



A Bayesian network approach for selecting translocation sites for endangered island birds

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ABSTRACT

Translocation has become increasingly important for conserving island species. Limited tools are available for guiding the selection of translocation sites, however, particularly when establishing rescue populations outside of historic ranges. We developed a Bayesian network model framework for translocation site selection for island birds. The model consisted of four primary components including ecological requirements for survival, anthropogenic threats at the population establishment site, effects the translocated species may have on native species, and operational support associated with the translocation process and ongoing management. We then used the model to identify potential sites for the establishment of a wild population of Guam Micronesian kingfishers (*Todiramphus cinnamominus cinnamominus*) on an island outside the bird's historic range. Conditional probabilities that guided model evaluations were allocated using information from the literature, expert opinions, and a training set of islands outside the region under consideration for releases. The model was used to evaluate 239 islands where a translocation population of Micronesian kingfishers could be established. Five islands, all in the Federated States of Micronesia, were identified as being suitable for assisted colonization, including Kosrae, Yap, Faichuk, Weno and Fefan. Sensitivity analysis showed a correspondence between model variables and island characteristics indicated by the literature as being the most important for successful translocation. We found the Bayesian network model to be a useful tool for translocation site selection despite limited information on the natural history of the Guam Micronesian kingfisher and the factors that impact the success of translocations.

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1. Introduction

During historic times island avifauna have had an extinction rate 40 times higher than their continental counterparts, and have represented over 90% of avian extinctions world wide (Johnson and Sattersfield, 1990). The trend is likely to continue with 140 Pacific island bird species listed as vulnerable, endangered, critically endangered, or extinct in the wild (IUCN, 2011). The rapid decline of island birds implores the development and use of new research and conservation technologies.

Translocations have been used as a conservation tool to establish rescue populations in areas where species do not currently occur (Derrickson et al., 1998; Griffith et al., 1989). Translocations used to reestablish populations at locations within historical ranges (Williams et al., 1988), are known as reintroductions. Conservationists often assume that locations within the historic range are suitable for reintroductions, even if populations were

previously extirpated (Osborne and Seddon, 2012). Although reintroduction has proven successful for establishing rescue populations for many species (e.g. Butler and Merton, 1992; Cade and Burnham, 2003; Clout and Merton, 1998; Hooson and Jamieson, 2003; Jones et al., 1995), limited suitable habitat may lead to failures to establish long-term and viable populations. For island birds, introduced predators, including *Rattus* spp. and cats (*Felis catus*) can impact populations enough that conservation biologists seek release locations void of these predators. Release sites can be limited, however, as islands small enough to effectively eradicate introduced predators may also be too small to maintain genetically robust populations (Jamieson, 2011), or because eradication efforts are unlikely to succeed (e.g. Clout and Veitch, 2002; Spurr, 1994; Brown Tree Snake Control Committee, 1996). The development of methods to select sites for establishing translocated populations outside of historic ranges will thus likely be essential to preventing the extinction of many island birds.

Translocation outside a species historical range, or assisted colonization (Ricciardi and Simberloff, 2009), has been discouraged by some (IUCN, 1998; Williams et al., 1988), with ecological and ethical arguments underpinning opposition (Sandler, 2009). Most assume that historical range boundaries are associated with

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ecological factors that promote survival and maintenance of viable populations, and therefore that locations outside historical ranges are less suitable (Huang, 2008). Others have argued that even if suitable sites exist outside the historic range, identifying those locations would be impossible without perfect ecological knowledge (Davidson and Simkanin, 2008; Ricciardi and Simberloff, 2009). Another argument against releases outside the historic range is rooted in the idea that assisted colonization exacerbates the invasive species problem, and the release of threatened or endangered fauna may have unintended impacts on target systems (Davidson and Simkanin, 2008; Ricciardi and Simberloff, 2009).

