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The first artificial intelligence algorithm for identification of bat species in Uruguay

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ABSTRACT

Acoustic bat identification is a complementary method to traditional mist-netting for chiropteran surveys. In this work, an algorithm based on artificial intelligence techniques was developed for bat species identification in Uruguay. An acoustic library of 662 search phase pulses of the 10 most common bat species in Uruguay was obtained. Random Forests, Support Vector Machines and Artificial Neural Networks algorithms were trained to predict bat species from acoustic variables. Variable selection was performed in an independent subset (one third) of the dataset, using the function varImpPlot of *randomForest* R package. Model performance was evaluated by means of the test error with the remaining two thirds of the data. To do this, data were split randomly into a training and a test set, then the model was trained with the training sample and its performance was assessed using the test sample. The procedure was performed 100 times and the test errors were averaged to have an unbiased measure of the performance of the models. The best predictor was a Random Forests classifier that considered 12 predictor variables. The achieved accuracy was comparable to other international published products. Additionally, a threshold value for classification probability was optimized to define an "unclassified" class that allows using this algorithm even when the training sample does not represent an exhaustive sample of local richness. A web application returning the predicted class and a confidence measure for a given observation was developed permitting the use of this tool by a broad spectrum of users, from biologist to technicians.

1. Introduction

The recent development of wind farms in Uruguay is a state policy for changing the energy matrix of the country (MIEM-DNETN, 2005; Uruguay, 2014). This type of energy is more environmentally sound, particularly in comparison to other sources such as fossil-based thermoelectric centrals. However, wind farms also have negative environmental consequences; in particular, bats and birds may be negatively affected by their development (Arnett et al., 2008, 2011; Barclay et al., 2007; Brennan et al., 2007; Kunz et al., 2006) since they are killed when collide with the moving blades. According to a recent study, globally, more than 40 species of bats have been affected by almost 300 mass mortality events related to windfarms (O'Shea et al., 2016). The Latin American and Caribbean Network for Bat Conservation has identified wind farms as an emerging threat to bats in this region (RELCOM, 2010). To minimize the negative impacts of wind farms on bat populations, exhaustive impact assessment studies should be conducted to determine which species use the airspace around the turbines and in what manner (e.g., migration patterns, feeding areas and massive roost sites). The use of acoustic surveys in these assessments is a powerful tool for determining the species present at each site because they provide large datasets of presence and activity (e.g., hunting) information. In addition, acoustic surveys minimize the biases of mist-net capture techniques, which may miss high-flying species (Frick, 2013; Macswiney et al., 2008; Weller and Baldwin, 2012). However, acoustic monitoring produces large datasets, and their analysis and correct interpretation may pose a challenge for researchers and policymakers in the absence of standardized procedures. Identification algorithms ensure standardized call classification, as they perform replicable, and tested procedures for species identification, unlike visual classification, which is more subjective. A recent study has shown that even when automated algorithms perform similarly to trained researchers in species identification, algorithms provide more consistent and reproducible results (Jennings et al., 2008). Moreover, a primary objective of these studies is to ensure that the identification of species from each pulse (or each pass: a sequence of pulses attributables to the same

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individual) is repeatable and explicit, which is better achieved by automated identification systems (Frick, 2013). Given the number of variables involved in bat identification and the violations of assumptions underlying classical statistical approaches, artificial intelligence techniques emerge as an attractive alternative to predict bat species from acoustic surveys. In fact, several studies have shown better results with artificial intelligence techniques than more classic techniques such as linear models (e.g. Armitage and Ober, 2010; Frick, 2013; Jennings et al., 2008; Redgwell et al., 2009).

Presently, there is no algorithm to identify bat calls from Uruguay based on local samples. In this study, we propose to develop the first semi-automated algorithm for bat identification in Uruguay using a local call library and three of the most effective machine learning techniques: Random Forests (Breiman, 2001), Support Vector Machines (Vapnik, 1998) and Artificial Neural Networks (Venables and Ripley, 2002). The presented algorithm considers an “unknown class” so that pulses that do not fit with the species included in the training set will not be classified incorrectly. Furthermore, this algorithm provides a measure of confidence in the classification for each observation. This measure is calculated from the proportion of votes assigned to the winning class and allows the technicians to explore in more depth those pulses with low confidence classifications.

