



Risk of invasion predicted with support vector machines: A case study on northern pike (*Esox Lucius*, L.) and bleak (*Alburnus alburnus*, L.)



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ABSTRACT

The impacts of invasive species are recognised as a major threat to global freshwater biodiversity. The risk of invasion (probability of presence) of two avowed invasive species, the northern pike (*Esox Lucius*, L.) and bleak (*Alburnus alburnus*, L.), was evaluated in the upper part of the Cabriel River (eastern Iberian Peninsula). Habitat suitability models for these invasive species were developed with Support Vector Machines (SVMs), which were trained with data collected downstream the Contreras dam (the last barrier impeding the invasion of the upper river segment). Although SVMs gained visibility in habitat suitability modelling, they cannot be considered widespread in ecology. Thus, with this technique, there is certain controversy about the necessity of performing variable selection procedures. In this study, the parameters tuning and the variable selection for the SVMs was simultaneously performed with a genetic algorithm and, contradicting previous studies in freshwater ecology, the variable selection proved necessary to achieve almost perfect accuracy. Further, the development of partial dependence plots allowed unveiling the relationship between the selected input variables and the probability of presence. Results revealed the preference of northern pike for large and wide mesohabitats with vegetated shores and abundant prey whereas bleak preferred deep and slightly fast flow mesohabitats with fine substrate. Both species proved able to colonize the upper part of the Cabriel River but the habitat suitability for bleak indicated a slightly higher risk of invasion. Altogether may threaten the endemic species that actually inhabit that stretch, especially the Júcar nase (*Parachondrostoma arrigonis*; Steindachner), which is one of the most critically endangered Iberian freshwater fish species.

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1. Introduction

The impacts of invasive species are recognised as a major threat to global freshwater biodiversity via a variety of adverse impacts, such as predation, hybridisation, vectoring diseases, food web alteration and interspecific competition (Almeida and Grossman, 2012). Therefore, several authors highlighted the importance of risk assessment and management for controlling these invasive species (Almeida et al., 2013). In Iberian rivers, native fish have suffered from multiple and recurrent introductions during the last century, which has been stressed as one of the main negative factors affecting the survival of these native, mostly endemic, species (Elvira

and Almodóvar, 2009). It is consequently the responsibility of conservationists to elucidate the link between the level and nature of propagule pressure and its potential impact on native species (Ribeiro et al., 2008).

In the Iberian Peninsula, most of the conducted research quantified the invasiveness degree of several fish species at the basin scale identifying key biological traits that would facilitate successful establishments (Almeida et al., 2013; Clavero, 2011; Ribeiro et al., 2008). Although ecological impacts such as changes in species survival, microhabitat selection or competition for spawning areas have been reported (Ribeiro and Leunda, 2012), very few studies have been performed at detailed scales (i.e., micro or mesohabitat scales) (Almeida et al., 2014a; Elkins and Grossman, 2014). In the Iberian Peninsula, introduced species are widespread and they are still expanding their distribution ranges (Ribeiro and Leunda, 2012). Furthermore, many of them are piscivorous species, which form a trophic group almost absent in the original ichthyofauna

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(Clavero et al., 2004; Ribeiro and Leunda, 2012). Damming of rivers has favoured the establishment of these typically lentic species by reducing the natural intra- and inter-annual flow variations (Clavero et al., 2004; Muñoz-Mas et al., 2016a). Thus the native fish communities are increasingly being cornered to the upper part of the stream networks, being isolated from one to another by these artificial barriers (Alcaraz et al., 2014; Aparicio et al., 2000). In this context, the basin scale can be too coarse resolution to render effective tools with management purposes.

The benefits of the mesohabitat scale have been highlighted among the other spatial scales to analyse fish habitat requirements (Costa et al., 2012; Vezza et al., 2015) because using this scale is possible to describe the environmental conditions around an aquatic organism not only limiting the analysis to the point where it is observed (Veza et al., 2015). Furthermore, mesohabitats – generally corresponding in size and location to Hydro-Morphological Units (HMU) such as, pool, riffle or rapid – can be used to describe fish ecology with a broader range of variables even including biotic predictors (Muñoz-Mas et al., 2015; Veza et al., 2015).

In numerous occasions, machine learning habitat suitability models proved to be adequate tools to understand the habitat requirements of fish species (Mouton et al., 2007; Olden et al., 2008). Thus, they can be considered adequate tools to characterize the suitability of the recipient mesohabitats allowing the evaluation of the risk of invasion. To date, the mesohabitat scale has been used in combination with several modelling approaches to predict the presence or abundance of fish, for instance, with logistic regression (e.g., Veza et al., 2014a), Support Vector Machines (SVMs) (e.g., Tirelli et al., 2012), or random forests (e.g., Veza et al., 2014a). The strengths and weaknesses of every machine learning technique must be considered; otherwise, the development of an inappropriate habitat suitability model may result in erroneous predictions (Lin et al., 2015). In this regard, SVMs produced very competitive results when compared with the best accessible classification methods (Fukuda et al., 2013; Sadeghi et al., 2014; Tirelli et al., 2012) and, in addition, they only need the optimization of very few parameters (Hoang et al., 2010; Sadeghi et al., 2014). Furthermore, SVMs rely on convex quadratic programming; thus, no local optima exist and efficient optimization procedures can be used to find the unique global optimum (Fukuda and De Baets, 2016). In accordance to previous statements, SVMs gained visibility in habitat suitability modelling in the last few years (Fukuda and De Baets, 2016; Fukuda et al., 2013; Hoang et al., 2010; Sadeghi et al., 2014; Fukuda et al., 2013; Hoang et al., 2010; Sadeghi et al., 2014) but, despite the existence of the aforementioned references, they still cannot be considered widespread in ecology (Hoang et al., 2010). Thus, within the ecological modelling discipline, it does exist certain controversy about the necessity of performing variable selection. Thereby, in ecology, some authors suggested it unnecessary (Hoang et al., 2010; Sadeghi et al., 2014; Tirelli et al., 2012) or explained it very cryptically (Poulos et al., 2012) whereas in machine learning or medical studies it has been stated as a fundamental step to improve generalization capability (Fröhlich et al., 2003; Guyon et al., 2002; Huang and Wang, 2006).