On the islands of Pacific Oceania, however, these same arguments may not hold true. The likelihood that an introduced species will negatively impact native fauna depends on the evolutionary exposure of native species to organisms with ecological roles similar to those of the introduced species (Simberloff, 1995). Most of the oceanic islands in the Pacific are likely to have hosted more bird species than currently exist, and to have had a similar composition of genera represented on islands of similar sizes (Steadman, 2006). Thus, conservationists may be able to use concepts from the theory of island biogeography (MacArthur and Wilson, 1967) to provide estimates of how many and what types of species an island may support.

Several authors have compiled guidelines for planning and executing translocations, emphasizing the importance of choosing suitable habitat (Griffith et al., 1989; IUCN, 1987). However, little advice is provided on determining what makes a habitat suitable for a particular species, or how to prioritize when choosing from among multiple sites (Osborne and Seddon, 2012). Determining ecological requirements of a species can also be tremendously complex, particularly when all populations are imperiled or when only captive populations remain. For island birds, extensive niche overlaps within superspecies groups (Mayr and Diamond, 2001), wide niche breadth, and generalist dietary and nesting requirements (Cox and Ricklefs, 1977; Lack, 1969) may allow for the transfer of ecological information between similar taxa (Kesler and Haig, 2007a).

Political and logistical infrastructure are often ignored or evaluated in a post hoc fashion when selecting population establishment sites, but these factors can greatly affect whether a conservation project is successful (IUCN, 1998). Political infrastructure includes the presence and activity of local government and non-government conservation agencies. These entities may have the power to create protected areas, assist with implementation and monitoring, and educate local residents on conservation issues. Garnering local support may be difficult for assisted colonizations (Serena and Williams, 1994), making the presence and support of these agencies essential. Logistical infrastructure is also important for moving birds and people to and from the translocation sites during releases and monitoring, and assisted colonizations are more likely to require elevated levels of management. Incorporation of political and logistical infrastructure into the site selection process should thus lead to more effective identification of translocation release sites and higher long-term conservation success.

The process of identifying translocation release sites outside a species' historical range would best be addressed through scientific, rigorous, and quantitative approaches for which analytical tools are key (Lindenmayer, 1994). Bayesian network models are increasingly being used as decision-aiding tools in conservation science, and may provide a suitable framework for selection of translocation sites. Bayesian network models can be used to calculate the probability of a particular outcome (e.g. the probability that translocation to a particular site will be successful) by taking into account a range of factors with potential to influence the outcome (e.g. the characteristics of the translocation site), and weighting factors by their impacts on the outcome (e.g. the presence of a

natural predator may have less of an impact than the presence of an introduced predator on the species being translocated) (Smith et al., 2007). Bayesian network models also allow prior probabilities and proxies to be used where information is unavailable (McCann et al., 2006). Bayesian networks have the flexibility to incorporate the many factors likely to be important when evaluating translocation release sites while simultaneously incorporating uncertainty associated with species requirements and site characteristics (Marcot et al., 2006). The models have been used to evaluate availability of habitat resources for species and alternative management strategies (Howes et al., 2010; Marin et al., 2003; McNay et al., 2006; Raphael et al., 2001; Smith et al., 2007), and several studies demonstrated their utility for identifying suitable habitat for threatened or endangered species (McNay et al., 2006; Smith et al., 2007).

We developed a Bayesian network model structure for site selection for the translocation of threatened or endangered island birds. We first outline the general model components, and then give an example of how the generalized model was fitted for a single species – the Guam Micronesian kingfisher (GMK; *Todiramphus cinnamominus cinnamominus*; US Fish and Wildlife Service, 1984) which is extinct in the wild but exists as a captive population.

1.1. Guam Micronesian kingfisher

Avian populations on Guam began to decline in the 1960s and all were precipitously reduced by the 1980s (Engbring and Ramsey, 1984; Wiles et al., 2003). Although many factors may have contributed to the population declines, the introduced brown tree snake (*Boiga irregularis*) was identified as the primary cause of 12 eventual extinctions and extirpations (Conry, 1988; Rodda et al., 1997; Savidge, 1984; Wiles et al., 2003). The GMK is among the species that are now extinct in the wild. Prior to its extirpation from Guam (Wiles et al., 2003), a coalition of captive breeding institutions, US federal entities, and Guam Department of Wildlife and Aquatic Resources collected 29 birds with the goal of establishing a captive population that would eventually serve as a source for reintroductions (Haig and Ballou, 1995).

