

Universidade Federal de Goiás



Instituto de Ciências Biológicas

Programa de Pós-graduação em Ecologia e Evolução

Tese de Doutorado

Efeitos da perda e fragmentação de habitat sobre felinos: ecologia e genética de paisagem como ferramentas para a conservação

Marina Zanin Gregorini

Orientador: Prof. Dr. Daniel de Brito C. da Silva

GOIÂNIA - GO

Março de 2014





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Marina Zanin Gregorini

Tese apresentada à Universidade Federal de Goiás, como parte das exigências do Programa de Pósgraduação em Ecologia e Evolução para obtenção do título de doutora.

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Ausência

Por muito tempo achei que a ausência é falta. E lastimava, ignorante, a falta. Hoje não a lastimo. Não há falta na ausência. A ausência é um estar em mim. E sinto-a, branca, tão pegada, aconchegada nos meus braços, que rio e danço e invento exclamações alegres, porque a ausência, essa ausência assimilada, ninguém a rouba mais de mim.

Desenho: Natália Gregorini

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v

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INTRODUÇÃO GERAL

O estudo da perda e fragmentação do habitat

A rápida conversão de hábitats naturais consiste na principal ameaça à biodiversidade da atualidade, afetando ecossistemas em todo o globo e espécies de todos os taxa (Foley et al. 2005). A substituição de habitats nativos por cobertura antrópica tem acarretado uma perda substancial de espécies (Foley et al. 2005), alcançando proporções somente observadas em eventos de extinção em massa (Johnson 2002). A perda e a fragmentação são processos inerentes da conversão do habitat (Lindenmayer & Fischer 2007; Ewers & Didham 2006; Fischer & Lindenmayer 2007), levando à transformação de manchas de habitat contínuos em fragmentos menores e isolados. Esses processos ocorrem principalmente em escala de paisagem (Fahrig 2003) e geram heterogeneidade espacial, composicional e estrutural no ambiente (Bennett et al. 2006).

Devido à importância e complexidade do tema, tem sido produzido um vasto conhecimento acerca dos efeitos diretos e indiretos das alterações antrópicas sobre a biodiversidade. Tais estudos possuem diferentes enfoques, que podem ser: abordagens experimentais (Mortelliti et al. 2011) ou teóricas (Reed 2004); respostas de espécies (Tian et al. 2011) ou táxons (Smith et al. 2011); padrões estruturais (Rodríguez et al. 2012) e relativos à escala (Hanski 2013); revisões e meta-análises sobre aspectos metodológicos (Debinski & Holt 2000; McGarigal & Cushman 2002), conceituais (Andrén 1994; Fahrig 2003; Fischer & Lindenmayer 2007) e padrões ecológicos (Jenkins et al. 2007; Watling et al. 2011).

A base conceitual e teórica dos efeitos da perda e fragmentação de hábitats surgiu, em um primeiro momento, a partir das aplicações da Teoria de Equilíbrio em Biogeografia de Ilhas (TBI) (MacArthur & Wilson 1967) no âmbito da Biologia da Conservação. Nesse contexto, compreendeu-se que fragmentos de habitat poderiam ser considerados como "ilhas" circundadas por um "oceano" de matriz inóspita. Assim, a dinâmica de colonização e extinção de espécies em comunidades terrestres também seriam explicadas pelos efeitos da área e isolamento previstos pela TBI (Haila 2002; MacArthur & Wilson 1967).

Poucos anos após a publicação de MacArthur e Wilson, Levins propôs um modelo simples para a compreensão da dinâmica de uma única espécie dentro de paisagens fragmentadas (Levins 1970). A partir do trabalho de Levins, surge a teoria de Metapopulação, que se assemelha as predições gerais da TBI, onde a área e o isolamento são os principais fatores responsáveis pela dinâmica de ocupação de fragmentos em uma paisagem (Hanski & Gilpin 1991; Hanski 1998). O desenvolvimento dessa teoria e dos modelos propostos por ela consistiu em outro marco para a evolução da compreensão dos efeitos da perda e fragmentação de habitat sobre as espécies (Hanski & Gilpin 1991; Hanski 2001; Hanski 2005).

