] to retrieve the Water Vapour content from the L1C image. This algorithm uses a ratio between band B8A and band B09.

The S2 Level 2-A (BOA – Bottom Of Atmosphere reflectance) processing consist in two parts: Atmospheric Correction (S2AC) mentioned above and Scene Classification (SC) which we used to mask the limited clouds in the images. The SC algorithm allows to detect clouds, snow and cloud shadows and to generate a classification map, which consists of 4 different classes for clouds (including cirrus), together with six different classifications: vegetation, soils/deserts, water, snow, shadows and cloud shadows. The algorithm is based on a series of threshold tests that use as input TOA reflectance from the S2 spectral bands [59].

To build the dataset for classification, 10 spectral bands (B2, B3, B4, B5, B6, B7, B8, B8A, B11, B12) were chosen for each analyzed image [52] by resampling and combining them into a single piled layer (raster stack). In addition to the multispectral bands, we also included in the stack a Digital Elevation Model (provided by Abruzzo region: http://opendata.regione.abruzzo.it/content/modello-digitale-del-terreno-risoluzione-10x10-metri) at 10 m per pixel and its derivative products such as Slope and Aspect. Finally, to obtain a more accurate classification, the NDVI (Normalized Difference Vegetation Index) [60,61] and a derivative product thereof, such as 'Texture' (Focal analysis) [62], were calculated for each analyzed image and added to the stacked raster. Focal analysis is one of the raster neighborhood analysis methods and is one of the cues that is used for visual classification and as additional information for automated classification. The method usually calculates the variability of pixel values in a certain neighborhood around a central pixel. The texture images obtained from the focal analysis provides a measure of the heterogeneity of the average (in our case) values of the pixels within a defined area of an image; it also provides a combination of desirable attributes for cover classes characterization on a landscape scale [63].

2.4 Field data

We carried out a data collection in the field and from other ancillary data (e.g. Catonica, *et al.* [64],Congedo, *et al.* [65],Copernicus [66]) to train the classifier and to validate the result of the classification process. Field data was collected using a GPS receiver 'GPSMap 60CSX' (positional error <2 m).

A random stratified sampling based on existing knowledge (land cover products) distributed over the entire studied area (mainly consisting by grasslands) was used, considering the altitudinal variability within the area, ranged from 1500 to 2000 m a.s.l.

Since these data are used as training and validation data, we took care that all recorded data had accurate location and thematic information. Our sampling framework considered positional errors in classified images by ensuring that sample points are not close to the edge of a class boundary (presence/absence classes).

The ground truth data was collected close the same date when the imagery used for the classification was acquired (2019-07), except for the image acquired in the late spring period (2019-06-20) where it was not possible to realize the sampling. This was done to ensure conditions on the ground have not changed significantly.

The samplings were made in homogeneous areas, so that no mixed pixel signal could interfere with the classification algorithm, including all the intra-class variability [62].

The presence sampled points were collected in a homogeneous patch of 100 m2, where *B. genuese* cover is higher than 90%.

Moreover, the same number of absence points of the target species on grassland habitats, plus a limited number of absence points in the other different cover classes (e.g. forest, bare soil, scree, urbanized), were collected both directly and indirectly in the field and through the previously mentioned layers of existing geographic information.

Consistent with the size of the study area, 40-point occurrences of *B. genuense* were collected. A total of 80 sample points were selected in the study area to create the training and accuracy assessment data sets.

2.5 Classification Analysis by Machine learning

To capture the extents of *B. genuense* in the study area, the Random Forest (RF) machine learning classifier [67] was used. RF is a machine learning algorithm that employs a bagging (bootstrap aggregation) operation in which a certain number of trees (ntree) are constructed based on a random subset of samples derived from the training data. Each tree is independently grown to maximum size based on a bootstrap sample from the training dataset without any pruning, and each node is split using the best among a subset of input variables (mtry) [68].

The supervised RF algorithm was used to relate the target species to the satellite and ancillary data. RF was chosen as the preferred classification method as it has frequently demonstrated its skill for vegetation mapping using various typology of data [69,70] and is less sensitive than other machine learning classifiers to the quality of training samples and to overfitting [71].

The 'superClass' function within the RStoolbox package [72] in R environment [73] was used to perform the RF classification analysis.

The Random Forest's tuning has been optimized by setting the default number of trees (500) and mtry to 6 considering the variables used for the classification, according to the papers of Duro, *et al.* [74] and Belgiu and Drăguţ [71].

We performed a binary classification using the presence points of the target species as a reference class and the absences points as all other classes considering a two-class binary scenario (presence/absence of target species). These binary classifiers, however, require a complete and exhaustively labelled sample set for model training [75]. In particular, the training set must typically contain labelled samples of all cover types that occur in the imagery, which are then divided into presence and absence sample subsets.