Captive breeding institutions are now at full capacity, and some have not paired birds because of funding restrictions. At the same time, brown tree snakes remain widespread on Guam, and thus reintroductions to the island are unlikely to be successful (Brown Tree Snake Control Committee, 1996). Alternative islands are being sought by the US Fish and Wildlife Service for assisted colonizations that will hopefully allow the kingfisher meta-population to grow, shorten the duration of the population bottleneck, and eventually serve as a source population for reintroductions to Guam. The large number of Pacific islands, along with their diverse ecological and political environments, makes selecting from among the possible sites at which a new population of GMK could be established tremendously challenging. Many Pacific islands likely hosted populations of *Todiramphus* spp. kingfishers that are now extinct (Steadman, 2006), so it is also likely that there are several islands with suitable resources for an introduced population of GMK.

2. Materials and methods

The generalized avian island site selection model is a tool for evaluating candidate sites based on their likelihood of hosting a translocated population of a particular species. Model construction occurred in six major phases. First, factors likely to influence the success of translocation were identified and were represented in an inference diagram as interconnected nodes (Fig. 1). Second, the inference diagram was customized for the GMK by incorporating nodes specific to the species. The third step was to

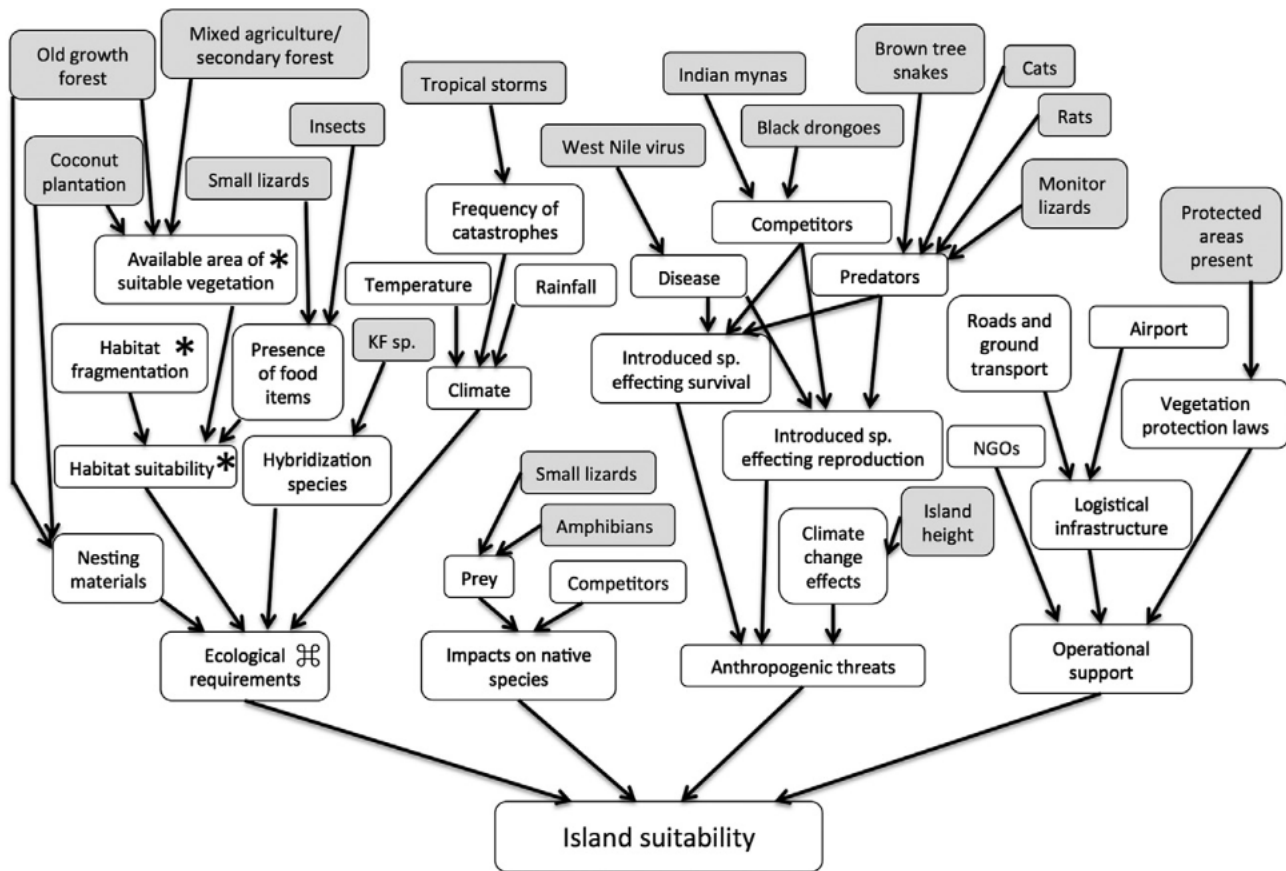


Fig. 1. Inference diagram depicting the relationships between island characteristics and the suitability of the island for establishment of translocated species. Asterisks indicate probabilities derived by learning from training dataset, and ⌘ indicates probabilities derived by training data set and literature review. Other probabilities were derived from literature review and expert opinion. Shaded boxes show nodes specific to Guam Micronesian kingfisher translocation site selection (KF = Kingfisher).

allocate probabilities to each node that were particular to the GMK's natural history and conservation situation. Once the model was developed, step four was to review and revise the model. The fifth step was to collect information on the candidate translocation sites and the final step involved presenting the model with island data and evaluating the candidate islands.