Entretanto, ainda nos anos 70 foi observado que o arcabouço teórico e metodológico da *Teoria de Biogeografia de Ilhas* e *Metapopulações* eram insuficientes para responder questões relativas à perda e fragmentação do habitat. Assim, entre as décadas de 70 e 80, a Ecologia de Paisagem ganhou destaque por sua abordagem no estudo das causas e consequências da heterogeneidade espacial e suas variações em diferentes escalas (Turner 2005; Turner 1989). A Ecologia de Paisagem permitiu um grande avanço na compreensão dos efeitos da perda e fragmentação de hábitat sobre o ambiente, uma vez que as atividades antrópicas relacionadas a conversão de hábitats consistem no principal fator de modificação na estrutura e composição das paisagens (Turner 2005; Turner 1989).

Posteriormente, outras disciplinas surgiram com o intuito de explorar novos níveis de resposta dos efeitos da perda e fragmentação do habitat; nesse contexto, a Genética de Paisagem também se tornou uma poderosa abordagem de estudo, especialmente pelo avanço dos marcadores genéticos (Holderegger & Wagner 2008). A Genética de Paisagem é uma disciplina recente que combina ecologia de paisagem e genética de populações por meio de uma abordagem que possibilita a compreensão de como as características da paisagem afetam processos microevolutivos (Holderegger & Wagner 2008; Manel et al. 2003). Dessa forma, a genética de paisagem permite um melhor entendimento dos efeitos das mudanças da paisagem, simultaneamente, sobre as respostas ecológicas e evolutivas (Wagner & Fortin 2013).

Como exposto, as consequências da perda e fragmentação do habitat sobre a biodiversidade pode ser estudado por meio de várias disciplinas e à luz de diferentes teorias ecológicas ou evolutivas. Em um contexto conservacionista, o uso de diferentes abordagens é a melhor estratégia para dimensionar o real efeito da perda e fragmentação sobre as espécies e/ou paisagens. Nesse contexto, essa tese usa o arcabouço teórico e metodológico da ecologia e genética de paisagem para estudar o efeito da perda e fragmentação do hábitat sobre as espécies.

Susceptibilidade à perda e fragmentação do habitat: escolha do grupo focal

Alguns trabalhos têm destinado esforços em identificar os fatores de risco de extinção das espécies (Cardillo et al. 2005; Cardillo & Bromham 2008; Machado & Loyola 2013), investigando se espécies ameaçadas são vítimas de 'maus genes ou má sorte' (Cardillo et al. 2005). A fragmentação aparece em todos os trabalhos como o principal ameaça, independentemente do táxon (Cardillo et al. 2005; Cardillo & Bromham 2008; Machado & Loyola 2013). No entanto, existem atributos intrínsecos às características bionômicas e traços ecológicos das espécies que retro-alimentam o risco de extinção

(Cardillo et al. 2005; Cardillo & Bromham 2008). Dentre eles tais atributos podemos citar: especialização quanto ao uso de hábitats, área de vida, capacidade de dispersão, tamanho corporal, densidade, tamanho da distribuição histórica e atual (Fischer & Lindenmayer 2007). A combinação dos fatores ambientais e biológicos em uma paisagem fragmentada pode acarretar no declínio da população e, em níveis mais drásticos, até mesmo em sua extinção por ação de eventos demográficos, genéticos ou estocásticos (Fischer & Lindenmayer 2007).

Felinos como objeto de estudo

Essa tese teve como grupo focal os felinos (Carnivora: Felidae), grupo composto por 36 espécies selvagens, separados filogeneticamente em 12 gêneros. Os felinos podem ser considerado uma das Famílias mais bem sucedidas da Ordem dos Carnívoros, uma vez que possuem uma ampla distribuição (Figura 1), habitando todos os continentes exceto a Antártica (IUCN 2013). Os felinos são mamíferos de hábito alimentar essencialmente carnívoro, frequentemente topo de cadeia alimentar (Wilson & Reeder 2005). Mesmo sendo composto por poucas espécies, o grupo possui grande heterogeneidade de traços ecológicos e história de vida, pois possuem espécies sociais e solitárias, de tamanho corpóreo menor que 1.5 kg a maior que 150 kg, áreas de vida que variam de pouco mais que um quilômetro à quase 300 km², distribuições restritas à continentais, especialistas e generalistas quanto ao habitat e dieta (Wilson & Reeder 2005).