2. Methods

2.1. Study area

All the acoustic recordings were obtained from bats captured in Uruguay (Fig. 1a). Uruguay is situated in southeastern South America, between 30°S and 35°S latitude, with coasts to the Atlantic Ocean and the Río de la Plata estuary (Fig. 1). This region has a subtropical climate, with a mean temperature of 17.5 °C and 1300 mm average annual rainfall. The dominant ecosystem is temperate grasslands, with varying levels of modification by agriculture, forestry and livestock production. Forests are mainly restricted to rivers banks and some hill areas (Evya and Gudynas, 2000; PNUMA, 2008). All the captures were performed in southern Uruguay except for one capture that was achieved in a northeastern locality where a large colony of *Tadarida brasiliensis* roost in an abandoned industrial facility (Fig. 1b).

2.2. Bat captures and recording of reference calls

An acoustic library was developed using reference calls from hand release or zipline recordings. All captures were made by mist-netting outside identified shelters or over water bodies. In some cases, captures were performed directly inside shelters using hand nets (Kunz et al., 2009). For hand-release and zip-line recordings, we followed the methodology proposed by Estrada-Villegas et al. (2014). All handling procedures were performed according to a protocol approved by an Institutional Animal Use and Care Committee and conducted by trained and authorized personnel. Reference calls were recorded using an EM3+ hand-held ultrasonic recorder (WildLife Acoustics Inc.). For each pulse, family, species and capture locality were recorded. Field species identification, based on external morphology, was made following González and Martínez-Lanfranco (2010).

For the *Myotis* species, only genus was recorded as there is some overlap in external characters between common species (*M. albescens* and *M. levis*). For the tribe Lasiurini, only one group was created, clustering calls from *Dasypterus ega* and *Lasiurus blossevillii*. In this work, only common species from southern Uruguay were considered.

2.3. Acoustic analysis and database building

From each recording, only searching phase pulses, as they are the pulses with most constant structural features within each species (Armitage and Ober, 2010; Jennings et al., 2008; Obrist et al., 2004), were identified and analyzed using Sonobat™ 2.9.7 (Sonobat Inc.) in 10- to 20-millisecond standard views. For each identified pulse, a set of 76 variables was automatically recorded by Sonobat™ into a plain text file (.txt). The files were joined into a dataframe in R 3.3.1(R Core Team, 2016) using RStudio 0.99.485 (RStudio Team, 2012). A database comprising 662 pulses from 96 individuals of 8 species was obtained. This dataset was split into two independent subsets, one for the variable selection (1/3) (see Methods: Variable selection) and a modeling set for