The generalized avian island site selection model was constructed in Netica™, a user interface developed for the construction and use of Bayesian networks (Norsys Software Corporation, 1998), and we followed the basic structure outlined by Marcot et al. (2006). Our Bayesian network model consisted of child nodes that represented single measurable factors that may influence the suitability of a site for translocation (e.g. “mean temperature”). Each node was in one of several possible states (e.g. the “mean temperature” node may have had two states “warm” and “cool”). Child nodes fed into associated parent nodes (e.g. child nodes “mean temperature” and “annual rainfall” may feed into parent node “climate”). Each combination of states for each child node corresponded to a probability that the parent node will be in a particular state (e.g. warm temperatures and high rainfall are likely to represent a high probability that the climate of a site will fall into the state “suitable climate for GMK” and a low probability that it will fall into the state “unsuitable climate for GMK”). These probability relationships between each of the node states, and among parent and child nodes, were organized into conditional probability tables. Models consisting of many nodes result in complex conditional probability tables and may lead to inaccuracies, so we limited the depth of the model to four layers and restricted the number of parent nodes for any given node to 3 or fewer wherever possible (Marcot et al., 2006).

2.1. Development of inference diagram

We first constructed an inference diagram incorporating island characteristics with potential to affect the success of a translocation (Fig. 1). We incorporated both the natural history requirements of birds that would be translocated to an island, and the potential impacts of translocated species on the fauna at the release site. We used primary literature and the limited information available about prior translocation successes. An overview of each model node is presented below and detailed in Appendix A.

We identified four model branches including ecological requirements for survival, impacts on native species, anthropogenic threats, and operational support for inclusion in the model. The first model branch addressed island characteristics and ecological requirements needed to support the translocated species. Within the ecological requirements branch we included habitat suitability, climate, nesting materials, and the presence of species with which the translocated birds may hybridize (Andrewartha and Birch, 1954; Lack, 1954; Rhymer and Simberloff, 1996). Habitat suitability was further broken down into the area of suitable vegetation, the degree of habitat fragmentation, and the presence of food items within the vegetated areas. Climate consisted of temperature, rainfall, and the frequency of catastrophes.