This study focuses on the Cabriel River, the main tributary of the Júcar River (eastern Iberian Peninsula). The Cabriel River has 220 km in length, 4754 km² of drainage area and 10.8 m³/s of mean flow. It harbours the most important populations, in terms of presence and fish density, of the Júcar nase (*Parachondrostoma arrigonis*; Steindachner, 1866) a fish species in imminent danger of extinction (Alcaraz et al., 2014). The Cabriel River is actually split into two main stretches of similar length (upper Cabriel and lower Cabriel) by a sequence of weirs and dams – the most noticeable the Contreras dam (Costa et al., 2012) – conforming a complex of storage and hydropower facilities. Both stretches harbour invasive species, but the larger amount of invasive species is hosted in the lower part

(Alcaraz et al., 2014). The most remarkable ones are the northern pike (*Esox lucius*; Linnaeus, 1758) and the bleak (*Alburnus alburnus*; Linnaeus, 1758) (Alcaraz et al., 2014; Costa et al., 2012) both categorized as highly invasive species (Almeida et al., 2013). Northern pike has been introduced in freshwater systems across the globe, and, in the Iberian Peninsula, it has been linked to the decline or extirpation of multiple fish species (Elvira et al., 1996; Ribeiro and Leunda, 2012; Rincón et al., 1990). Conversely, the impacts of bleak introduction have been poorly documented; especially taking into account that the species has shown an incredible high fecundity allowing bleak to outcompete other species (Vinyoles et al., 2007). Thus, it has been only confirmed that the species is able to easily hybridize with the calandino (*Squalius alburnoides* complex; Steindachner, 1866) and the southern Iberian chub (*Squalius pyrenaicus*; Günther, 1868) (Almodóvar et al., 2012) and to proficiently compete for feeding resources (Almeida et al., 2014b). In the Iberian Peninsula, the northern pike was introduced in 1949 with recreational purposes, whereas the introduction of bleak took place in 1992, principally to provide forage for large predator fish (e.g., northern pike) (Elvira and Almodóvar, 2001). Reservoirs favour the establishment and rearing of these invasive species (Ribeiro and Leunda, 2012), and, in the current situation, the Contreras complex can be considered the bridgehead in their invasion of the upper part of the Cabriel River.

As a consequence, the study aim was (i) to infer the habitat preferences of the northern pike and bleak at the mesohabitat scale (based on data collected in the lower part of the Cabriel River), and (ii) to predict the risk of invasion of these species in the upper part of the Cabriel River (upstream of the Contreras complex of storage and hydropower facilities) whereas (iii) the triviality of the variable selection procedures was ruled out in a subsidiary way. To achieve these aims, habitat suitability models (i.e., probability of presence estimation) were developed by means of SVMs optimized simultaneously performing the variable selection and the parameter tuning with a genetic algorithm. Then, the optimal SVMs (i.e., the aforementioned SVMs trained with data collected throughout the downstream river segment) were used to assess the risk of invasion (potential suitable habitat) in the upper part of the Cabriel River.

2. Methods

2.1. Previous knowledge on northern pike and bleak ecology

The northern pike is a large ambushing predator (maximum body length ≈150 cm) with circumpolar origins (Harvey, 2009). Northern pike has shown an opportunistic diet (Sepulveda et al., 2013). Consequently, it can become a keystone predator able to control fish community composition (Kobler et al., 2008). In accordance with the interest and the aftermath of its introduction northern pike has profusely been the subject of ecological modelling from the plain univariate habitat suitability criteria (Inskip, 1982) to the more complex cellular automata (Pauwels et al., 2013) or individual-based models (Baetens et al., 2013). However studies on habitat requirements have usually focused on lentic environments (Casselman and Lewis, 1996; Kobler et al., 2008 and references therein) and only few studies have been carried out in lotic ecosystems (Inskip, 1982; Kerle et al., 2001; Zarkami, 2008). Although results partially differ between sites, it has been stated the imperative necessity for aquatic vegetation, submerged or emerged (i.e., reeds) (Harvey, 2009; Inskip, 1982; Kerle et al., 2001), and the preference for large depths (up to 5 m) (Kerle et al., 2001; Stojkovic et al., 2014).

On the other hand, bleak is a small cyprinid (maximum body length ≈30 cm) with a wide natural distribution in Europe, from the north-eastern slopes of the Pyrenees to the Urals (Vinyoles et al.,

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