2.6 Accuracy Assessment

One of the most important steps in a classification process is accuracy assessment. The aim of accuracy assessment is to quantitatively assess how effectively the pixels were sampled into the correct cover classes. Considering the paper by Foody, *et al.* [76] we focused more on the class of interest (presence of *B. genuense*) so that even a small and inexpensive training dataset can be used to obtain the desired information. Considering the total extension of the study area (~ 9400 ha) we used a small training dataset. It is widely demonstrated in the literature that even the use of a small training dataset relative to the study area size, can lead to excellent results [77-79]. For the accuracy assessment, we kept 80% of the data for training the model and the remaining 20% for validation. Performance tuning and estimation were performed using random 10-folds cross-validation using the 'superClass' function in RStoolbox. In addition, the Overall accuracy (OA), Kappa, Sensitivity and Specificity [80] were obtained through the same function.

Since the model has no knowledge of the environments in which the classification is made, estimating the area to which a classification model can be reliably applied is required. To this end we used the method proposed by Meyer and Pebesma [81] which consists in the calculation of the 'Applicability Area' (AOA) which is defined as the area, for which, on average, the cross-validation error of the model is applied. To calculate the AOA, the 'dissimilarity index' (DI) based on the minimum distance from the training data in the multidimensional predictor space is required, with the predictors weighted by their respective importance in the model [82]. The AOA is derived by applying a threshold based on the DI of the training data in which the DI of the training data is calculated with respect to the cross-validation strategy used for training the model. The 'CAST' package [83] was used for the estimation of the AOA in the R environment. This function estimates the DI and the derived AOA of spatial prediction models by considering the distance of new data (i.e. a Raster Stack of spatial predictors used in the models) in the predictor variable space to the data used for model training.

The spatial association of the classified *B. genuense* patches were tested using the Local Indicators of Spatial Association (LISA) analysis. This analysis provides for each observation an indication of the extent of significant spatial clustering and the sum of LISAs for all observations can be considered as a global indicator of spatial association [84].

2.7 Conversion of plant associations into NATURA 2000 habitats

The plant associations in the study area were extrapolated from 'La vegetazione di Campo Imperatore (Gran Sasso d'Italia)' [47]. Through an expert-based process, the plant associations have been converted into their respective habitats (N2k). The plant associations were transformed in N2k habitat according to the 'Interpretation Manual of European Union Habitats - EUR28' [2] and the 'Interpretation Manual of Italian Habitats' [85]. The complex vegetation systems like those of the sinkholes, that occur in small area, cannot be reported as one habitat type thus were named 'Mosaic'.

2.8 GIS analysis of the spread of B. genuense *on habitats NATURA 2000*

To evaluate the spread of *B. genuense* on habitat N2k, we calculated the area of *B. genuense*'s cover map obtained by classification analysis. All spatial processes and geographic analyses were managed through QGIS 3.4.13 [86]. The raster obtained from classification process has been polygonized and intersected with another vector layer of the N2k habitats. This post-modelling analysis was performed to investigate the spatial relationship between the *B. genuense* and the N2k habitats. To assess how each habitat was affected by the spread of *B. genuense*, the cumulative contribution of the patches in each habitat and the differences between 'realized' cover with 'expected' cover was calculated. The realized cover is the real cover of the target species in each habitat while the expected cover is an equal repartition of *B. genuense* cover proportional to the area of each habitat, thus the target species results equally distributed among the habitats. The 'expected' cover in each habitat (Expected cover$_{(i)}$) was calculated by using the following formula:

$$\textbf{Expected Cover}_{(\mathbf{i})} = \frac{\textbf{AreaH}_{(\mathbf{i})} * \textbf{TotAreaBra}}{\textbf{TotArea}}$$

Where the AreaH$_{(i)}$ is the total area of each habitat, TotAreaBra is the total area covered by *B. genuense* and TotArea is the entire study area.

Moreover, to investigate how the distribution of *B. genuense* is associated in the ecotones among habitats, 'moving windows' approach was used. The 'moving window' process consists of a window of a given size (the neighbourhood) that is moved across the image. It stops for each pixel and calculates a summary statistic for the neighbourhood and then moves on to the next pixel. In our case, we calculated the 'standard deviations' to identify the ecotones among the habitats. The presence/absence data of *B. genuense* was recorded in these ecotonal areas and compared with core areas of the habitats. To test if *B. genuense* is associated to the ecotones among Habitats, three different buffer area were used: 3x3, 5x5 and 7x7 [62].

2.9 Topographic niche model

Species distribution models (SDMs) were used to investigate the topographic drivers of the investigated species. They are a group of numerical tools that combine observations of species occurrence with environmental estimates [30].

The topographic variables calculated are elevation, eastness, northness, slope, topographic wetness index (TWI), roughness, terrain ruggedness index (TRI), topographic position index (TPI) and solar radiation. All these variables were extrapolated from digital elevation model (DEM) at 10 m per pixel, free available for the Abruzzo Region. The occurrences data were extrapolated from the RS classification. To avoid high spatial autocorrelation, we reduced the presence point by topographic similarity. Through clustering based on topography information of points, the occurrences were classified into 100 classes and within each class was sampled the 5 % of points obtaining a total of 884 presence points. To assess the spatial autocorrelation among occurrences Moran's test were performed in R studio using the 'usdm' package [87].