The second model branch addressed the impacts that translocated species might have on other native threatened and endangered populations (Gibbons et al., 2000; Johnson and Sattersfield, 1990; van der Geer et al., 2010). An island was considered an unsuitable release site if the translocated bird was likely to impact other native species. The literature was used to pinpoint native taxa upon which translocated species are likely to prey, or native

species with which it might compete. Endangered species within these taxa were then identified using the IUCN red list. The third model branch encompassed anthropogenic threats to translocated species, including introduced predators, competitor species, and diseases (Wolf et al., 1998), which can disproportionately impact island fauna (Whittaker and Fernández-Palacios, 2007). Global climate change and associated changes in sea level were also included as they have the potential to severely impact and inundate habitat on islands (Mimura, 1999). The final model branch incorporated factors needed for the operational support of translocation and management programs (Wolf et al., 1998, 1996). Support included transportation infrastructure for release animals, program personnel, equipment and supplies. Additionally, support from local residents in the form of pre-existing conservation organizations and legislation can facilitate translocation programs and reduce persecution of released birds (IUCN, 1998).

2.2. Customizing inference diagram for the Guam Micronesian kingfisher

Very little was published about habitats used by the GMK before the birds were extirpated from Guam. We thus drew information from the literature, from captive populations, and from related taxa (*T. c. reichenbachii*; Kesler and Haig, 2007a,b,c; and *T. gambieri*; Coulombe et al., 2011; Kesler et al., 2012, in press). Nodes were then added to the general avian translocation inference diagram to customize the model for GMK translocation (Fig. 1). For example nodes associated with the presence of small lizards and insects were added as parent nodes to the food items node reflecting the specific dietary requirements of GMK. Details about node additions for GMK translocation are provided in Appendix A.

2.3. Developing model probability relationships

We used two methods to allocate conditional probabilities for each node in the GMK translocation site selection model (indicated in Fig. 1). The first method used an analysis of islands that are currently inhabited by congeneric kingfishers, and those that are not, to identify correlations between island characteristics and kingfisher occurrence. We used a set of 156 islands in the Society, Marquesas, and Tuamotus archipelagos of French Polynesia and the Cook islands as a training set. *Todiramphus* spp. kingfishers occurred on 11% of the training islands. The same range of ecological characteristics was collected from training islands as from the candidate islands. The EM learning function of Netica™ was used to evaluate the training set of islands and inform conditional probabilities in our model. The function uses an expectation maximization (also known as an expectation maximization or EM) algorithm to estimate maximum likelihood values from incomplete data (less than 4% of values for data input nodes were missing) (Dempster et al., 1977). We also used the literature as a second method for allocating conditional probabilities. We first built a qualitative rationale for the importance of each factor using citations from the literature (Appendix A), and then translated this into a quantitative relationship between the factors (Appendix B Tables A.4–A.16).

2.4. Model assessment

We used two methods to evaluate translocation site selection model performance. Model robustness was assessed with sensitivity analysis (Lui and Chen, 2006), which determines how the model output (*Island suitability node*) is affected by state changes at each of the input nodes. Sensitivity analysis measures how influential each node is in determining island suitability for assisted colonization. We measured sensitivity using mutual information, which calculates the amount of information in one node that is provided

by another. When one node heavily influences another, a high mutual information value results, nodes with high mutual information values with the final output node therefore have large influence on model outcome. The program Netica automatically calculated mutual information values. We then ranked the effects of each node on the outcome node, which represented the predicted island suitability for hosting a translocated population of GMK. Ordered rankings from the sensitivity analysis were then compared to conditional probability tables (Appendix B) derived from the literature (Appendix A) and to opinions provided by an expert panel (Appendix D). The expert panel was comprised of conservation biologists, captive husbandry experts, US Fish and Wildlife Service staff from the GMK recovery group (Micronesian Kingfisher Recovery Committee Meeting, 2000, Honolulu), and staff from captive breeding facilities housing the birds (see acknowledgments). The panel was asked to rate the importance, on a scale of one to ten, of each node for determining an island's suitability for GMK translocation. Rationales for node inclusions were also provided to panelists. Sensitivity analysis rankings were then qualitatively compared to expert panel ratings.

We presented the model with data reflecting our best estimate of conditions on Guam prior to the introduction of the brown tree snake, and when the GMK population was stable in the wild, to evaluate model performance (Beck and Savidge, 1990; Savidge, 1987, 1984; US Fish and Wildlife Service, 2004). We predicted that if the model was performing well, the historic conditions on Guam would be identified as a suitable site for GMK.

