

# Predicting global habitat suitability for *Corbicula fluminea* using species distribution models: The importance of different environmental datasets



M. Gama<sup>a,\*</sup>, D. Crespo<sup>b</sup>, M. Dolbeth<sup>b,c</sup>, P. Anastácio<sup>a</sup>

<sup>a</sup> MARE – Marine and Environmental Sciences Centre, Departamento de Paisagem Ambiente e Ordenamento, Escola de Ciências e Tecnologia, Universidade de Évora, Portugal

<sup>b</sup> CFE – Centre for Functional Ecology, Department of Life Sciences, University of Coimbra, Portugal

<sup>c</sup> CESAM & Department of Biology, University of Aveiro, Portugal

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## ABSTRACT

Niche-based models (NBMs) are increasingly being used to predict the biological distribution of species, as well as the importance of different environmental variables on their habitat adequability. Here, we investigate the reliability of these models in predicting habitat suitability for *Corbicula fluminea*, an important freshwater bivalve invasive species. In order to determine the influence of topographic vs. climatic variables, three datasets were used: (1) *Corbicula*TOPO with topographic variables (altitude, slope and a compound topographical index); (2) *Corbicula*MIX, combining climatic (annual mean temperature, mean temperature of warmest quarter, mean temperature of coldest quarter and annual precipitation) and topographic variables and (3) *Corbicula*CLIM with only the climatic variables. Nine different types of models, implemented in BIOMOD2, were used and an ensemble of NBMs was built. We aimed to know how climatic suitability for these invaders changes when using different datasets of environmental variables; if the predictive reliability is similar between datasets; and which environmental variables better explain habitat adequability. Model performance was very similar between *Corbicula*MIX and *Corbicula*CLIM. *Corbicula*TOPO was the dataset with the least accurate predictions. Mean temperature of the coldest quarter and altitude were the variables that influenced *C. fluminea* distribution the most. The use of an ensemble of predictions allowed us to clearly identify areas with potential to be invaded by the bivalve, in which records are not yet detected. This information can be used in management, to implement measures to delay or prevent invasions, as well as for the identification of the environmental variables that favor that invasive potential.

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## 1. Introduction

The species *Corbicula fluminea* (Müller, 1744) is considered one of the most efficient freshwater invaders worldwide and is currently found in the 5 continents (Ituarte, 1994; Mouthon, 2001; Ciutti and Cappelletti, 2009; Bódis et al., 2012; Früh et al., 2012; Lucy et al., 2012). This bivalve species is normally found in well oxygenated waters (Belanger, 1991) and is intolerant to high salinity values (McMahon, 1999), low pH (Lucy et al., 2012) and low calcium concentrations (Karatayev et al., 2007). It tolerates a wide range of water temperatures (Lucy et al., 2012) and prefers sand and silt sediments with higher organic matter content (Sousa et al.,

2008a). The occurrence of pelagic and benthic life stages enables *C. fluminea* to spread over long distances by ballast water transport in boats (Paunović et al., 2007; Bódis et al., 2012), by currents, and locally by diffusion due to sand extraction (Belz et al., 2012). Passive transport by aquatic birds between water bodies was also observed (Darrigran, 2002; McMahon, 2002). For all these reasons this particular species has a high invasive potential.

Distribution models may be used to assess the spreading potential of invasive species allowing scientists to prioritize biodiversity conservation plans and mitigate invasion impacts. Despite the increasing area of distribution of *C. fluminea* in a small amount of time, little is known about the geographical and climatic characteristics of the areas that are potentially being invaded. Ensemble distribution models have been used recently to explore these issues for other species (Capinha et al., 2011). To account for uncertainty in single Niche based models, scientists have been recently joining

\* Corresponding author. Tel.: +351 266 745334/745385; fax: +351 266 745395.  
E-mail address: [ana.gama@ci.uc.pt](mailto:ana.gama@ci.uc.pt) (M. Gama).

single models in ensemble analysis combining individual predictions in consensus predictions (Capinha and Anastácio, 2011).

This study models the worldwide distribution of *C. fluminea* using an ensemble of Niche-based models (NBMs) of nine modeling techniques that are implemented in the BIOMOD modelling framework (Thuiller, 2003). The effects of three environmental datasets on the accuracy of the models were explored. We aimed to answer the following questions: (i) how will the climatic suitability change for these invaders by using different environmental variables datasets; (ii) is the predictive reliability similar between tested datasets; (iii) which are the environmental variables that better explain habitat adequability?