Three sets of 1000 pseudo absences were randomly sampled in all the area where the classification does not identify the *B. genuense* occurrences. For the species distribution model were used 2 different algorithms: Generalized Linear Models (GLM; type = "quadratic", interaction level = 2) and Generalized Boosting Model, also known as Boosted Regression Trees (BRT; number of trees = 10000, interaction depth = 3, cross-validation folds = 10). The choice of these techniques permitted to explore responses from different classes of models, ranging from more classical statistical techniques (GLMs) to machine learning-oriented approaches (BRT) [31,88]. GLMs are based on parametric linear functions [89,90]. BRT combines the regression-tree and boosting algorithms to optimize predictive performance from an ensemble of trees sequentially fitted focusing on residuals from the previous iterations [91]; this technique in general results in high discrimination performance and fit of accurate function [29]. The SDMs for the investigated species was performed using BIOMOD2 [92] and ECOSPAT [93].

3. Results

3.1 Classification output and Accuracy assessment

The coverage map of *B. genuense* (Figure 2), obtained through the RF classifier, showed a large spread of this species within the study site. The classification algorithm detected 776.98 ha of *B. genuense* area out of the 9402.84 ha total study area (8.26% of the total area).

Before performing the classification process, we estimated the spatial areas for which the classification model should provide reliable predictions, through the calculation of the AOA. Forecasts outside the AOA (Appendix S2) were strongly limited in the North-Western sector of study area. In the context of presence-absence, the best result obtained on the Campo Imperatore upland plain, provided values of overall accuracy (OA) of 90.91% with a Kappa of 80.53% (Tab.1). More data about the classification results were reported in Appendix S3 and in general, the RF classifier showed relatively consistent overall performance at the study site.

The analysis on spatial association of *B. genuense* shows as most of the patches have a high clustering value. Even though the general pattern is 'clustered', there are also some not clustered patches mainly distributed in the central and western parts of the study area (see Appendix S4). This section may be divided by subheadings. It should provide a concise and precise description of the experimental results, their interpretation, as well as the experimental conclusions that can be drawn.

3.2 Conversion of plant associations into Natura 2000 habitats

As observed by Figure 3, the dominant vegetation cover in the study area is represented by high altitude grasslands and meadows (N2k habitats 6170, 6210*, 6230*).

Based on Habitat N2k (Appendix S5) the plant associations, overlapped with *B. genuense* distribution, were divided into 5 habitats. The 6170, 6210 e 6230 are grassland habitats, two of them are priority (6210* e 6230*), one is for scree habitat (8210) and one for shrubs habitat (4060).

3.3 Overlay analysis output

Following the overlay analysis (Figure 3), *B. genuense* classified in the study area (8.26% of the total area) was found in 5 different types of habitats (Tab. 2). The differences between 'realized' and 'expected' cover of *B. genuense* in each habitat shows as the most affected by the spread of *B. genuense* is the 6210* (Semi-natural dry grasslands and scrubland facies on calcareous substrates - *Festuco-Brometalia* - *important orchid sites) with 255 ha more than expected. Moreover, the 74.04% of total *B. genuense* distribution was detected within this habitat. On the other hands the less affected is the Alpine and subalpine calcareous grasslands (6170) with 3.45% of *B. genuense* cover. The other habitats (6230*, Mosaic and 8120) have slight differences between 'expected' and 'realized' cover. These habitats have shown a cumulative contribution of 5.17% in 6230* (Species-rich *Nardus* grasslands, on siliceous substrates in mountain areas and submountain areas, in Continental Europe), 1.90% in 'Mosaic' (habitats 6170/6210*/6230*) and 0.48% in 8120 (Calcareous rocky slopes with chasmophytic vegetation).

The results obtained using the moving windows techniques identify the ecotonal area among habitats. Compared the *B. genuense* cover between the core and the ecotonal areas it was observed a slight difference (≈1.6 %). The three different moving windows size (3x3, 5x5, 7x7) give the similar results and in the core area the percentage of *B. genuense* ranges from 7.1 % to 7.4 % while in the ecotonal areas ranges from 8.7 % to 8.9 %.

3.4 Topographic model output

Ensemble model to investigate the topographic driver of *B. genuense* distribution shows high accuracy with sensitivity higher than 95 and about 85 of specificity (Tab. 3).

Six topographic variables with a Pearson correlation coefficient < 0.75 were selected [90,94]: elevation, eastness, northness, slope, topographic wetness index (TWI) and solar radiation (Figure 4). The main topographic drivers are elevation, slope, solar radiation and TWI in order of importance. Indeed *B. genuense* shows a strong preference of slight slope area with an elevation between 1500 and 2000 m a.s.l. Moreover, the target species prefers humid areas as highlighted by (TWI) that is the most commonly topographic index used, to describes the tendency of a cell to accumulate water [95]. Moreover, this species shows a slight preference for areas with high solar radiation.