Apesar dessa heterogeneidade, os felinos podem ser generalizados como espécies de altos requerimentos ecológicos, o que os tornam sensíveis às alterações antrópicas em seus ambientes naturais (Cardillo et al., 2005). Morrison et al. (2007) lista cinco felinos (*Acinonyx jubatus, Panthera leo, Panthera pardus, Panthera onca e Puma concolor*) entre as 20 espécies de grandes mamíferos com maior redução na distribuição devido aos impactos antrópicos, demonstrando que esse é um dos grupos de mamíferos mais ameaçados pela conversão do hábitat. Atualmente, todos os felinos estão ameaçados pela perda e fragmentação de hábitats e 16 deles estão classificados sobre algum *status* de ameaça devido primariamente a esses processos (IUCN 2013). Essa situação tende a ser agravada nos próximos anos, pois as regiões de grande diversidade de felinos estão inseridas em países economicamente emergentes que compõem o G-20 de países em desenvolvimento e que apresentam hoje as maiores taxas de conversão habitat (Hugueney 2004; Figura 1). Esse panorama geral revela a urgência em compreender os efeitos da perda e fragmentação do habitat sobre os felinos, motivando e fundamentando sua escolha como grupo focal desse trabalho.

Conteúdo do trabalho

Nosso trabalho teve como objetivo investigar o efeito da perda e fragmentação de habitat sobre os felinos (Carnivora: Felidae), testando hipóteses relacionadas ao tema, bem como fazendo inferências para a conservação. Apresentamos aqui três capítulos no formato de artigo científico e uma breve discussão geral, que consiste na compreensão geral proveniente dos resultados dos três primeiros.

Iniciamos essa tese com uma revisão sistemática e quantitativa da literatura sobre o efeito da perda e fragmentação do habitat sobre felinos. Esse trabalho consistiu no passo inicial dessa tese, pois permitiu identificar as lacunas de conhecimento, tendências gerais e metodologias eficientes a serem aplicadas nas outras etapas do trabalho. No entanto, nossa revisão se estende além da avaliação do "estado da arte", pois testamos também hipóteses relativas a alocação do esforço de pesquisa.



Figura 1. Riqueza de espécies de felinos ao longo do globo (cores quentes denotam uma maior riqueza). Rachurado, destacamos os países que compõem o G-20 de países em desenvolvimento, que constituem em 20 países emergentes de grande desenvolvimento agrícola (Hugueney 2004).

Já no segundo capítulo, avaliamos os efeitos da perda e fragmentação do habitat para uma única espécie, a onça-pintada (*Panthera onca*). Nesse estudo, investigamos o efeito sinergético e isolado da perda e fragmentação de hábitat sobre a probabilidade de sobrevivência da espécie. Para tal, utilizamos uma abordagem teórica que fez uso de simulações de dinâmica populacional em paisagens reais e hipotéticas, que nos permitiu também estimar limiares de perda e fragmentação de habitat para as populações.

O terceiro capítulo utiliza uma abordagem mais recente na pesquisa do efeito da perda e fragmentação de habitat, que consiste na genética de paisagem. Nesse trabalho, avaliamos o efeito da complexidade da paisagem na estrutura genética de duas espécies, a onça-pintada e a onça-parda (*Puma concolor*), testando hipóteses sobre o efeito da capacidade de dispersão no fluxo gênico.

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CAPÍTULO 1

Esse artigo segue o padrão de formatação da revista Oryx, na qual foi aceito para publicação (Anexo 1).

1	What we (don't) know about the effects of habitat loss and fragmentation on
2	felines
3	
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17 What we (don't) know about the effects of habitat loss and fragmentation on

