ALS DATA FOR DETECTING HABITAT TREES IN A MULTI-LAYERED MEDITERRANEAN FOREST

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KEY WORDS: Habitat Trees; Forest Biodiversity, LiDAR, Tre-Related Microhabitat; Sustainable Forest Management

ABSTRACT

Among the wide pool of ecosystem services provided by forests to human wellbeing, biodiversity conservation represents one of the most important topics of Sustainable Forest Management. Monitoring forest biodiversity is a challenging task as it includes all the life forms that can be found in a forest. However, the availability of inventory data is often inadequate to assess the biodiversity value of forests, therefore requiring improvements in monitoring activities and methods. In the last decades, several improvements have been made to reduce costs for collecting data and supporting monitoring and management activities. Particularly, remote sensing techniques have provided a significant contribution to forest and natural resource management and planning. Nevertheless, most of the information concern to the forest canopy and photosynthesis responses quantified through vegetation indices. Few information are available about tree habitats and other important ecological features. This study aims to demonstrate how ALS data can contribute to assess forest biodiversity through the detection of Habitat Trees. We use the Tree-Related Microhabitats, such as cavities, dead branches, injuries and woods, as a proxy to identify Habitat Trees and correlate them to the ALS metrics. Four statistical models were implemented to assess and map the biodiversity value in a mixed and multi-layered forest in Central Apennine.

1. INTRODUCTION

Monitoring forest biodiversity is not only linked to the tree species diversity, but refers to all the life forms that can be found in the forests (Conference Of the Parties; COP 2 Decision II/9). Several authors focused on developing methods to assess and correlate forest structure and biodiversity. Nevertheless, the most common set of Indicators for Sustainable Forest Management, and in particular those related to criterion 4 "*Maintenance, conservation and appropriate enhance-ment of biological diversity in forest ecosystems*" (MCPFE 2002), are mostly concerned with the assessment of tree species diversity, regeneration, naturalness, introduced tree species, deadwood, genetic resources, forest fragmentation, threatened forest species and protected forests. These Indicators represent the most common tool to assess forest biodiversity across Pan-European countries, although information is rather limited to assess the habitat value of forests for several reasons. Firstly, field inventory activities are strongly expensive and time consuming. Moreover, there are no information about "all life forms", as Indicators focused only on the trees species.

As regards the first point, remote sensing techniques have been recognized as very valuable tool in supporting biodiversity monitoring. In fact, they provide significant contribution to monitor and assess forest biodiversity, especially for forest fragmentation (Chirici *et al.*, 2012; Santi *et al.*, 2017) and naturalness (McRoberts *et al.*, 2012) with relative low costs.

As concerns the amount of information provide by Indicators, many authors agreed on the fact that Tree-Related Microhabitats (TreMs) are strongly important to increase forest biodiversity as they represent ecological niches of several living organisms (Bütler *et al.*, 2013; Kraus and Krumm, 2013; Larrieu *et al.*, 2018). Since 1993, different classification systems have been developed across Europe in order to assess their occurrence, frequency and habitat value (Winter and Möller, 2008; Kraus *et*

al., 2016; Larrieu *et al.*, 2018). For these reasons, it is strongly important to develop automatic methods to recognize and assess the habitat values of both single trees and forests. For this purpose, monitoring activities should move from the forest structure to the tree structure target, as many living organisms live in the particular niches that are present on the tree' trunks and crowns.

Since monitoring single trees is a demanding challenge, we describe an experimental approach to detect the abundance of TreMs using LiDAR could points. The frequency and abundance of these particular niches allow to identify Habitat Trees, which play a significant role for the conservation of biodiversity. Thus, the aim of this study is to verify whether or not Airborne Laser Scanner (ALS) data can support the prediction of Habitat Trees within a mixed and multi-layered Mediterranean forest. Habitat Trees are trees hosting TreMs as cavities, injuries and wounds, bark structure, deadwood, growth form or epiphytes.