2.5. Collection and synthesis of island data

We used only political affiliates of the United States as candidate translocation islands. These included islands in the Commonwealth of the Northern Mariana Islands, the Federated States of Micronesia, Republic of Palau, American Samoa, Samoa, the Republic of the Marshall Islands, Palmyra Atoll, Wake Island, and Johnston Atoll. Within each region, islands were identified using numerous sources including databases, maps, and systematic searches on geographic information systems (GIS; Arc GIS 9.3, ESRI, Redlands California; Google Earth, Google, Inc., Mountain View, CA). We excluded islands smaller than 1 km², because of their inability to support a large enough population of kingfishers to remain viable. We gathered the characteristics of each island from the literature, online searches, and government websites (detailed in Appendix C Table A.25). Fields with missing data were left empty with the exception of presence/absence of cats and rats, which are widespread throughout the Pacific and predicted to be on all islands where eradications have not occurred (Loope et al., 2001).

2.6. Potential model outcomes

We defined five categories to encompass the range classifications that might be applied to islands under consideration for a translocation. The *preferred islands* category was defined by all the characteristics that were considered to be optimal for the persistence of a translocated population of GMK (Appendix A). The *very suitable* category was defined by preferred ecological characteristics, but some of the political or logistical features were in a less than ideal state. The *suitable with management* category was defined by very high, high or moderately suitable ecological characteristics, with very low, low or moderate anthropological threats (e.g., presence of predators), and therefore some management would be required. The category *suitable with extensive management* consisted of islands with high anthropological threats and therefore required substantial predator management. The final category consisted of *unsuitable* islands and included characteristics that met few of the ecological requirements to support a

GMK population, islands with other kingfisher species, or those with threatened species likely to be impacted by a translocated population of GMK.

2.7. Evaluation of islands by model

Island information was presented to the model, which used the conditional probability tables to calculate whether each island was most likely to be categorized as preferred for translocation, very suitable for translocation, suitable with management, suitable with extensive management, or unsuitable for translocation. The model predicted the probability that each island should fall into each class, so results included five probabilities for each island.

We also divided the analysis into five potential recovery strategies, which were based on island size and the mean territory size of a Micronesian kingfisher (8.1 ha; Kesler and Haig, 2007c). Predicted GMK population sizes were estimated by dividing the area of high quality habitat on each island by mean territory size (8.1 ha), and by dividing the area of suitable but lower quality habitat by territories that were 20% larger (9.72 ha). We assumed that a pair of birds inhabited each territory. Islands were grouped based on the size of the population they could support; those with a potential population of >2000 would support a full recovery (US Fish and Wildlife Service, 2004); those supporting a smaller recovery population of 1000–2000 individuals; and islands supporting a minimum number for the maintenance of genetic diversity of 500–1000 individuals (Soulé, 1980). Additionally, we evaluated islands with enough habitat to support temporary management populations of 200–500 kingfishers, and islands with habitat to support 100–200 birds.

3. Results

We assessed 239 islands for their suitability to host a translocated GMK population. No islands fell into the preferred or very suitable classes, and the bulk were classified as unsuitable (Table 1). The model identified five release candidate islands in the Federated States of Micronesia as suitable with management or suitable with extensive management. The islands were Yap, Kosrae, Weno, Fefan, and Faichuk (Table 1).

Sensitivity analysis (Table 2) indicated that the way the model classified island suitability was most influenced by the same factors identified by the literature (Appendix A) and the expert panel (Appendix D) as being key to the establishment and persistence of a population of GMK. Impacts on native species, presence of other kingfisher species, the area with suitable vegetation, and the presence of brown tree snakes had the highest sensitivity values, and they were also ranked by the panel as being among the factors most likely to influence translocation success (Appendix D Fig. A.26). The panel also included the presence of rats, small lizards, insects, and temperature to be among the top 8 most important factors. These other four factors did not rate highly in the sensitivity analysis, however, there was little variation in the values across the candidate regions. All islands have insects, small lizards, tropical temperatures, and few are rat-free, so these nodes had little impact on model outcome. Sensitivity analysis also indicated that ecological factors exerted greater influence on model outcome than operational support. Finally, the model ranked an island characterized by the conditions on Guam prior to the introduction of brown tree snakes as being suitable with management for hosting a population of GMK.