On the other hands the distribution seems not affected by aspect, indeed both eastness and northness shows flat response curves.

4. Discussion

One of the aims of the study was to distinguish the grasslands dominated by *B. genuense* from other types of vegetation throughout a binary classifiers approach. We used a small training and validation samples and a multi-variable approach using optical and ancillary data (NDVI, DEM, Slope, Aspect, Texture). Furthermore, to distinguish the target species from other plant coverings, we observed the phenological variations of *B. genuense* by using multitemporal satellite data.

The result of the classification allowed us to distinguish the species with overall accuracy values > 90%, in agreement with other studies conducted on widely spread grasslands and invasive species, where the accuracy values achieved ranged from 70 to 90% [96-99]. Our results suggest as binary classifier approach (presence/absence) well perform also with small training samples, in accordance with recent literature [77-79].

In the study area, some plants species, such as *Bromopsis erecta* and *Festuca circummediterranea*, could alter the measure of the spectral signature of *B. genuense*, contributing to the overall classification error. Any overestimation of the distribution of *B. genuense* in some habitats may be due to the copresence of plant species with similar phenology and/or environmental needs that cause spectral mixing [100]. Despite this, the high accuracy values of the RF classification may be due to the decrease in abundance of early and mid-flowering species, as the invasion of *B. genuense* decreases the heterogeneity of the vegetation from the phenological point of view [101]. Another factor that could explain the high performance of the model may be due to the physiological peculiarities (silica-rich and hairy leaves) [102] of the target species which allow its overabundance compared to other species as it is not palatable by domestic herbivores (sheep and cattle) in understocking conditions [103]. Through the sampling in homogeneous areas mainly dominated by the target species, the multitemporal analysis and efforts concentration on two cover classes, we have limited the spectral mixing as much as possible.

Furthermore, it is well known that the spatial resolution of the images must be carefully chosen with respect to the spatial scale of the analysed object [104]. Notwithstanding, the S2 data with a spatial resolution of 10 m per pixel were able to map the target species. Through a careful ground-based survey campaign at the same time as the acquisition of images by satellite sensors, we have shown how maps deriving from S2 can also be a powerful source of information, as confirmed by Feilhauer, *et al.* [105].

The topographic model suggests as a high-resolution digital elevation model strongly improve knowledge of plant species distribution [106]. The results obtained are in accordance with the ecology of *B. genuense*, indeed a preference of humid areas (high value of TWI) with high value of solar radiation suggest the competitiveness of this species [36,107]. Topography can be considered as an important determinant of distribution patterns in dry grasslands and controls soil moisture and pH. Thus, TWI is an excellent candidate to be a priority driver of local plant diversity patterns in grasslands [108]. These findings suggest the key role of hydrology in species distribution [109,110]. Moreover, the effect of topography on pH distribution could explain the strong effect of TWI in shaping *B. genuense*. Indeed, this species shows a small pH interval ranged from 6.17 and 7.2 [107]. However, the direct effect of solar radiation on local temperatures [111,112] may also contribute to its effects on local vegetation patterns. Finally, the elevation and slope variables suggest as this species is limited by high elevation and high slope probably due to the combination of environmental constraints: decrease of soil depth, low temperature, and winter stress [37].

The overlay analysis on N2k habitats identify the most occupied habitat by *B. genuense*, this result can be important to address management policy and conservation strategies for nature conservation. Concerning the relationship between species and N2k habitats, the most suitable habitat for *B. genuense* spread are the semi-natural grasslands referred to *Festuco-Brometalia* (habitat 6210*) which are one of the most threatened habitats in Europe [5,113]. The strong diffusion of *B. genuese* on the habitat 6210* is probably due to the variation in the livestock types (from sheep to cows/horses) and/or to the reduction of extensive grazing in the study area. The increase of *Brachypodium* (*B. pinnatum*, *B. genuense*, *B. rupestre*) distribution cause reduction in grasslands biodiversity [35,37,101,114,115]. Indeed, as shown in a recent study [116] when *B. genuense* and/or *B. rupestre* becomes dominant (cover > 80%) a strong reduction in biodiversity was observed. Moreover, as said above, many plant communities in the study area constitute habitats of interest for biodiversity conservation and hosting several plants of high naturalistic value that could be threatened by *B. genuense* spread.

Other habitats, such as 4060 and 6230*, have shown high *B. genuense* percentage. The high values in these habitats can be associated both to specific topographic characteristics and the limited area occupied by these habitats. Indeed, the differences among realized and expected cover is less than 20 ha. The 8120 and 6170 habitats have shown the low percentage of *B. genuense* cover; these results could be explained by the altitudinal distribution of these habitats that go up to 2000 m a.s.l where the investigated species decrease its suitability.