18 felines

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20 HLF effects on felines

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22 **1.** Abstract

23 Habitat loss and fragmentation (HLF) are among the main threats to biodiversity. However, some taxa are more susceptible to HLF due to intrinsic ecological traits, 24 leading to local extinctions and range contractions. The goal of this study was to 25 26 compile the current knowledge of HLF effects on felines, by describing trends, investigating research effort allocation, and identifying knowledge gaps. We searched 27 28 the scientific literature in scientific databases and classified the articles according to 29 conceptual and methodological approaches. We reviewed a total of 162 articles and observed that scientific knowledge is unevenly distributed among important topics and 30 species. Habitat suitability and patch-landscape configuration are the most studied 31 topics, comprising 56% of studies. The allocation of research effort is unrelated to 32 variables that describe conservation priorities, such as threat status and habitat 33 34 availability within the species range. However, it is related to body size, suggesting that charismatic attributes influence the choice of target species. Moreover, the countries 35 with lower research effort are also those with lower economic development, making 36 North America and Europe the centers of knowledge generation on HLF studies on 37 felines. The responses of sixteen felines to HLF remain unknown. Among these, 38 Leopardus jacobita, Pardofelis badia, Prionailurus planiceps, and Prionailurus 39 viverrinus have the highest urgency of research because they are threatened with 40 extinction. We suggest that theoretical approaches, through modeling exercises, as a 41

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- 42 first step to decrease the lack of information about HLF effects on felines, especially
- 43 those species with larger knowledge gaps.
- 44
- 45 Keywords: Felidae, fragmentation, gap analysis, habitat loss, landscape,
- 46 metapopulation

47 **2. Introduction**

48 Habitat loss and fragmentation are rising at an alarming rate due to the growth of human activities that convert natural landscapes into human-modified mosaics (Lord & 49 Norton, 1990; Ritters et al., 2000). Habitat loss and fragmentation (HLF) reduce 50 wildlife-adequate habitat and create dispersion barriers; they affect the size and spatial 51 configuration of fragments (Fahrig, 1997; Ewers & Didham, 2006) from the local (Lord 52 53 & Norton, 1990) to the global scale (Ritters et al., 2000). Not surprisingly, they are listed as the main threats to biodiversity and have become central issues in conservation 54 biology (Foley et al., 2005). Due to the importance of these issues, many reviews and 55 56 meta-analyses have been published with the objective of clarifying terms (e.g. Andrén 1994, Fahrig 2003, Fischer & Lindenmayer 2007), methodological aspects (Debinski & 57 Holt, 2000; McGarigal & Cushman, 2002), ecological processes (Jenkins et al., 2007; 58 59 Watling et al., 2011), and their effects on target taxa (Mortelliti et al., 2010). Susceptibility to human alteration of the environmental is related to life-history 60 and ecological traits of species (Davidson et al., 2009; Ockinger et al., 2010; Thornton 61 et al., 2011). Therefore, it is expected that certain evolutionary lineages are more 62 vulnerable to HLF than others. Felines (Carnivore: Felidae) are a phylogenetically and 63 ecologically homogeneous taxon composed of 36 wild species (Johnson et al., 2006; 64 Morales & Giannini, 2010). These taxa share traits that potentially make them 65 vulnerable to HLF, such as: high trophic levels, large home ranges, low population 66 densities (Sunquist & Sunquist, 2002), and continued persecution by humans 67 (Woodroffe & Ginsberg, 1998; Inskip & Zimmermann, 2009). Felines are an interesting 68 model to study HLF impacts on wildlife populations due to their high susceptibility to 69 70 such impacts, their key ecological roles within ecosystems, and their charisma.

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71 Our objective was to review the global literature about HLF effects on felines, 72 investigating biases and trends in knowledge. To achieve this goal, our study focuses on three targets. First, we charted the state of knowledge concerning feline HLF studies, 73 74 discussing weak points and potential solutions to correct such weaknesses. Second, we identified the allocation of research effort across species and countries, providing a 75 76 global picture of feline HLF studies; we choose these taxonomic and geopolitical scales 77 because they are the levels for which conservation actions could be planned a later implemented on the ground. In a species-specific context, we expected species with 78 higher conservation priorities (e.g. threatened species) to be better studied, and those 79 80 with high rates of habitat reduction would be studied more extensively. On other hand, charismatic attributes and logistic easiness could be influencing in the choice of target 81 felid species, making large-bodied and widespread species to be more studied. 82 83 Considering the allocation of research effort across countries, we expected that countries with better economic development would have a greater research effort, 84 85 whereas research in less-developed countries would have been led mainly by investigators from developed countries. Finally, we created an index based on our 86 results, which allowed for the ranking of species and required studies according to the 87 88 lack of information associated with them. 89

90 **3.** Methods

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3.1 Trends in the knowledge about HLF effects on felines

We searched the scientific literature for articles that quantify or describe HLF
effects on felines, through a combination of search strings in three scientific publication
databases: ISI Web of Science, Cat Library, and Google Scholar (see Appendix A for a

96 complete list of search keywords). All articles published up to and including November
97 2012 were analyzed and classified according to their conceptual and methodological
98 information. We based this classification in key points previously appointed by
99 Mortelliti et al. 2010 in a review of the state of knowledge to European mammals, but
100 modified for felids necessities.