Although Habitat Trees are not included in the indicators set for SFM developed by Forest Europe process, they could be considered as valid ecological indicators. In the last decade, the topic of TreMs has become common among forest researchers, with several studies evaluating the occurrence and abundance of TreMs, and correlating their frequency with different forest management systems or with the forest ownership regimes, developing practical classifications systems currently used at the European level. Importantly, TreMs are not only linked to the deadwood, which is the most common biodiversity indicator used at European scale, but also to the living trees. This is very important as Habitat Trees are among the largest trees occurring in a forest, also representing potentially conflictual trees because of their value for biodiversity and timber production. Data on the TreMs occurrence and frequency can support forest technicians to balance timber production and conservation of biodiversity and thus to address the selection of trees for harvesting activities.

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2. MATERIALS ANS METHODS

2.1. Study area

The study was carried out in Bosco Pennataro (Figure 1), a mixed and multilayer forest in Molise Region, Central Apennine, Italy. Bosco Pennataro is characterised by a high number of trees species (Figure 1), though *Quercus cerris* L. and *Fagus sylvatica* L. are the most frequent ones. At regional level, the forest plays a significant ecological and cultural role as it is one of the five regional forests, it is part of the Natura 2000 site (code IT7212124), and it has been recognized as a core area of the *Collemeluccio - Montedimezzo Alto Molise* Man and Biosphere reserve. Currently, the forest management system is high forest with continuous canopy cover and uneven aged trees.
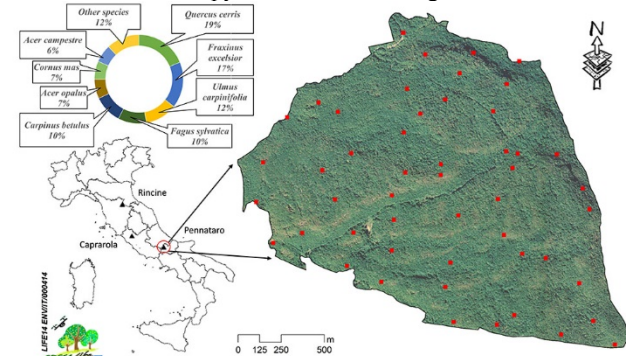

Figure 1. Study area. Geographical location of Bosco Pennataro and the other sites of FRESh LIFE project. Distribution of sampling plots across Bosco Pennataro (red squares). Tree species composition of forest (top-left).

2.2. Field data collection

We collected field data of tree diameter at breast height, tree height, crown length, tree vitality and tree position using Field-Map technology (http://www.fieldmap.cz). TreMs were observed using the classification system by Winter and Möller (2008), considering only the TreMs of standing trees and leaving out the TreMs on fallen deadwood (Figure 2). Data was collected during the demonstration FRESh Life project (*LIFE14 ENV/IT/000414*).
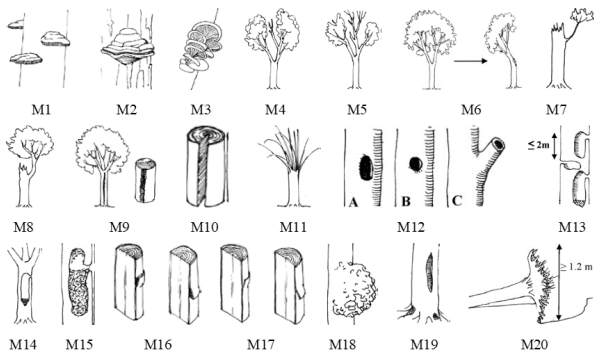

Figure 2. Tree-related Microhabitats (TreMs) classification used for the field survey. Further detail on the TreMs description can be found in Winter and Möller 2008.

2.3. ALS data acquisition

The ALS dataset was collected using YellowScan LiDAR, mounted on a light conventional helicopter. Data were taken in a single flight, on March 2016 and the LiDAR instrument was operated by Oben srl (www.oben.it). Dimensions, weight and autonomy of YellowScan LiDAR are $17 \times 21 \times 15$ cm^3, 2.1 kg, and 3 h, respectively. The system provides up to three echoes per shot, allowing to get topographic information under vegetation cover.

The sensor was set with a maximum scan angle of +/-50°, and a pulse frequency of 20 KHz, resulting in an average density of 30 pulses/m^2. The raw ALS data were elaborated using LAStools software (https://rapidlasso.com).

From the original points cloud, 38 canopy metrics were extracted using LAStools to be correlated with biodiversity variables such as Habitat Trees and TreMs.