5. Conclusions

RS can be considered an effective approach to assess the distribution and spread of dominant plant species such as *B. genuense* that can affect habitat biodiversity. Our results show that the binary classification integrated with SDMs is affordable and reliable method for characterize both distribution and topographic niche of *B. genuense*. Indeed, the occurrences data obtained from RS classification can be used to calibrate niche models, useful for studying the drivers underlying the species distribution.

Our results, on *B. genuense*, highlight as some variables such as elevation and slope are the main distribution drivers followed by solar radiation and TWI.

The overlay analysis between *B. genuense* coverage and N2k habitats shows that the target species spreads across all habitats with a strong preference for 6210*. The monitoring of potentially invasive species is fundamental for the management of the N2k habitats, especially in the protected areas where the conservation of biodiversity is one of the priority goals.

In this sense, further studies, using high resolution RS data and multitemporal diachronic analysis could strongly improve the knowledge on the spread of *B. genuense*. Moreover, the approach presented in this study may be extended to larger areas and to other plant community for a more effective habitats management.

Supplementary Materials:

Appendix S1. Satellite images used for the analysis.
Appendix S2. Results of the 'Area of Applicability' (AOA) analysis.
Appendix S3. Accuracy statistics.
Appendix S4. Maps of spatial aggregation using LISA.
Appendix S5. Transformation of plant association into Habitats Natura 2000.

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Tables

RF classification	
Overall accuracy (OA)	0.9091
Sensitivity	1.0000
Specificity	0.8667
Kappa	0.8053

Tab. 1

HABITAT	Habitat (ha)	*B. genuense* (ha)	% *B. genuense*	Realized cover - Expected cover (ha)	Cumulative contribution of *B. genuense* %
4060	197.62	30.61	15.49	14.28	3.93
6170	3254.98	112.34	3.45	-156.52	14.45
8120	721.11	3.72	0.51	-55.84	0.48
*6210	3874.06	575.3	14.85	255.30	74.04
*6230	291.39	40.21	13.8	16.14	5.17
Mosaic	1063.67	14.79	1.39	-73.07	1.90
TOTAL	9402.84	776.98	8.26		