101 The key points studied were: (1) the attention designated to study HLF effects on 102 felines, which can be expressed through total number of publication, the intention to 103 evaluate directly their effects on felines (which considered those articles with a clear objective centered on the topic and the inclusion of variables that measure such 104 105 processes within a statistical framework), and temporal trends in the publications; (2) taxonomical level of analyses; (3) characteristic of HLF evaluated (habitat reduction or 106 subdivision per se, human buildings as barriers, and climatic changes; see Table 1); (4) 107 108 methodological approach (review, theoretical or empiric; see Table 1); (5) ability to separate habitat loss from fragmentation processes; and (6) sub-discipline studied 109 110 (conservation medicine, demographic viability, genetic viability, habitat selection, 111 landscape genetic, movement ecology, patch-landscape configuration, road ecology, and systematic conservation plan; see Table 1 for definitions of the sub-disciplines). 112 113 Poaching of felines or their prey could have been included as a sub-discipline due to the indirect effects of HLF. However, this topic is more complex and commonly studied in 114 the context of conservation conflicts and should be evaluated in an independent study; 115 so, we decided do not considered the poaching in this study. 116

In order to investigate temporal trends in feline reviewed publications, we divided the number of articles investigating HLF on felines by the total number of articles published each year, assessing the relative growth of knowledge in this area in relation to the advancement of science in general. We used the total number of articles

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indexed in ISI Web of Science in each year as an estimate of the annual total number ofpublications.

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3.2 Allocation of research effort

We investigate whether research effort was allocated across species according to 125 ecological and conservation variables, which were: threat status (IUCN 2011), body size 126 127 (Wilson & Reeder, 2005), range distribution size (IUCN 2011), and suitable habitat 128 within the species range (measured as the absolute area of suitable habitat and the proportion of the range holding suitable habitat). Variables of suitable habitat measure 129 130 different ecological and conservation attributes, since a species could have a large absolute area of remaining habitat, but also a low proportion of suitable habitat within 131 132 the range. The proportion of suitable habitat was calculated as the suitable habitat area 133 inside the range distribution relative to total range size. We considered as suitable habitat types those listed by IUCN (IUCN, 2011), and the total area was calculated from 134 135 available land cover maps (Bontemps et al., 2011).

136 We performed an analysis of covariance (ANCOVA) to valuate if the number of publications is equal among groups of threat status (categorical variables), measuring 137 138 and controlling the effect of the others (continuous variables). The results of ANCOVA clarify about the relation of response variable and each one of descriptive variables; 139 even same one or more descriptive variables are not interacting to predict the response 140 variable (Zar, 2010). Research effort across the countries was measured in two different 141 142 ways: the proportion of felines studied relative to the national feline richness; and the proportion of the range distribution studied. These metrics evaluate different aspects of 143 national research effort; the first represents the knowledge of HLF effects on species 144 while the second may provide information regarding populations that can suffer distinct 145

HLF pressure. We mapped the locations of research article study areas to obtain a
global distribution of the studies. We divided species ranges using a 0.25 decimal
degree grid and selected grid cells that overlapped with study areas, creating a presence
and absence matrix of the studies. Using this matrix, we calculated the number of
species and the area studied in each country; the feline richness and range distribution
area of countries were calculated through range distribution maps (IUCN 2011).

152 We categorized the countries into classes according to their economic development, which were described by the annual Gross National Income per capita -153 GNI (World Bank, 2010). The classes were ≤ 10 , > 10 and ≤ 30 , and > 30 times the 154 income needed to live at the poverty line (\$ 540.5 person/year; Ravallion et al., 2009). 155 We compare the research effort variables to the economic development classes through 156 non-parametric methods. Thus, Kruskal-Wallis was performed to evaluate the mean 157 158 variation among groups and a Nemenyi test was performed to identify the different groups. Nemenyi test is an analog of the Turkey test to non-parametric analysis, which 159 160 does a posteriore comparison of the groups (Zar, 2010).