## 2. Methods

### 2.1. Data sources

An extensive compilation of worldwide native and invasive records (Fig. 1) (412 presences) was obtained from literature. To describe the environmental conditions, we selected up to 4 different climatic variables, with a cell resolution of 5 arc-min from the worldclim datasets (<http://www.worldclim.org/1.4> datasets; Hijmans et al., 2005; accessed May, 2014). The climatic variables included were annual mean temperature (AnnMeanTemp), mean temperature of warmest quarter (MeanTempWarmQt), mean temperature of coldest quarter (MeanTempColdQt), and annual precipitation (AnnPrecip), chosen from a set of 19 different climatic variables. These were chosen in order to determine the influence of temperature and precipitation patterns in the determination of habitat suitability. It was considered that the selection of these particular climatic variables were ecologically meaningful for *C. fluminea*. In addition, several topographic variables were also added to the model to allow the representation of landscape characteristics. The chosen variables were altitude and slope and a compound topographical index was also calculated. Altitude (alt) and slope give us an indication of other environmental factors such as stream size and velocity, known to influence, for example, oxygen availability (Hynes, 1970). Altitude was obtained from the WORLDCLIM datasets. The compound topographical index (CTI) was calculated based on Cooley (2013) and was previously used for freshwater species (Capinha and Anastácio, 2011). The CTI (Moore et al., 1991)

or “soil wetness” transformation can be used to model aspects of hydrologic systems and is strongly correlated with soil moisture, providing indirect information on water availability. The value of each cell in the CTI output raster is the value in a flow accumulation raster for the corresponding DEM (digital elevation model), meaning that higher CTI values represent drainage depressions and lower values represent ridges. The topographical variables’ slope and CTI were spatially modeled in ArcGIS (version 10), using the digital elevation model of the United States Geological Survey (USGS) HYDRO1k geographical dataset (Verdin and Jenson, 1996). Posteriorly, these data were resampled to match the remaining variables in R. To avoid collinearity among variables, Pearson correlation coefficients were calculated for all pairs of predictors and the environmental variables included were the ones not highly correlated ( $r < 0.83$ ). Several published papers refer distinct  $r$  values to define high correlations, for example  $r < 0.80$  (Gallardo and Aldridge, 2013),  $r < 0.85$  (Capinha and Anastácio, 2011),  $r < 0.80$  (Capinha et al., 2012) and some studies indicate that variables with  $-0.70 < r < 0.70$  should be excluded (Domisch et al., 2013 following Green, 1979). In this study only one pair of pairwise variables had an  $r$  outside this range being the remaining lower than 0.7. We chose to keep it because we believe that the variables were considered relevant for the distribution of *C. fluminea*.

To determine the influence of topographic vs. climatic variables, three ensemble models with increasing complexity (with respect to the number of environmental variables selected) were created: *Corbicula*TOPO, with alt, slope and CTI; *Corbicula*CLIM, with AnnMeanTemp, MeanTempWarmQt, MeanTempColdQt and AnnPrecip; and *Corbicula*MIX, with AnnMeanTemp, MeanTempWarmQt, MeanTempColdQt and AnnPrecip, alt, slope and CTI.

### 2.2. Ensemble distribution models

To model the potential distribution of *C. fluminea*, 9 different algorithms in the BIOMOD2 package (Thuiller, 2009) were used, in R software (version: 2.14.0; R Development Core Team, 2011). Algorithms were SRE (surface range envelop or BIOCLIM), CTA (classification tree analysis), RF (random forest for classification and regression), MARS (multivariate adaptive regression spline), FDA (flexible discriminant analysis), GLM (generalized linear models), GAM (generalized additive models), GBM (generalized boosted

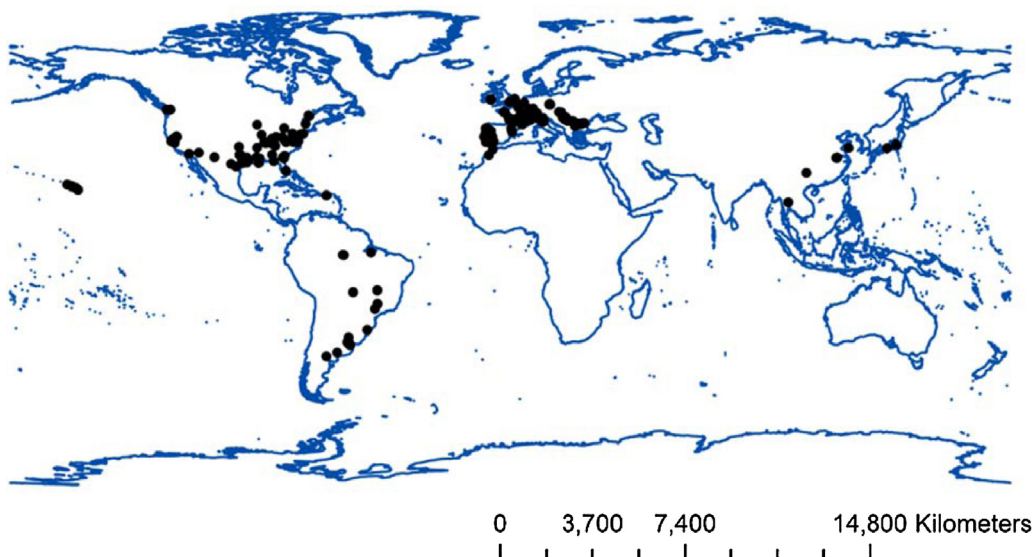


Fig. 1. Records of *C. fluminea* presence worldwide, used to model the current distribution of the species.

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