

# Sex dependent spatially explicit stochastic dispersal modeling as a framework for the study of jaguar conservation and management in South America



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## ABSTRACT

The jaguar (*Panthera onca*) inhabits most of the lowlands (<2000 m) of central and South America in small and numerous fragmented populations. This species now occupies only 50% of its historic range and is included in IUCN red list. Current conservation and management plans rely on the identification and preservation of corridors and potential areas for species dispersion that provide gene flow. Over the last decade, expert-based knowledge consolidation and computational modeling complemented with radio-telemetry and camera-trapping analysis defined suitable areas for jaguar long-term survival and corridors for preserving jaguar connectivity. However, none of these static models incorporate jaguar population dynamics and assume that current population distribution is at steady state equilibrium. Here, we analyze jaguar metapopulation dynamics with a spatially explicit stochastic dispersal model to predict jaguar population distribution and density at a continental level. We also incorporate other biological features in the model such as gender differences regarding movement patterns and include the effect of human–jaguar conflict. This dynamic model provides a good framework for jaguar conservation analysis by providing new insights into jaguar migration and species viability.

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## 1. Introduction

The jaguar (*Panthera onca*) is the largest neotropical felid (Kitchener, 1991), and is considered 'near threatened' by the IUCN red list (IUCN, 2013). It now occupies only around 50% of its historic range, which covered the southern United States throughout the Argentinean Patagonia (Swank and Teer, 1989). Their major threats are habitat loss due to high deforestation rates, forest fragmentation, retaliation from attacks on livestock, and hunting of its prey base (Sanderson, 2002; Zeller, 2007).

Large carnivores such as the jaguar are keystone species that maintain the structure of an ecological community in diversely forested habitats and protecting biodiversity (Berger et al., 2001; Terborgh et al., 2001). Jaguars are, however, relevant not only ecologically but also culturally as they have served as a cultural icon for many indigenous American people (Benson, 1998; Cristancho and Vining, 2004; Reichel-Dolmatoff., 1975).

Conservation and management plans are highly dependent on the ability to identify and preserve corridors and potential areas for species dispersion, which provide gene flow, genetic variability and avoidance of endogamy. These are highly important properties because of the high historical reported levels of gene flow and the absence of deep geographical subdivisions throughout the species range (Ruiz-Garcia et al., 2006; Eizirik et al., 2001).

Over the last decade, expert-based knowledge consolidation and computational modeling have been complementing radio-telemetry and camera-trapping analysis in the field. These parallel theoretical approaches have been a useful tool for the definition of suitable areas for the jaguar's long-term survival and have served as a guide in identifying priority areas for preserving its connectivity. Sanderson et al. (2002) presented a first approach to metapopulation-based conservation analysis, using an expert-based eco-geographic framework for setting the jaguar priority areas. Their goal was to find the most important sites for ecologically distinct populations using the jaguar's geographic regions as a geographical proxy. This study was later extended by Zeller (2007), who added data from the 2006 survey on Jaguars in the New Millennium meeting. The study showed that healthy populations of jaguars still existed throughout their range, but that many of them

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were in decline due to anthropogenic threats. However, these techniques were still prone to errors due to the subjective nature of expert-based priority-setting systems.

More recently, computational models were included in the analysis. Rabinowitz and Zeller (2010) worked on jaguar connectivity and used a least-cost model based on a spatially explicit permeability matrix that reflected how costly it would be for a jaguar to cross each cell with a set of landscape characteristics. The model determined the shortest weighted distance between two patches with an accumulated cost algorithm. Subsequently, Torres et al. (2012) estimated the potential geographical distribution of the jaguar using different species distribution modeling (SDM) methods based on occurrence records and environmental data.

However, none of these static models incorporated jaguar population dynamics and assumed that current population distribution was at steady state equilibrium. For this reason, connectivity analyses did not generate information about the sustainability of proposed corridors and about whether corridor characteristics were ecologically optimal for an individual to cross. Torres's SDM models ignored that a species may not occur in a potentially suitable habitat because there are barriers to species dispersion, or because the species has not yet arrived to the area. Similarly, the analysis did not include the possibility of a species occurring in areas in which they are not well suited and may not maintain viable populations in the long term (Fitzpatrick et al., 2007). Hence, this static approach could cause under and over-prediction of the potential range estimations of a species.

Some dynamic models have been previously developed for felid species. Revilla and Wiengand (2008) analyzed interpatch processes in a spatially structured population of Iberian lynx, by using an individual-based spatially explicit model. Recently, Bernal et al. (2011) applied a reaction-diffusion model in two dimensions with logistic growth for jaguars, to analyze the sustainability of pre-identified suitable areas and possible corridors in Colombia. Results supported the hypothesis that connectivity between populations from Central and South America is highly threatened. However, model boundary conditions ignored dispersion from other countries, and therefore the estimations of population density were therefore biased and probably too low. Also, important biological features such as sex-biased dispersion were not included in the model.

