JAV-01527
Appendix 1

Table A1. Details of the predictor variable “Density of exotic tree species” representing the spatial distribution of exotic tree species on which *Psittacula krameri* is known to feed.

<table>
<thead>
<tr>
<th>Exotic tree species</th>
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<tbody>
<tr>
<td><em>Albizia julibrissin</em></td>
<td>(FERA 2009)</td>
</tr>
<tr>
<td><em>Butia capitata</em></td>
<td>(Fraticelli 2014)</td>
</tr>
<tr>
<td><em>Cupressus sempervirens</em></td>
<td>(Fraticelli 2014)</td>
</tr>
<tr>
<td><em>Diospyros sp.</em></td>
<td>(Clergeau et al. 2009, Clergeau and Vergnes 2011)</td>
</tr>
<tr>
<td><em>Ligustrum sp.</em></td>
<td>(Clergeau et al. 2009, Clergeau and Vergnes 2011)</td>
</tr>
<tr>
<td><em>Liriodendron tulipifera</em></td>
<td>(Claes and Matthysen 2005)</td>
</tr>
<tr>
<td><em>Magnolia grandiflora</em></td>
<td>Expert knowledge</td>
</tr>
<tr>
<td><em>Melia azedarach</em></td>
<td>(Fraissinet et al. 2000, Fraticelli 2014)</td>
</tr>
<tr>
<td><em>Morus sp.</em></td>
<td>(Fraissinet et al. 2000, Fraticelli 2014)</td>
</tr>
<tr>
<td><em>Phoenix canariensis ; Phoenix dactylifera</em></td>
<td>(Fraticelli 2014)</td>
</tr>
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<td><em>Populus alba</em></td>
<td>(Clergeau et al. 2009, Clergeau and Vergnes 2011)</td>
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<tr>
<td><em>Prunus sp.</em></td>
<td>(Clergeau et al. 2009, Clergeau and Vergnes 2011, Fraticelli 2014)</td>
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<td><em>Sophora japonica</em></td>
<td>(Fraticelli 2014)</td>
</tr>
<tr>
<td><em>Tilia sp.</em></td>
<td>(Claes and Matthysen 2005, Clergeau et al. 2009, Clergeau and Vergnes 2011)</td>
</tr>
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<td><em>Washingtonia filifera</em></td>
<td>(Fraticelli 2014)</td>
</tr>
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</table>
Table A2. Raw relative contribution of the predictor variables used in the ensemble modelling for eight years (from 2009 to 2016) for *Psittacula krameri*. The mean importance value of all the predictors was calculated and the most important predictors were defined as those with an importance score above this mean value (highlighted in bold).

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<td><strong>0.065</strong></td>
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Table A3. Raw relative contribution of the predictors used in the ensemble modelling for eight years (from 2009 to 2016) for *Corvus monedula* The mean importance value of all the predictors was calculated and the most important predictors were defined as those with an importance score above this mean value (highlighted in bold).

<table>
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Figure A1. Habitat suitability maps for *Psittacula krameri* for each year modelled (a) 2009 (b) 2010 (c) 2011 (d) 2012 (e) 2013 (f) 2014 (g) 2015 using an ensemble modelling approach.
Figure A2. Habitat suitability maps for *Corvus monedula* for each year modelled (a) 2009 (b) 2010 (c) 2011 (d) 2012 (e) 2013 (f) 2014 (g) 2015 using an ensemble modelling approach.
Figure A3. Suitability curves along the gradients of the most important predictors for *Psittacula krameri* for an eight-year period (from 2009 to 2016).
Figure A4. Suitability curves along the gradients of the most important predictors *Corvus monedula* for an eight-year period (from 2009 to 2016).
Appendix 2: Description and parametrization of the models

Four machine learning SDMs were used in this study: **Random Forests** (RF, Breiman 2001), **Maximum Entropy** (MAXENT, Phillips et al. 2006), **Generalized Boosting Model** (GBM, Friedman 2001) and **Artificial Neural Networks** (ANN, Ripley 1996). All the SDMs were run using **BIOMOD2**, an ensemble-modelling R package developed by Thuiller et al. (2009), in R 3.1.3 (R Development Core Team 2016). The outputs of models were averaged based on the weighted average consensus (Marmion et al. 2009) to produce a single predictive map of occurrence probability.

**Random Forest** (RF) is an extension of classical Classification Trees in which multiple decision trees are grown with random subsets of the data. Each random subset is selected from the initial complete dataset by a procedure called bagging (in which each data point has an equal probability of being selected) and all random subset have the same number of data points. RF is one of the most accurate machine learning algorithms which has the advantage of maintaining accuracy even when a large proportion of the data is missing. RFs were run using a maximum of 750 trees and the number of predictors randomly sampled as candidates calculated as the square root of the total number of predictors in the model (default setting in Biomod2).