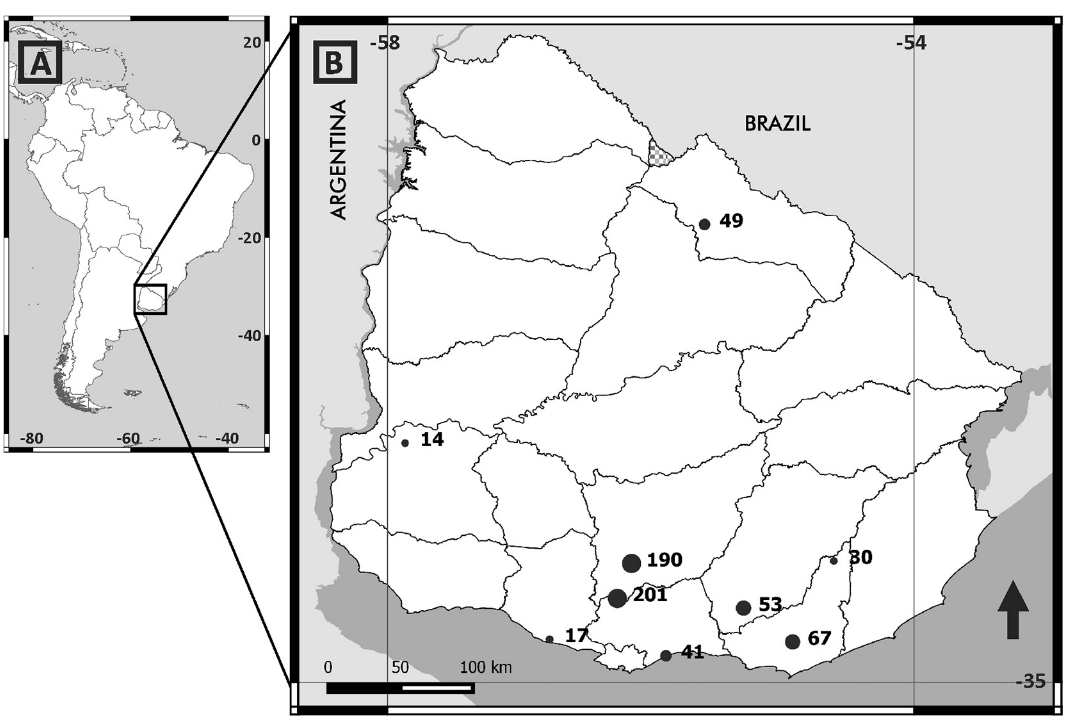

Fig. 1. A. Continental relative location. B. Distribution of the capture localities for both samples in Uruguay. The point size and numbers represent the number of calls analyzed from each site.

the training and testing (2/3) of the models (see Methods: Model building).

2.4. Variable selection

From the 76 quantitative variables provided by SonoBat™, four were discarded due to incompleteness or because they were not informative for the classification, namely: "TimeInFile" (position of the analyzed pulse in the original file), "PrecedingIntrvl" (Time interval between the analyzed pulse and the previous one), "CallsPerSec" (Estimated number of pulses per second) and "Quality" (Quality index [0;1] assessed by SonoBat for the analyzed pulse). The remaining 72 variables were included in the variable selection process. As the variable selection process was performed using the varImpPlot function of the *randomForest* R package, and in order to avoid biases in the models' performances afterwards, it was achieved in an independent subset of the data: 1/3 of the data were sampled using a by-species stratified random sampling.

A forward selection process was implemented. The 72 predictor variables were included in the model one by one, from the most to the least important, following the importance order provided by the varImpPlot function (Liaw and Wiener, 2002). This function calculates the predictor variables importance considering the mean decrease in Gini index (i.e., the average gain of purity by splits of a given variable) (Cutler et al., 2007). Global performance of all the nested models was evaluated using the Out of the Bag (OOB) error (Breiman, 2001). The model with the minimum OOB error was used to choose the final set of variables to include in the models.

2.5. Models building

Three modeling approaches were used to predict bat species: 1) Random Forests (hereafter RF), 2) Multiclass Support Vector Machines (hereafter SVM), and Multiclass Artificial Neural Networks (hereafter ANN). All the models were built using the same set of predictor variables (see Results: Variable selection). To assess the performance of the models, the modeling set (2/3 of the original dataset) was split randomly and stratified by species, in halves into a training and a test sample, then the model was trained with the training sample and it performance was assessed using the test sample. The procedure was performed 100 times and the test errors (i.e. the proportion of misclassified observations over the test sets) were averaged to have an unbiased measure of the performance of the models.

The RF model was performed considering 5000 trees, and SVM model was trained using a probability model and a Radial Basis Kernel (Karatzoglou et al., 2004). For the ANN, one hidden layer and 10 neurons were used. For each model, a matrix of predicted probabilities with 217 rows (observations) and 8 columns (species) was obtained. The class (i.e. species) that maximized the probability was retained as the final prediction. An observation was classified as "unknown" when the maximum probability did not reach a defined threshold (see Methods: Definition of the unknown class).

All the models were performed in R software (R Core Team, 2016). RF models were trained using the package *randomForest* (Liaw and Wiener, 2002). SVM models were trained using the *kernlab* package (Karatzoglou et al., 2004) and ANN models were trained using *nnet* package (Venables and Ripley, 2002).

2.6. Definition of the "unknown" class

For the best performing model, an "unknown" class was created by setting a threshold on the probabilities of belonging to each class: if the winning class was not predicted with a higher probability than the defined threshold, an "unknown" was assigned as the resulting class. The value of the threshold was optimized considering the model global accuracy in final model. For the optimization process, an error function was calculated. For each observation, this function takes value of 0 for a correctly classified observation, 1 for misclassification or 0.5 for pulses assigned to the "unknown" class. We selected the threshold value (from a sequence from 0 to 1 with a 0.01 incremental step) that minimized the global sum of the error function.

2.7. Algorithm availability and web application

The optimal model (see Results) was implemented in an R function (Botto Nuñez et al., 2018), included in an open Web application developed using Shiny (Chang et al., 2016), freely available at the shinyapp website (https://german-botto.shinyapps.io/bats_UY_v2/).

The web application takes a plain text file (.txt) from a SonobatTM analysis and returns a downloadable comma separated values file (.csv) containing the species and the probability for each observation. It also shows an absolute frequency bar graph in a graphic interface, representing the number of observation per class in the analyzed file.

