



Predictive analytics of tree growth based on complex networks of tree competition



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ABSTRACT

Competition between individual trees is a major factor influencing the development of forests. However, due to the complexity of such interactions, that span over vast geographic areas, systematic analysis of competition has only recently become possible through the concepts of so-called predictive analytics. The rationale behind the utilised approach is that a prediction model, which is capable of forecasting future increments of tree development parameters accurately, contains knowledge about the underlying relationships that govern them. The analysis of such model, therefore, holds the potential to reveal new insights into the critical factors that influence forest developments. Within this study, we utilise an Evolutionary Algorithm in order to enable predictive analytics based on a complex-network representation of competition. This allowed us to study the patterns related to spatial distribution of individual trees. We discovered that triplets of competing trees, and their betweenness centralities, have significantly greater influence on the development of each individual tree than traditionally observed parameters like the number of a tree's competitors and distances between them. While this indicates preferable spatial patterns for optimal forest development, the introduced methodology proved to be an efficient predictive analytics tool that allows for their discovery.

1. Introduction

Network-based analyses are becoming one of the main trends in the studies of biological communities and interactions between individuals (Jacoby and Freeman, 2016). The theory of complex networks was already used to unveil new insights into various ecological processes (Proulx et al., 2005; Urban et al., 2009; Dale and Fortin, 2010; Bohan, 2016). Early approaches into the subject, such as (Bascompte et al., 2003), mostly examined plant-animal mutualistic networks. Fortuna and Bascompte (2006), developed a patch-model to describe plant-animal communities and explored their persistence, while Fontaine et al. (2011) outlined a conceptual framework for studying networks composed of more than one type of interaction. The latter demonstrated an improved understanding of the patterns and processes taking place in biological communities. Subsequently, network-based approaches have gained their popularity in studies of social interactions in animal groups. A review of emerging issues related to animal social networks was presented by Kurvers et al. (2014) through a discussion on the effects of social network structure on evolutionary dynamics and social evolution. While network-based studies have also been used for

examining the behaviour of sharks (Guttridge et al., 2010; Wilson et al., 2015) and defining social shark communities (Jacoby et al., 2010; Mourier et al., 2012), this contextual interaction aspect has, surprisingly, been ignored for years in plant competition research, as reported by Nakagawa et al. (2016). Despite their obvious importance, the network-based analyses have, thus, only recently been emerging in the studies of plant societies and the competitions within them (Kikvidze et al., 2011).

Guimarães et al. (2011) exposed the role of networks of interacting plant-animal assemblages in shaping co-evolutionary processes, while Poisot et al. (2012) used complex networks for describing the varying species' interactions through space and time. Golubski et al. (2016) demonstrated the influences of the real-world coffee agroecosystem on the environment, and vice versa. Lately, Nakagawa et al. (2016) used complex network analysis to reveal some essential properties of competition among individuals in an even-aged multi-individual stand of the Sakhalin fir (*Abies sachalinensis*). The role of individual nodes (and their removal) has been examined in studies on the context-dependencies (Golubski et al., 2016) and plant interactions (Brose et al., 2005), while the dimensionality of the network (trait-axes) has proved

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to play a critical role in predicting the interactions between species in different ecological networks (Eklöf et al., 2013). It has, furthermore, been shown, that the strength of interactions between species influences the structure and dynamics of ecological systems strongly (Vazquez et al., 2015). However, while we are witnessing a global growth of pressures on natural resources, the need to understand and mitigate the impacts on the environment is becoming increasingly important (Evans et al., 2013). Consequently, utilisation of complex networks for environmental modelling and predictive analytics is coming into focus. Several attempts have already been made towards achieving this goal.

Jeger et al. (2007) proposed a network-based model for spreading of plant diseases in order to achieve their efficient prevention, while several studies in biology (Tarca et al., 2007), microbiology (Škraban et al., 2013), and ecology (Tamaddoni-Nezhad et al., 2015) have explored the possibilities of machine learning for discovering of new knowledge about the natural phenomena. Unfortunately, the use of these traditional techniques is still limited. While the methods like artificial neural networks and support vector machines result in uninterpretable prediction models that do not allow for knowledge discovery (Devos et al., 2009), classifiers like decision trees (Škraban et al., 2013) and random forests (Mascaro et al., 2014) do not allow for quantifying the relationships between the observed variables (Nokelainen et al., 2007). In order to overcome these limitations, a new complex network-based analysis was developed, and is presented in this paper.