4. Discussion and conclusions

The Bayesian network model of Pacific island bird translocations efficiently and effectively assessed 239 islands upon which a translocated population GMK could be established. The island

characteristics identified in the sensitivity analysis as having the most influence on island suitability classification by the model were the same characteristics that were ranked as being most important to GMK population establishment by the expert panel. Further, the model correctly determined that the ecological conditions on Guam prior to the introduction of brown tree snakes were generally suitable for the kingfishers. However, the model ranked Guam as suitable with management, rather than preferred or very suitable, because Guam already had been impacted by humans and introduced species prior to the introduction of the brown tree snake (Savidge, 1987). Together, results, expert opinions, sensitivity analyses and the simulated Guam validation indicated that the model provided a useful evaluation of potential GMK translocation sites.

Islands that were ranked by the model as being suitable for establishing a population of GMK had several characteristics that set them apart from the unsuitable islands. Model input data showed islands identified as potential release sites were larger and they had lower levels of habitat fragmentation. Larger islands also host larger human populations and the associated infrastructure that could benefit a release. Indian mynas (*Acridotheres tristis*), black drongoes (*Dicrurus macrocerus*) and other kingfisher species (*Todiramphus* spp.) were absent from the suitable islands, but all islands were assumed to have populations of *Rattus* spp. and cats.

Program Netica's ability to extract information from the training island set provided a straightforward method for populating conditional probability tables, which greatly enhanced model utility. However, caution should be used to ensure that the training dataset captures key species-environment interactions. Relationships defined with training data are purely correlative, and they can thus incorporate spurious relationships, which in turn influence model performance. By using training data, the importance of habitat type, habitat area, and fragmentation were quantitatively incorporated into the model. These same habitat features identified by the training data are well documented in the literature for their influence on population establishment and persistence (Andrén, 1994; Bender et al., 1998; Kesler et al., 2012). The conditional probabilities derived from the training dataset indicated that kingfisher population persistence is only likely to be high if an island had enough habitat to sustain more than 200 individuals. This value is much smaller than the estimated historical population on Guam (13,400–6500; Laws and Kesler, in preparation), the population size set as the recovery goal ($n = 1000$; US Fish and Wildlife Service, 2004), and the number considered sufficient to prevent serious losses of genetic diversity over time (500; Soulé, 1987). However, an assisted colonization population of 200 birds might be large enough to be robust against environmental and demographic stochasticity, and inbreeding depression, for a short time (Soulé, 1987). Further, some questioned whether genetic factors affect island populations in the same way that continental species are impacted (Brook et al., 2006; Jamieson, 2007), so a 200 bird population may indeed be robust in the long term as well. Ecological relationships captured by the kingfisher training dataset corresponded well with literature.

The Bayesian network framework integrated political, infrastructure, and ecological factors into a single model. There are risks associated with releasing a species into an assisted colonization site, and those risks were incorporated into our model. The model automatically excluded from consideration islands with other kingfishers, and those with species that might be impacted by a release population. Logistical and political factors are often considered in a process separate from the evaluation of biological features when designing conservation strategies (Wolf et al., 1996). However, the century-long conservation experience of many nations indicates that policy can be key to biodiversity preservation (Possingham and Shea, 1999; Rudd, 2011). Our site visits to Yap and

Table 1

Suitability of Pacific islands under consideration for the establishment of a wild population of Guam Micronesian kingfishers (GMK). Predicted GMK population sizes were estimated by dividing the area of high quality habitat on the island by mean territory size (8.1 ha), and by dividing the area of suitable but lower quality habitat by territories that were 20% larger (9.72 ha), and by assuming that pairs of birds inhabited each territory. Probabilities for preferable island category and very suitable category were all <0.01 and were therefore not shown.