Here, we present a similar approach to analyze the jaguar's population distribution, density and connectivity at a continental level to complement previous studies on jaguar conservation. Our

approach incorporates population dynamics that could be useful for conducting meta-population analyses in a more realistic manner. We simulate jaguar dispersion and connectivity in 54 Jaguar Conservation Units (JCU) in South America, which represent areas previously identified as important for long-term survival (Zeller, 2007). For this, we use a spatially explicit stochastic dispersal model based on reaction-diffusion equations.

We incorporate other biological features in the model such as gender differences regarding movement patterns. The effect of the human–jaguar conflict is also included, as jaguar hunting is still a major threat, despite laws prohibiting it. The spatially explicit stochastic dispersal model is implemented in Matlab® and is based on a permeability matrix for South America that includes habitat characteristics related to the jaguar's movement behavior.

## 2. Methods

Fig. 1 shows a summary of the subsections detailed below.

### 2.1. Study area

Our area of study extended from northern Panamá to northern Argentina, including information from Argentina, Bolivia, Brazil, Colombia, Ecuador, French Guiana, Guyana, Panamá, Paraguay, Peru, Suriname and Venezuela (see Fig. 2). Jaguars use an incredible vast array of habitat types and range over a large geographical area (Swank and Teer, 1989; Sanderson et al., 2002; Zeller, 2007; Rabinowitz and Zeller, 2010). The studied habitats varied from tropical moist and dry forest to shrub lands, grasslands and savannas. Areas not used by jaguars such as glaciers and bare areas were also included and subsequently identified as barriers in permeability analysis. Other habitat characteristics that are correlated with human activities affecting jaguars were also included. In general, layers (see Table 1) were geo-processed using ArcGIS v10 software and resampled to a 30 km<sup>2</sup> grid.

Within the study area, 51 important areas for jaguar conservation known as Jaguar Conservation Units (JCUs) were identified, based on a geographic atlas of jaguar data created by a panel of experts panel (Zeller, 2007) (see Fig. 2). These areas were seen as possibly having an adequate habitat with a stable diverse prey base or sustainable jaguar populations of at least 50 breeding individuals.

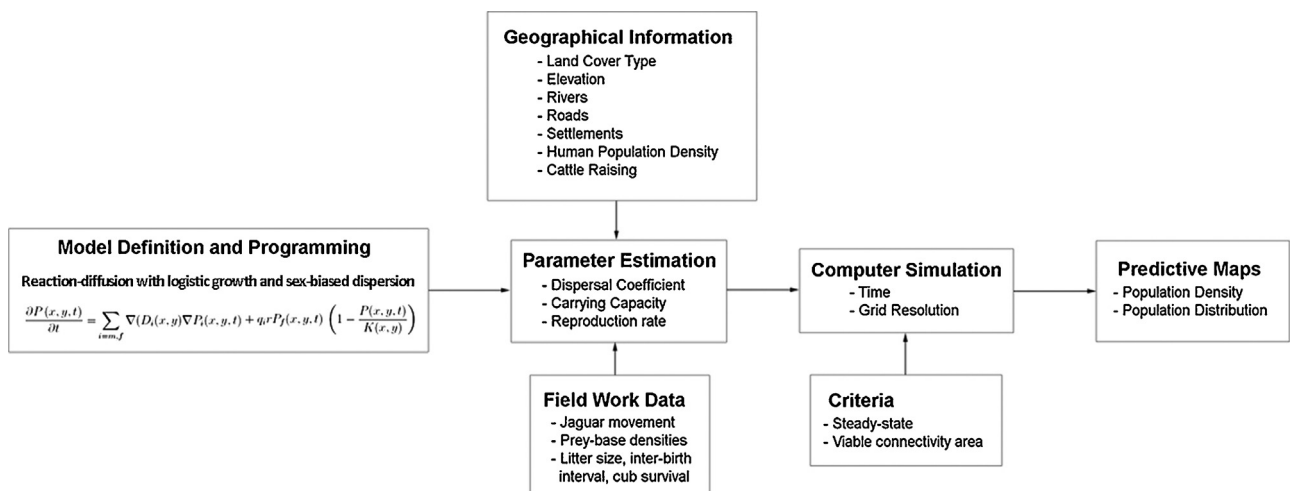


Fig. 1. Conceptual diagram of the model implemented.

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