**Maximum Entropy** (MAXENT) is a modelling algorithm that applies the principle of maximum entropy to predict species potential distributions. Maxent compares the known locations of species to the overall corresponding environment in the study area by finding the distribution closest to uniform. Maxent is a widely used and powerful algorithm that showed good performances in many fields and for many applications. Maxent was used with default settings.

**Generalized Boosting Model** (GBM, also called Boosted Regression Trees) is a combination of decision trees and boosting methods which used a recursive partitioning algorithm to develop a final model by repeatedly fit decision trees. For each new tree add in the model, the input data are weighted in such way that data that was poorly modeled by previous trees has a higher probability to be selected in the new tree. Interaction depth, which controls the number of split in each tree and whether
interactions between predictors and response variables are fitted, was set to 2. The other parameters of
GBM was leave as default setting in BIOMOD2.

**Artificial Neural Network** (ANN) has a high predictive power and is able to model non-linear
associations between response variables and predictors. In other hands, it is sensitive to missing data
and outliers.

---

GBM = list( distribution = 'bernoulli',
            n.trees = 2500,
            interaction.depth = 2,
            n.minobsinnode = 5,
            shrinkage = 0.001,
            bag.fraction = 0.5,
            train.fraction = 1,
            cv.folds = 0,
            keep.data = FALSE,
            verbose = FALSE,
            perf.method = 'OOB'),

ANN = list( NbCV = 5,
            size = NULL,
            decay = NULL,
            rang = 0.1,
            maxit = 200),

RF = list( do.classif = TRUE,
           ntree = 750,
           mtry = 'default',
           nodesize = 1,
           maxnodes = NULL),

MAXENT = list( path_to_maxent.jar = "",
               memory_allocated = 1024,
               maximumiterations = 200,
               visible = FALSE,
               linear = TRUE,
               quadratic = TRUE,
               product = TRUE,
               threshold = TRUE,
               hinge = TRUE,
               lq2lqpthreshold = 10,
               l2lqthreshold = 10,
               hingethreshold = 15,
               beta_threshold = -1,
               beta_categorical = -1,
beta_lqp = -1, 
beta_hinge = -1, 
defaultprevalence = 0.5)

MigClim

MigClim model (Engler and Guisan 2009) is based on a cellular-automaton which allows implementing dispersal constraints into predicted species distribution. It can be used under environmental change scenarios or in stable environments to simulate colonization of suitable cells. MigClim requires two data input: a binary layer of the species initial distribution corresponding to the year 0 and indicating respectively presence (coded ‘1’) and absence (coded ‘0’) of the target species ([iniDist]) and one or more habitat suitability maps which can be either binary or probabilistic ([hsmap]).

We used MigClim R package (Engler et al. 2012) with the following parameters. In each time step, unoccupied cells are colonized with the combined probability of a propagule colonizing the cell given the distance to a seed source, the probability of propagule production as a function of time and sexual maturity age ([iniMatAge]), and the suitability of the cell (habitat suitability map). We assumed that both of our studied species can disperse once a year. The maximum regular dispersal distance of the ring-necked parakeet and the jackdaw were respectively 400m (Butler 2003) and 600m (Withey et al. 2005) which correspond respectively to 8 and 12 cells since our input data have a spatial resolution of 50m. We assumed no barriers to dispersal given that jackdaws and parakeets are strong fliers. As our aim was to model the spread of expanding species through our study area, simulations were run without environmental change ([envChgSteps]) and by year 2066. We assumed that all age classes have the same probability of propagule production ([PropaguleProd]) of one. For the parakeet and the jackdaw, the frequency of long distance dispersal events ([lddFreq]) was set to 0.01. For the parakeet, the range of long distance dispersal events was set with a minimum ([lddMinDist]) of 450m (i.e. 9 cells) and a maximum ([lddMaxDist]) of 350m (i.e. 15km). For the jackdaw, ([lddMinDist]) was set to 650m (i.e. 13 cells) and ([lddMaxDist]) to 22km (i.e. 440 cells). A negative exponential dispersal kernel (formula 3, (Engler and Guisan 2009)) was used to estimate the probability a propagule dispersed from each occupied cells to adjacent cells until the maximum dispersal distance of species is
reached. For both of our species, the initial maturity age ([iniMatAge]) was set to two. We ran 10 replicate simulations.
References


FERA 2009. WM0104: Rose-Ringed parakeets in England: a scoping study of potential damage to agricultural interests and management measures.