2.4. Modelling approach to estimate forest biodiversity variables

From the initial set of 38 ALS metrics, we applied a multicollinearity filter by retaining only variables exhibiting a variance inflation factor ≤ 5 (Zuur, Ieno and Elphick, 2010), and obtained the following ten ALS metrics: *min, std, kur, b10, b90, c00, c02, d00, dns_gap and max*, which were scaled to unit variance. Since the selected forest attributes were calculated as count data, we tested their statistical relationship with the ALS metrics by using Generalized Linear Models (GLM). In particular, we fitted two GLMs (Figure 3) for each forest biodiversity attribute, i.e. one with a Poisson and another with a Negative Binomial distribution of errors, both including linear and quadratic terms. For each GLM, we run a stepwise variable selection procedure based on the Akaike Information Criterion (AIC; Akaike, 1974), as implemented in the R package "MASS" (Venables and Ripley, 2002). In addition, we evaluated the effect of potential outliers on the resulting GLMs by calculating the Cook's distance *D* (Cook, 1977). Specifically, we dropped all the observations showing a Cook's *D* greater than three times the average *D* value calculated among all the observations (Cook, 1977), then refitting GLMs with the remaining data. For each GLM, we evaluated the goodness-of-fit by calculating the coefficient of determination (R^2) and the Root Mean Square Error (RMSE). RMSE was also used in a *leave-one-out* procedure to quantify GLMs predictive performance.
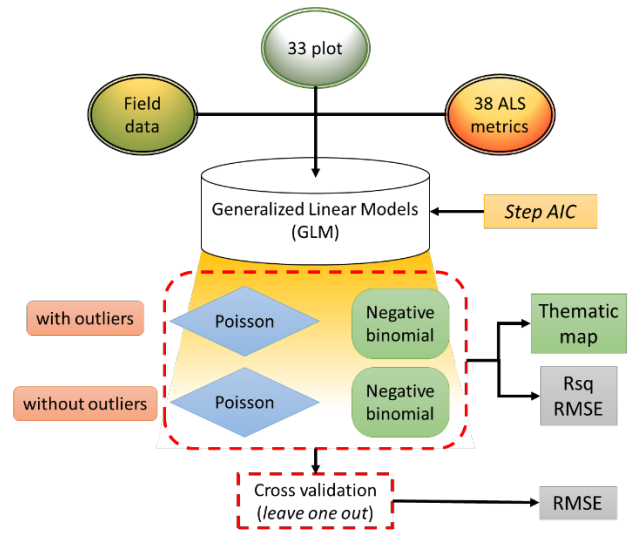

Figure 3. Modelling framework.

Subsequently, for each forest biodiversity variable, a raster map was provided for displaying the biodiversity value of Bosco Pennataro.

2.5. Results and discussion

Tree species composition partly confirms Bosco Pennataro biodiversity value. In fact, forest biodiversity is also stressed by the high variability of tree density, mean tree height and mean tree diameters among plots as well as basal area (G) and tree volume (Table 1). The past forestry interventions favoured an increase of complexity in forest structure across the forest. Historically, Bosco Pennataro represented an important source of timber and Non-Timber Forest Products, even if over the years,

particularly after the shift of forest ownership from the State to regional administration, forestry interventions have decreased. Nowadays, harvesting activities regards only fire prevention, sanitation cutting to allow recreational activities and few forestry interventions for scientific purposes. The abandonment of forestry interventions has contributed to the aged of forest stands with consequent shifting of forest structure from even-aged to uneven-aged and a high variability of number of trees per hectare among forest stands.

Nevertheless, beyond the forest structure, tree structure offers a deeper evaluation of forest biodiversity. Results show that there is also a high variability of Habitat Trees, ranging from 4 to 32 per plot, abundance of TreMs ranging from 6 to 61 per plot, and TreMs types, which range from 2 to 8 per plot.

The most frequent TreMs encountered in the forest are: cavities, broken stems and trees with <50% of the crown broken.