Estimated GMK population size	Island (Country)	Probability of suitability		
		Suitable with management	Suitable with extensive management	Unsuitable
2000+	Kosrae (FSM)	0.74	<0.01	0.26
	Savai'i (Samoa)	0.00	0.00	1.00
	Upolu (Samoa)	0.00	0.00	1.00
	Pohnpei (FSM)	0.00	0.00	1.00
	Guam (CNMI)	0.00	0.00	1.00
	Tutuila (US AS)	0.00	0.00	1.00
1000–1999	Yap (FSM)	0.74	<0.00	0.26
	Saipan (FSM)	0.00	0.00	1.00
	Tinian (CNMI)	0.00	0.00	1.00
	Rota (CNMI)	0.00	0.00	1.00
	Agrihan (CNMI)	0.00	0.00	1.00
500–999	Tau (US AS)	0.00	0.00	1.00
	Faichuk (FSM)	0.00	0.74	0.26
200–299	OfuOlosega (US AS)	0.00	0.00	1.00
	Weno (FSM)	0.74	<0.01	0.26
100–199	Pagan (CMNI)	0.00	0.00	1.00
	Fefan (FSM)	0.00	0.74	0.26

Federated States of Micronesia (FSM), Commonwealth of the Northern Mariana Islands (CNMI), American Samoa United States of America (US AS).

Table 2

Results from sensitivity analysis showing the effect of nodes on predicted island suitability for establishing a population of the Guam Micronesian kingfisher. Nodes are ordered from greatest effect to least effect. Mutual information values represent the effect of each node on model outcome.

Node	Mutual information
Kingfisher species	0.01938
Impacts on native species	0.01938
Available area of suitable vegetation	0.01104
Brown tree snake	0.00839
Island height	0.00376
West Nile virus	0.00127
Habitat fragmentation	0.00099
Nesting materials	0.00077
Airport	0.00061
Rats	0.00037
NGO's	0.00035
Protected areas present	0.00035
Small lizards	0.00031
Roads and ground transport	0.00028
Black drongoes	0.00015
Indian mynas	0.00015
Cats	0.00001
Monitor lizards	0.00001
Frequency of catastrophes	<0.00001
Insects	<0.00001
Rainfall	<0.00001
Temperature	<0.00001

Kosrae, which occurred after modeling was complete, emphasized the extreme role that local infrastructure and non-governmental conservation groups can play in conservation planning (Laws and Kesler, 2011). Visits revealed that conditions on the islands of Yap, Kosrae, and Faichuk were well represented by the input data. However, Fefan and Weno were unlikely to be suitable locations because of degraded habitats and a lack of political support that was encountered during site visits (Laws and Kesler, 2011). We believe that limited island-specific information led to the discrepancy between model classifications and determinations based on site visits. Further, the experience emphasized the paramount role of candidate data, and of conducting site visits for verification.

A lack of information hindered composition of the Bayesian network site selection model. Identifying island characteristics likely

to impact GMK translocation success was relatively straightforward, but quantifying the effects of those factors was challenging when conditional probabilities could not be drawn from the training data. Similarly, information on candidate islands was limited and often restricted to the presence or absence of features, rather than measures of density or influence. Therefore it is important to evaluate the information available before constructing a model, and to determine if sufficient site information and species natural history exists before proceeding. The literature provides some guidance, but general information on the factors influencing translocation success is largely missing (Seddon et al., 2007). The large margin of uncertainty surrounding the impacts of climate change, particularly in the Pacific region, similarly limited our ability to incorporate climate change into the model.

With the continual spread of invasive species, and habitat alteration from development and climate change, an efficient method is needed to assess management options for multiple species. We feel that the Bayesian network modeling approach to translocation site selection provides one option for reintroduction or assisted colonization site selection. Our generalized model can be applied to suites of imperiled avian species in the Pacific region and it can be customized to incorporate specialized ecological, political, infrastructure requirements. Modeling tools cannot replace common sense or local knowledge when selecting translocation sites, but models can be useful for narrowing candidate release sites to a manageable number of options.

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Appendix A. Supplementary material

Supplementary data associated with this article can be found, in the online version, at <http://dx.doi.org/10.1016/j.biocon.2012.05.016>.

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