Tab. 2

	Sensitivity	Specificity
KAPPA	97.541	85.053
TSS	97.600	85.003
ROC	97.600	85.003

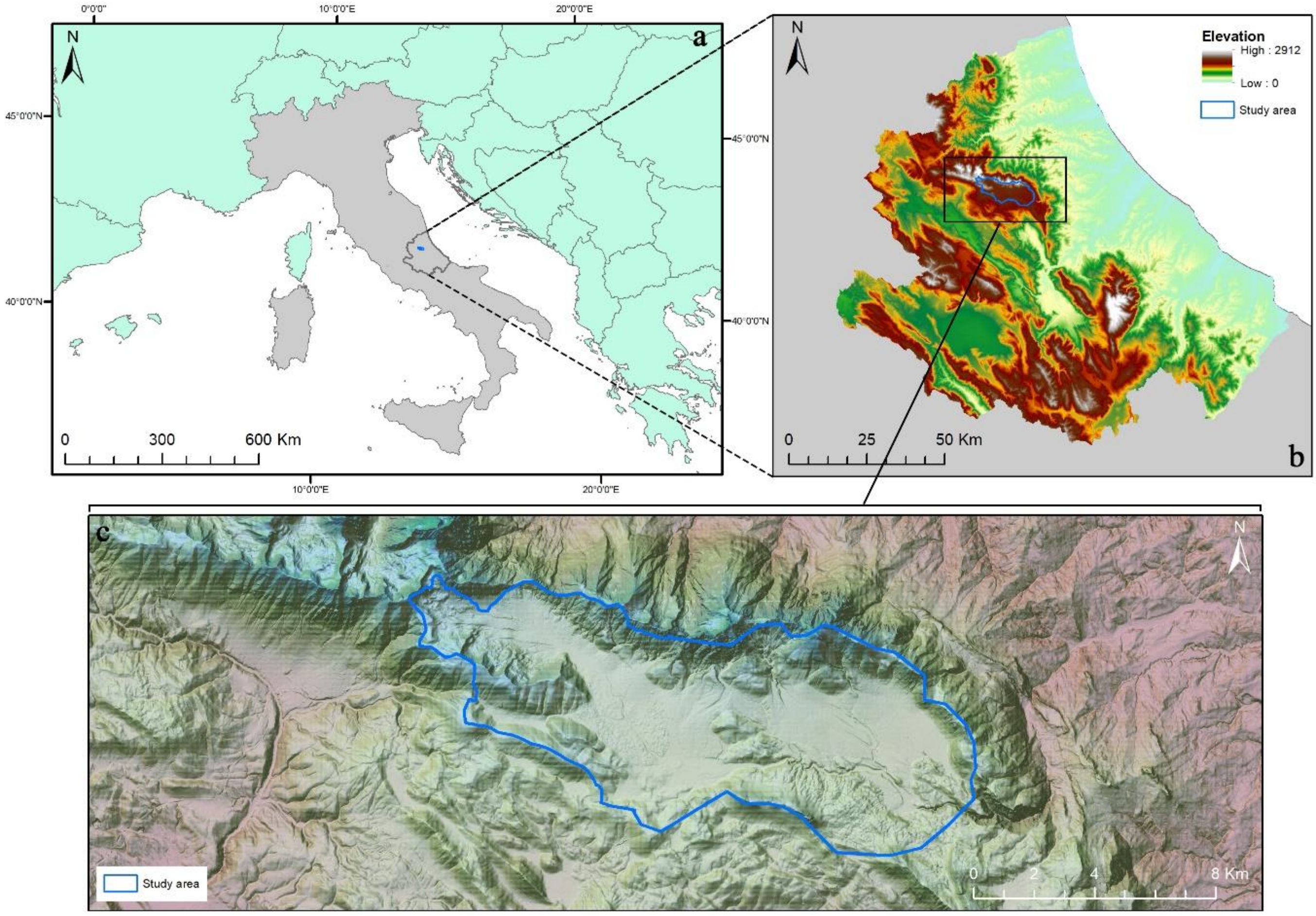
Tab. 3

Table captions

Tab. 1 Measurements of Overall accuracy (OA), Sensitivity, Specificity and Kappa against RF classification.

Tab. 2 Results from overlay analysis, total hectares of each habitat; hectares of *Brachypodium genuense*; the relative percentage; the differences between realized cover and expected cover, negative values indicate that *B. genuense* is less than what expected (8.26% in each habitat) while positive value indicate a higher cover compared to the expected ones; the percentage of *B. genuense* patches in each habitat compared to the total hectares covered by the species.

Tab. 3 Results of the topographic niche model. Measures of sensitivity and specificity (Kappa, TSS, ROC).



a
b
c
N
0°0'0"
10°0'0"E
20°0'0"E
45°0'0"N
40°0'0"N
0 300 600 Km
Elevation
High : 2912
Low : 0
Study area
0 25 50 Km
0 2 4 8 Km