3. Results

3.1. Database

For the complete database, 662 pulses for 8 taxonomic groups (species or genus: *Desmodus rotundus*, *Eptesicus furinalis*, *Eumops bonariensis*, *Histiotus montanus*, *Lasiurus sp.*, *Molossus molossus*, *Myotis* sp. and *Tadarida brasiliensis*) were obtained. The distribution of pulses by species in the datasets for variable selection and model training and testing is shown in Table 1. Fig. 1b shows all the capture localities and the number of pulses obtained from each site.

3.2. Variable selection

Twelve time, frequency, and derived predictor variables were selected to perform the models: Duration of the call (CallDuration), Final Frequency (EndF), Frequency of maximum power (FreqMaxPwr), Maximum Frequency (HiFreq), Minimum Frequency (LowFreq), Total amplitude of the third quartile of the call (Amp3rdQrtl), Bandwidth at 5 dB (Bndw5dB), Bandwidth at 15 dB (Bndw15dB), Maximum Slope (SteepestSlope), Mean of the fourth quartile amplitude (Amp4thMean), Percentage of the entire call duration at which the maximum amplitude occurs (PrcntMaxAmpDur), and Characteristic frequency (Fc). The performance of the 72 trained nested models is showed in the Supplementary material (Fig. S1).

3.3. Model evaluation

To compare different models (RF, SVM, and ANN), the test error calculated over the test sample was used. Fig. 2 shows the distribution of test errors for the three models over the 100 partitions of the data. The RF model outperformed both SVM and ANN, showing lower

Table 1
Distribution of analyzed pulses in the samples for variable selection (1/3) and modeling set (2/3), split randomly in halves 100 times into training and testing sets. The subseting was performed using a stratified random sampling. The *Lasiurus* group comprises *Dasypterus ega* and *Lasiurus blossevilli* samples. The *Myotis* group comprises *M. albescens* and *M. levis* individuals.

Taxonomic group	Variable Selection	Train/Test Resampling	Total
Desmodus rotundus	10	19	29
Eptesicus furinalis	32	63	95
Eumops bonariensis	22	45	67
Histiotus montanus	53	106	159
Lasiurus	8	15	23
Molossus molossus	24	47	71
Myotis	47	95	142
Tadarida brasiliensis	25	51	76
Total	**221**	**441**	**662**