	Min	1st Qu	Median	Mean	3rd Qu	Max
Tree (N/plot)	24.00	43.25	57.00	68.94	93.25	196.00
Tree (N/ha)	454.0	817.5	1077.5	1303.2	1762.8	3705.0
Tree species (plot)	3.00	7.00	7.50	7.68	9.00	11.00
Average DBH (cm)	10.00	13.00	16.00	16.42	19.00	27.00
H max (m)	17.60	24.80	28.40	28.10	31.07	39.60
G (m²/ha)	19.90	33.17	37.60	37.62	42.20	53.10
V (m³/ha)	142.0	311.2	372.5	387.2	447.8	647.0
Habitat Trees	4.00	11.00	15.00	16.56	20.75	32.00
TreMs	6.00	17.25	23.50	25.14	30.00	61.00
TreMs Type	2.00	5.00	5.00	5.38	6.00	8.00

Table 1. Ground data summary results. Descriptive statistics of the main forest structure and biodiversity variables from the ground.

As regards the modelling approach, results show that outliers affect models implementation, providing better results when GLMs have been fitted without outliers (Table 2). Moreover, Negative Binomial is the best performing modelling approach in all the cases.

	Model	df	AIC	R^2	RMSE	Pred. RMSE
Habitat Trees	*M_pois*	13	222.5	0.7	4.5	179.2
	M.NO_pois	15	**201.8**	**0.8**	**3.4**	**333.8**
	M_nb	14	223.8	0.6	4.5	14.8
	M.NO_nb	16	**203.8**	**0.8**	**3.4**	**12.5**
TreMs	*M_pois*	17	252.4	0.7	6.4	164.1
	M.NO_pois	15	**226.2**	**0.8**	**5.9**	**25.1**
	M_nb	14	248.9	0.6	6.9	16.0
	M.NO_nb	12	**225.6**	**0.7**	**6.3**	**16.3**
TreMs Type	*M_pois*	1	136.4	0.0	1.3	
	M.NO_pois	1	123.7	0.0	1.2	
	M_nb	2	138.4	0.0	1.3	
	M.NO_nb	2	125.7	0.0	1.2	

Table 2. Modelling approach summary results. Main statistical results of the model approaches implementation. M_pois "Poisson model"; M_nb is "Negative Binomial model"; NO is "no outliers". Bold character indicates the best performant model.

In detail, for detection of Habitat Trees, both Poisson and Negative Binomial GLMs show similar performances (Figure 4) in terms of RMSE and R^2 (3.4 and 0.8 respectively). Nevertheless, the AIC values seem to tend towards the Poisson rather than the Negative Binomial approach (201.8 and 203.8 respectively), while the difference is significantly relevant for prediction accuracy (333.8 and 12.5 respectively). Thus, the Negative Binomial is better than Poisson model at predicting Habitat Trees (Figure 5).
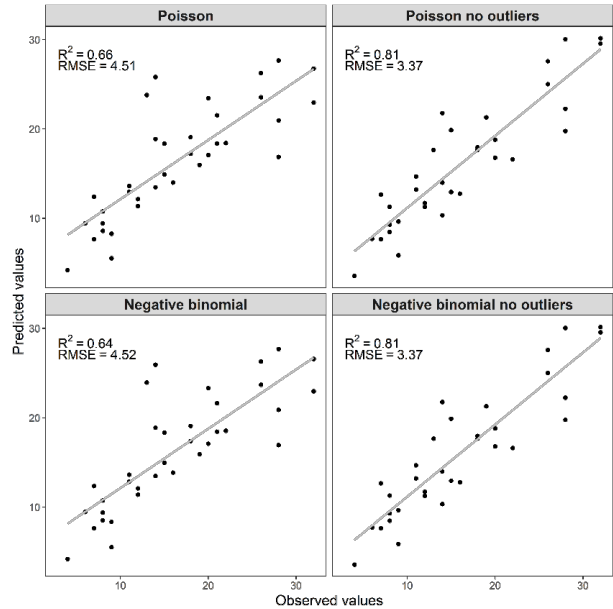

Figure 4. Goodness-of-fit for Habitat Trees. Comparison of the observed vs. predicted values for the 4 modelling approaches for detection of Habitat Trees.
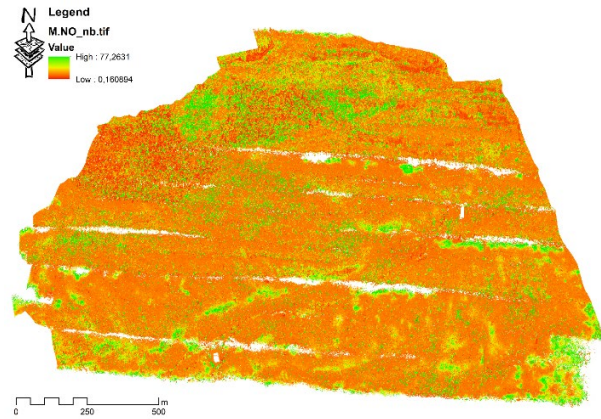

Figure 5. Habitat Trees prediction. Prediction of the Habitat Trees according the Negative Binomial no outliers approach.