The objectives of this study were (1) to test a complex network-based analysis method for predicting growth of individual trees using the concepts of machine learning (Muys et al., 2010) and (2) to propose a new regression analysis, which allows for human interpretation and, thus, enables knowledge discovery. The rationale behind the proposed

approach is that a prediction model, which is capable of foreseeing radial and height increments of individual neighbouring trees in a forest accurately, contains knowledge about the underlying ecological interrelations that govern it. A new algorithm was, therefore, designed that enabled the extraction and quantification of those relationships between the determinative topological metrics of tree competition. That allowed for making accurate predictions about future growth of each individual tree in several different uneven-aged multi-layered forests. We show that the interpretation of such prediction model may reveal new insights into the forests' dynamics, in particular, the role of competition among trees within them. The proposed approach could, thus, assist in foreseeing future growth of individual trees or forest stands and, consequently, support the decision-making processes in forest management by advancing on the known concepts of the predictive analytics (Lexer et al., 2005; Shmueli and Koppius, 2011).

2. Material and methods

2.1. Field data

The field data used in this study (see Tables 1–3) are a part of the monitoring network of the Intensive Monitoring of Forest Ecosystems provided by the Slovenian Forestry Institute (Vilhar and Žlindra, 2017), which is included in the International Co-operative Program on Assessment and Monitoring of Air Pollution Effects on Forests (ICP Forests), the United Nations Economic Commission for Europe Convention on Long-Range Transboundary Air Pollution (De Vries et al., 2003; Dobbertin and Neumann, 2010). For the purposes of the study, data from ten natural forest ecosystem plots (of size 50 m × 50 m) were examined at different ecological regions with different composition of tree species, as well as the stand structures. In accordance with the ICP

Table 1
Proportion of tree species per forest plot.

Forest ID	Ecological region	Tree species mixture							
		<i>Picea abies</i> [%]	<i>Abies alba</i> [%]	<i>Pinus nigra</i> [%]	<i>Pinus sylvestris</i> [%]	Other coniferous [%]	<i>Fagus sylvatica</i> [%]	<i>Quercus robur</i> [%]	Other broadleaves [%]
1	Alpine	100	–	–	–	–	–	–	–
2	Dinaric	–	–	–	–	–	100	–	–
3	Sub-Mediterranean	–	–	89	–	–	–	–	11
4	Pre-Alpine	0.2	–	–	95.5	–	–	2.4	1.9
5	Dinaric	–	–	–	–	–	84.7	–	15.3
6	Pre-Alpine	9.6	–	–	1.9	1.4	77.4	–	9.7
7	Dinaric	–	18.2	–	–	–	62.6	–	19.2
8	Pre-Pannonian	–	–	–	–	–	–	45.3	54.7
9	Pre-Pannonian	–	–	–	–	–	–	70.7	29.3
10	Pohorje	46.4	–	–	–	–	49.7	–	3.9

Table 2
List of forest plots in the years 2004, 2009 and 2014, where *min.* and *max.* represent minimal and maximal *dbh* value of a tree in a plot, accordingly, while σ is the corresponding variance, \overline{dbh} is quadratic mean of tree diameters at 1.3 m height and $\overline{\Delta dbh}$ is average five year increment.

Forest ID	2004					2009					2014				
	min. [cm]	max. [cm]	σ [cm]	\overline{dbh} [cm]	$\overline{\Delta dbh}$ [cm]	min. [cm]	max. [cm]	σ [cm]	\overline{dbh} [cm]	$\overline{\Delta dbh}$ [cm]	min. [cm]	max. [cm]	σ [cm]	\overline{dbh} [cm]	$\overline{\Delta dbh}$ [cm]
1	33.6	70.3	7.2	50.1	–	37.7	73.4	7.1	51.3	1.01	38.2	74.8	7.2	52.7	1.23
2	5.9	47.4	7.7	33.7	–	5.1	48.7	9.4	33.7	0.58	5.7	49.5	9.8	34.2	0.62
3	5.3	53.1	13.6	24.2	–	5.7	53.5	13.7	14.9	0.46	5.1	53.5	13.4	25.3	0.53
4	9.6	44.3	7.2	27.8	–	5.1	46.1	9.2	19.1	1.43	5.1	47.8	12.1	28.8	1.32
5	5.6	48.9	12.3	29.7	–	6.1	50.3	12.6	24.1	0.79	6.4	51.9	12.9	32.3	0.76
6	10.3	54.4	8.5	27.1	–	12.9	54.4	8.5	28.9	0.61	12.9	54.8	8.6	29.7	0.52
7	5.7	72.3	14.7	27.8	–	5.1	73.2	16.3	30.2	0.63	5.1	75.1	15.5	25.9	0.57
8	5.3	82.2	19.3	35.8	–	6.4	84.1	19.2	40.5	0.78	7.1	85.6	19.8	41.7	1.11
9	5.7	64.3	14.7	26.1	–	5.9	70.1	15.9	28.7	0.81	5.9	74.3	16.5	29.6	1.01
10	–	–	–	–	–	10.1	65.3	12.9	37.8	–	11.1	66.8	12.9	39.1	0.86

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