Figure 1

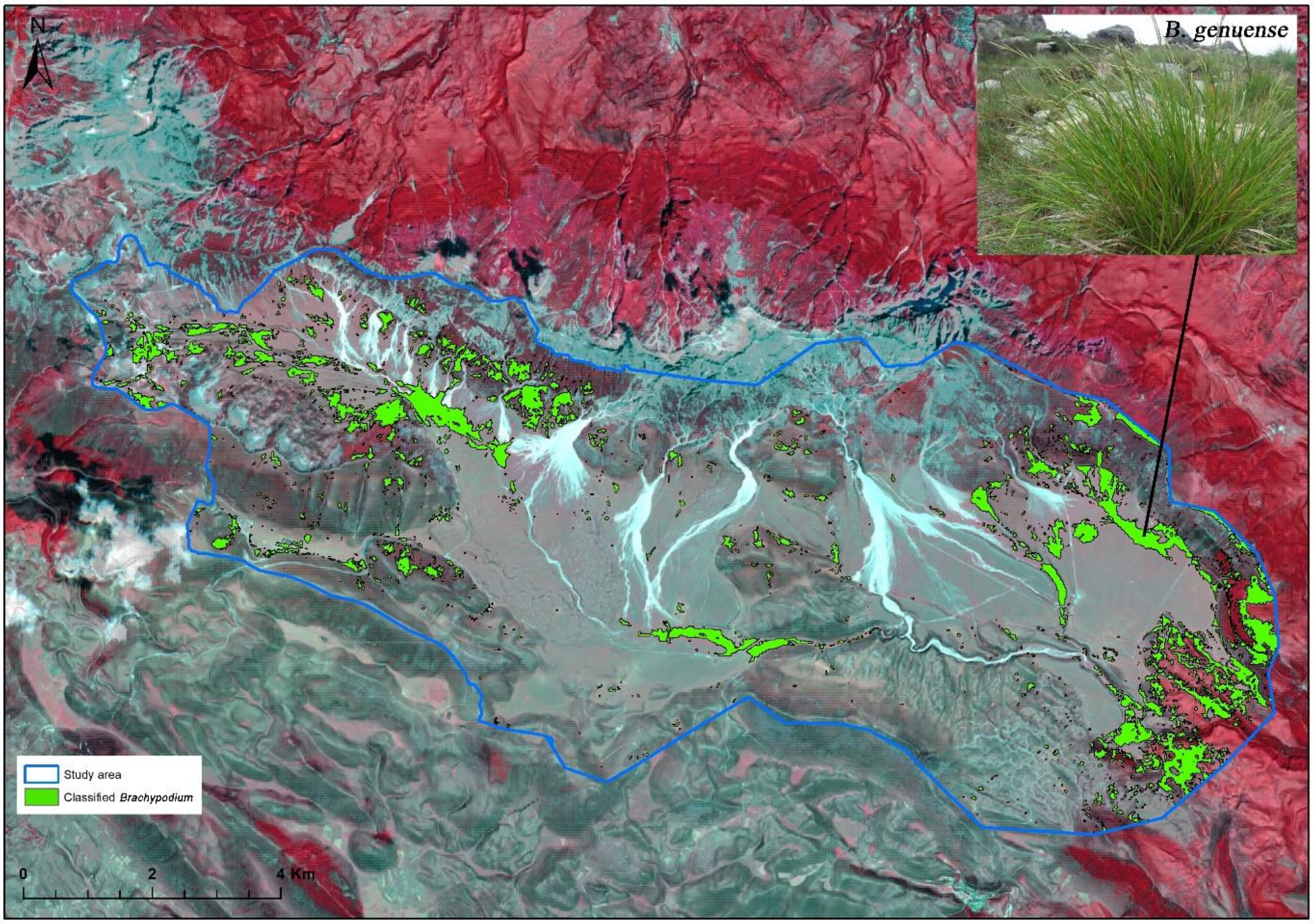
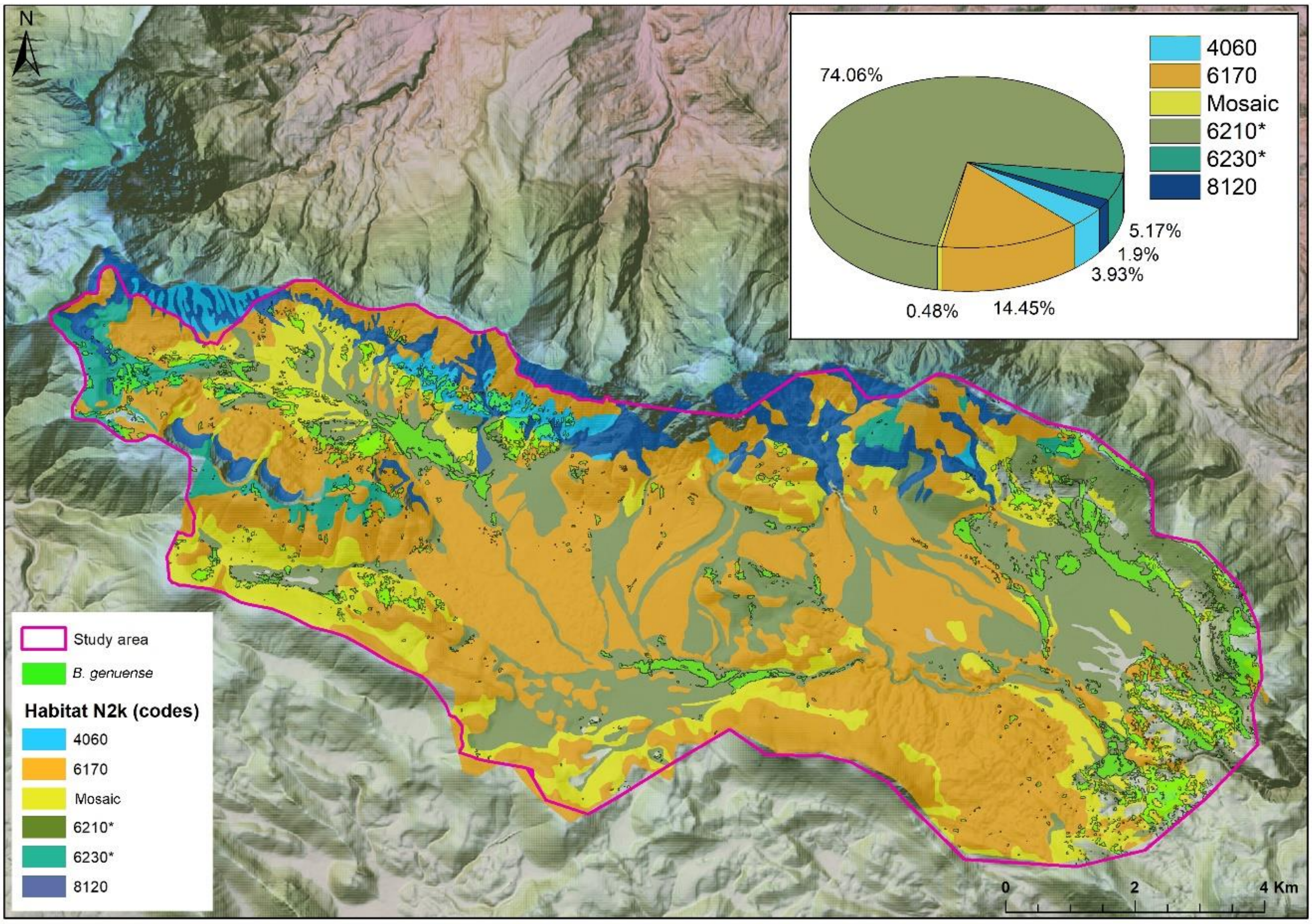


Figure 2



N
74.06%
4060
6170
Mosaic
6210*
6230*
8120
5.17%
1.9%
3.93%
0.48%
14.45%
Study area
B. genuense
Habitat N2k (codes)
4060
6170
Mosaic
6210*
6230*
8120
0
2
4 Km