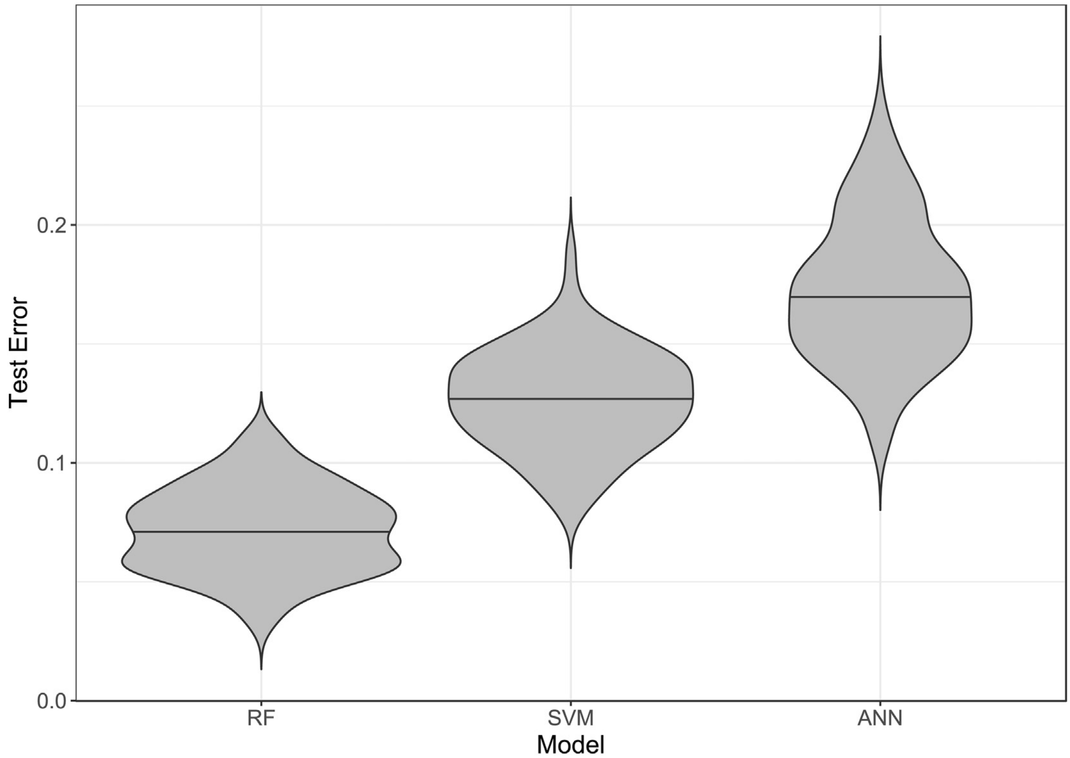

Fig. 2. Errors distribution over the 100 test samples for the three evaluated models: RF: Random Forests; SVM: Support Vector Machines; ANN: Artificial Neural Networks. Horizontal lines inside plots show medians.

average error and less dispersion. Mean test error over the 100 test samples (± SD) were respectively: 7.1 ± 1.8%, 12.7 ± 2.0% and 17.2 ± 2.9%.

Having identified RF as the best performing model, the "unknown" class was added to this model. The threshold value for the assignation to the "unknown" class was optimized as described before (see Methods subsection: Definition of the "unknown" class). The optimization process showed a minimum error with a probability threshold of 0.43 (last global minimum). Fig. 3 shows the results of the optimization process.

Once the selected threshold was applied, the global error of the model was 7.37% (201 correctly classified over 217 observations). This error results from observations that were classified as incorrect species, (11 misclassified over 217 observations), and observations assigned to the unknown class (5 over 217 observations) in which the probability of belonging to the assigned group was lower than the threshold.

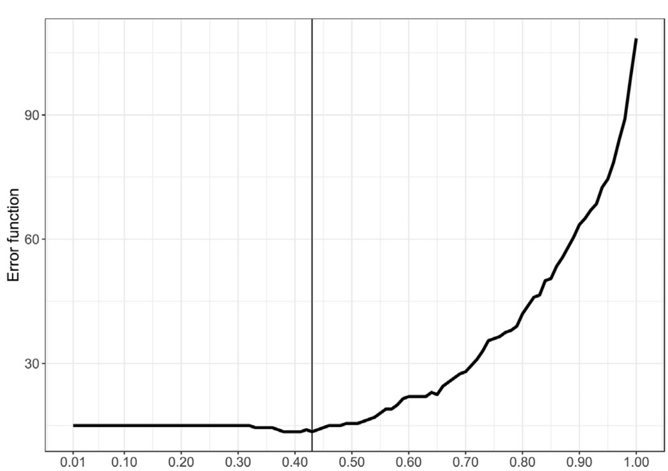

Fig. 3. Optimization process of the threshold value for the Random Forests classifier. A non-homogenous error function was constructed with different values for a complete error (assignation to an erroneous group, error = 1) and for the assignation to the "unknown" group (probability of belonging to the predicted class below the threshold, error = 0.5). The last global minimum of the error function is 13.5; the corresponding threshold value is 0.43 (vertical line).

The RF model with the threshold was retained as the best model and was implemented in the web application for public use.

4. Discussion

The RF model was the best model showing good classification performance for the identification of bats in Uruguay from their acoustic calls. The results are comparable to those of other published studies which considered different type of methods (Armitage and Ober, 2010; Basil et al., 2014; Britzke et al., 2011; Rodríguez-San Pedro and Simonetti, 2013; Walters et al., 2012). For example, Britzke et al. (2011) compared several discriminant functions with Neural Networks, finding that Neural Networks outperformed all discriminant functions. However, these authors used two calculation methods for assessing the global error, one considering the individual pulses (the same approach used here) and the other taking into account passes (sequences of pulses). For individual pulses, the best model showed an 87% accuracy (Britzke et al., 2011), similar to that obtained in this work. Armitage and Ober (2010) showed that the performance of the algorithms depends on the considered ensemble of species. In that case, in three out of the five ensembles considered, Random Forests outperformed the other algorithms: Neural Networks (with and without Principal Components Analysis for the predictor variables), SVM and Discriminant functions. In the remaining two ensembles, Neural Networks outperformed the other techniques (Armitage and Ober, 2010). It is interesting to note that in the three ensembles where RF outperformed the other algorithms over an independent test sample, it performed worst when considering the training sample (Armitage and Ober, 2010), showing less overfitting of the RF algorithms in those examples. The best accuracy reached in that study was 96%, for genus-level classification or for species-level classification, using Random Forests classifiers, but grouping all the *Myotis* species (Armitage and Ober, 2010). Neither of these two studies included an unknown class in the output (Armitage and Ober, 2010; Britzke et al., 2011).