As regards the detection of TreMs, the Poisson approach shows value of R^2 and RMSE slightly better than Negative Binomial (Figure 6). Nevertheless, the Negative Binomial results are somewhat better performing to prediction of TreMs (Figure 7), since the RMSE is moderately lower.

Finally, as regard the detection of TreMs Type, the study reveals that all the modelling approaches failed. We have two main reasons for this. Firstly, to image that ALS data can distinguish different type of cavities or different type of fruiting bodies on the trees is rather difficult. Second, the scarcely occurrence for some TreMs hinder their detection and of course their prediction.

By contrast, this non-result demonstrates that the approach is robust because it works only with a consistent quantity of data. This leave a light to think that a deeper investigation could provide more detailed data allowing a better detection of single TreMs. Maybe the integration of ground data, with ALS, Terrestrial laser scanning data and multispectral images could improve the detection and prediction of TreMs and thus support the SFM.
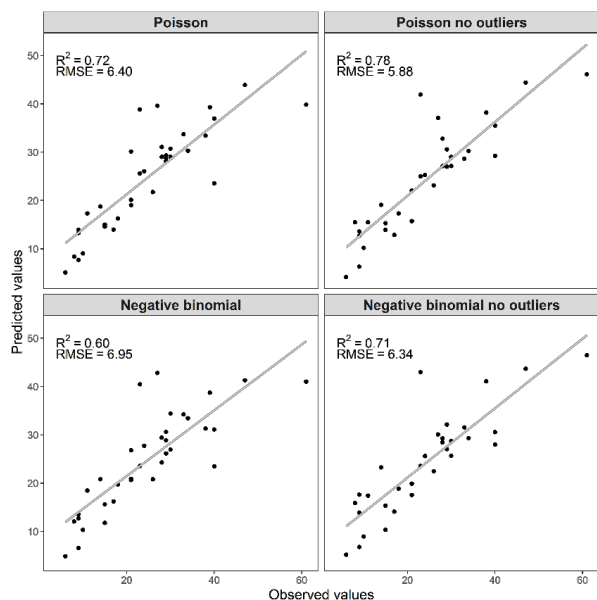

Figure 6. Goodness of fit for TreMs. Comparison of the observed vs predicted values for the 4 modelling approaches for detection of TreMs.
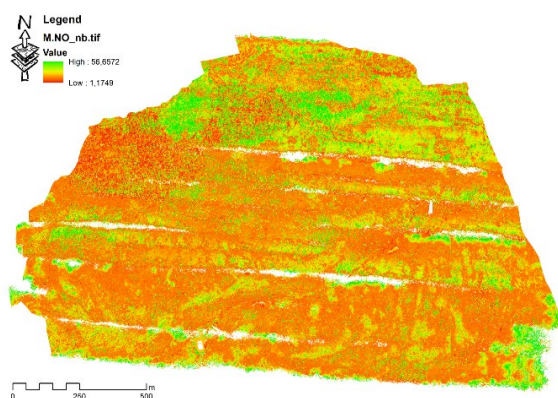

Figure 7. TreMs prediction. Prediction of the TreMs according the Negative bionomial no outliers approach.

3. CONCLUSION

This study introduces an approach to assess forest biodiversity based on the occurrence and abundance of Tree-Related Microhabitats.

Some weaknesses are still present and a deeper investigation is necessary. Maybe the integration of different source of remote sensing data could improve the detection approach. However the study shows a good results for Habitat Trees, and frequency of TreMs. Nevertheless, it was observed that the prediction of single microhabitats depends from their frequency, because without a significant number of occurrences the analysis failed.

In conclusion, ALS data are useful to detect Habitat Trees, and thus to support forest decision makers and managers in the assessment of forest biodiversity.

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