Figure 3

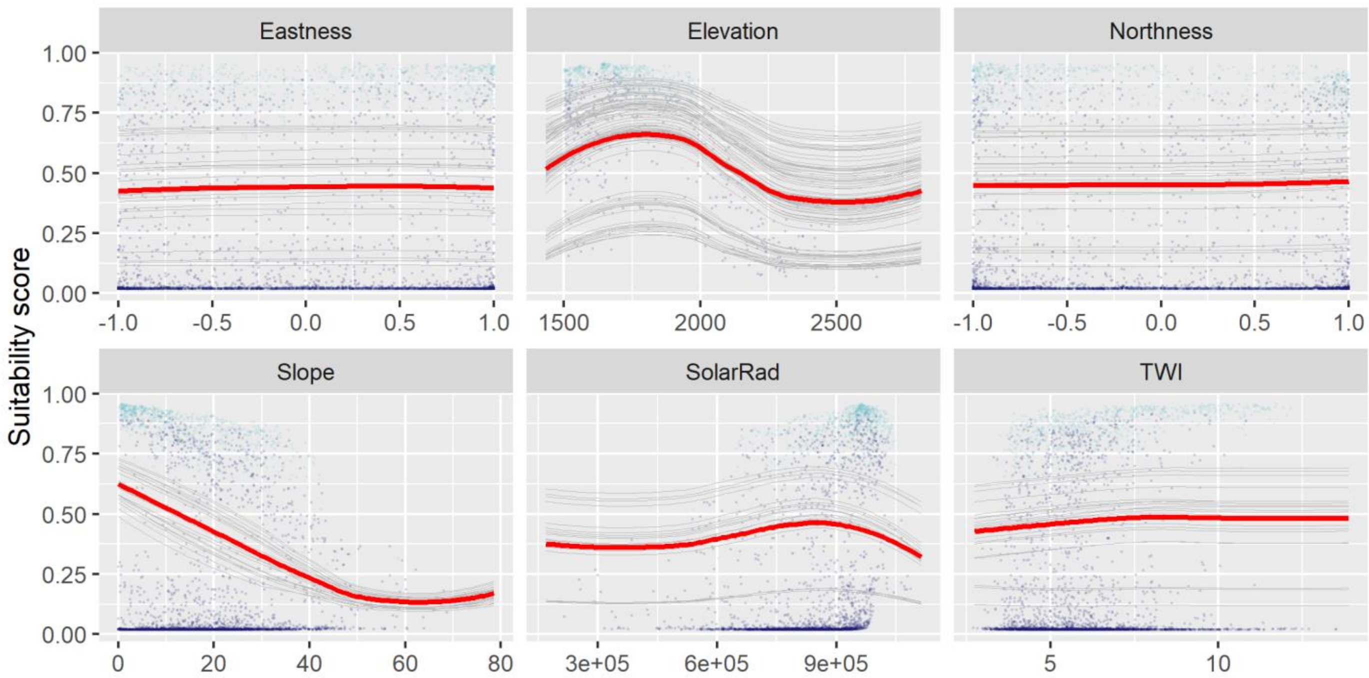


Figure 4

Figure captions

Figure 1. a) Large scale framework. b) Regional scale framework: digital elevation model of Abruzzo region. c) Local scale framework: views of the area's morphology. The study area located on the Gran Sasso and Monti of Laga National Park (Central Apennine, Abruzzo, Italy), are marked in light blue in all panels.

Figure 2 The cover map for *Brachypodium genuense* in Campo Imperatore showing this grass in light green. The background image is a false color image by Sentinel-2 (NIR, Red, Green) highlights the most active vegetation at the date of acquisition (25 July 2019). The study area is marked in light blue. In the upper right part, there is the target species.

Figure 3 Distribution of *Brachypodium genuense* on habitat map (Natura 2000) obtained by the expert-based conversion process (see Materials and Methods). The numeric codes of the habitats in the legend correspond to: Alpine and Boreal heaths (4060), Alpine and subalpine calcareous grasslands (6170), Semi-natural dry grasslands and scrubland facies on calcareous substrates (*Festuco-Brometalia*) (* important orchid sites) (6210*), Species-rich *Nardus* grasslands, on siliceous substrates in mountain areas and submountain areas, in Continental Europe (6230*) and Calcareous rocky slopes with chasmophytic vegetation (8210). The pie chart (top left in the figure) shows the split percentage by habitat of the *B. genuense* distribution identified in the study area. The study area is marked in purple.

Figure 4 Inflated response curve of topographic variables for *Brachypodium genuense* in the study area. The red line is the average of the 100 inflate curve randomly selected. The presences (azure dots) and pseudo-absences (dark-blue dots) used to calibrate the model. X-axis: Northness = cosine(aspect) and Eastness = sine(aspect); Elevation = m a.s.l.; Slope = degrees; Solar Radiation = WH/m^2; Topographic Wet Index (TWI), high values indicates humid areas and low values indicates dry areas.