Available software for bat calls analysis provide a large set of variables from each pulse (e.g. SonoBat provides 76 quantitative variables), stressing the relevance of the variable selection issue in this kind of problems. Previous studies have used different strategies for variable selection ranging from a priori selection based on expert knowledge (Parsons and Jones, 2000, Britzke et al., 2011, Russo and Jones 2002, Rodríguez-San Pedro and Simonetti, 2013) to comparison of intragroup variances and F ratios among potential predictor variables (Walters et al., 2012). In one of the works where a priori selection was performed, PCA was used to reduce the correlation of the variables (Britzke et al., 2011) while other studies dismissed the correlation's negative impact (Walters et al., 2012). Our approach directly uses the relevance of each variable through the variable importance estimation from RF. This appeared to be a suitable tool for the forward selection process and was similar to that used by Fox et al. (2017). Even though unlike the other models (ANN and SVM), it is possible to add more variables to RF without decreasing performance (Breiman, 2001; Cutler et al., 2007; Fox et al., 2017), the selection process allowed us to use the same set of predictor variables for the three algorithms used. The number of variables used as predictor variables by the previously cited works were not very different from our approach and were noticeably lower than 76 (number of variables available in SonoBat): from six variables in Russo and Jones (2002) to 24 in Walters et al. (2012). To our knowledge, this is the first study that considers this strategy for variable selection to predict bat species from acoustic variables.

Overall, Random Forests is a powerful predictive tool which showed best accuracy in several comparative ecological studies (Cutler et al., 2007). Furthermore, it provides an explicit tool to assess the variable importance. The fitting of Random Forests is easier in comparison with other machine learning techniques as Supporting Vector Machines and Artificial Neural Networks and the computational requirements for these models are covered by most personal computers (Breiman, 2001; Cutler et al., 2007).

The use of a threshold over the probability of belonging to the predicted class allows the model to identify calls from other species as “rare” instead of assigning them to one of the known classes. Walters et al. (2012) used a threshold to prevent a pulse to be classified with a low fraction of the votes in an ANN classification model. In that case, pulses with low proportion of votes to one species, were treated as unclassified. The use of thresholds to favor unclassification over misclassifications is recommended also by Russo and Voigt (2016). In the same sense, Rydell et al. (2017) proposed the use of automated classification to resolve the common species identification and reserve the dubious pulses for manual identification by an experienced technician. The work by Walters et al. (2012) showed that increasing the threshold not only decreased the proportion of misclassified calls, but greatly increased the likelihood of a pulse of not being assigned to any species. Then, we chose an explicit method to optimize the threshold for assigning to the “unknown” class rather than using an arbitrary threshold value.

The selected model included in the web application also provides the probability of belonging to the assigned class, which could be used as a confidence measure for each prediction. These confidence measures are especially important in the context of wildlife surveys in which the animal is not captured.

This web application is the first tool for automated identification of bats in the area, which is especially relevant as the identification procedures may be sensitive to both geographical variation and species diversity (Britzke et al., 2013). Given the rapid increase of wind farms in the country (MIEM-DNETN, 2005; Uruguay, 2014) and the subsequent need of improved and reproducible environmental impact assessments, our algorithm provides a tool that can be used in Uruguay, with a potential positive and significant impact on bat conservation and policy creation. The developed algorithm is freely available through a web application for public use in wildlife studies in Uruguay https://german-botto.shinyapps.io/bats_UY_v2/.

Supplementary data to this article can be found online at https://doi.org/10.1016/j.ecoinf.2018.05.005.

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Authorship information

The original research proposals were written by GBN, GL and MMW. GBN wrote the initial algorithm and the first draft of the manuscript. GL, MMW, ALR, EMG and CCK contributed with revisions. GBN and MMW developed the final model and the web app. GBN and GL built the data base. GBN, ALR and GL worked in sound files analysis and parameter estimation. GBN, GL, ALR and EMG performed the captures and field recordings. CCK is the academic advisor and provided fundamental support for numerical analysis and model development. GBN, MMW and CCK revised the corrections and edits.

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