161 The influence of researchers from developed countries, in other hand, was 162 investigated though the economic power of the paper's authorship. We divided the 163 publication into the economic classes based in the GNI of the country where the study 164 area is located; we evaluated the GNI from the country of the first author and the author 165 from the country with the highest economic power (highest GNI).

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3.3 Gap analysis of HLF knowledge on felines

Gap analysis is a term conventionally used to identify 'gaps' in the protected areas network by classification of biodiversity and its demands (Jennings, 2000), which results in information used to plan conservation priorities. In this study, we adapted the objective of traditional gap analysis to investigate the 'gaps' of knowledge concerning
HLF effects on felines. These results could clarify the information needed for planning
conservation actions.

To that end, we converted the relevant topics to be studied (see below, Figure 3A-P) into an index that ranks species by lack of information. The basic index of Gap Knowledge (GK) consisted of the sum of 'knowledge distance' - the difference between the maximum number of articles for a given issue and the number of articles for species for the same issue. The variables were linearly transformed (varying from zero to one) to have the same weight in the index. Therefore, the index was calculated according the following equation:

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$$GK = \sum_{i=1}^{n} 1 - \left(\frac{x_{ij}}{x_{j \max}}\right)$$
 Equation 1

where *i* are felids species; *j* are the key points. The gap analysis regards only those
articles evaluating directly the effect of HLF on felines. This index rates the gap of
information for each species

To create a more realistic rank of species according their priority to be studied,
we included in this index other items that affect species knowledge and conservation
following equations

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$$GK_{PR} = \left(\sum_{i=1}^{n} 1 - \left(\frac{x_{ij}}{x_{j \max}}\right)\right) * PR$$
 Equation 2

189 $GK_{TS} = \left(\sum_{i=1}^{n} 1 - \left(\frac{x_{ij}}{x_{j\max}}\right)\right) * TS$ Equation 3

190 $GK_{PR/TS} = \left(\sum_{i=1}^{n} 1 - \left(\frac{x_{ij}}{x_{j \max}}\right)\right) * PR * TS$ Equation 4

where *PR* is proportion of species range not studied and *TS* is the threat status of
species. The inclusion of proportion of species range not studied is a way to include the

193	spatial gap of information in the score and, with this, an indirect representation of the
194	regions or populations not studied until now. In the equations, TS assume values
195	hierarchically distributed to IUCN threat status (Least Concern – 0.2; Near Threatened –
196	0.4; Vulnerable – 0.6; Endangered – 0.8; Critically Endangered – 1.0), representing the
197	current species susceptibility to extinction and the urgency of study for the species. The
198	last equation (Equation 4), which considers both the proportion of range studied and the
199	threat status, provide a final rank regarding the knowledge gap on the topic and the
200	urgency of study the species.
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202	4. Results and Discussion
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204	4.1 Trends in the knowledge about HLF effects on felines
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206	4.1.1 Trends in the attention designated to study HLF effects on felines
207	We found a total of 162 published articles concerning HLF on felines
208	(Appendix A). This is a relatively small number, considering the number of feline
209	species, the threat that these processes represent to the taxa, and the charisma of the
210	group. If we analyze the objectives and methodologies of these studies, we observe that
211	the effective number of articles is less than half (Figure 1A), as many of them only
212	provide indirect inferences of these anthropogenic alteration on felines. Consequently,
213	the knowledge about HLF effects on felines is small, even though felids are among the
214	best studied mammal groups (Amori & Gippoliti, 2000).
215	The modest attention given to the topic is also demonstrated by the date of the
215 216	The modest attention given to the topic is also demonstrated by the date of the first publications (Ferreras et al., 1992; Rodríguez & Delibes, 1992), since the

2002). However, the number of publications has grown throughout the years (Figure 2),
showing that researchers have paid more attention on the topic recently, probably due to
its importance to feline conservation.

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4.1.2 Taxonomic level of analysis

Most articles have a single-species approach (Figure 1B); however, the effects of HLF on felines have not been studied using a single species approach for 61% felines (Figure 3A). When that is not the case, the focus group of the research was frequently carnivores (13.9%) or mammals in general (19.6%), and only two studies investigated HLF effects on sympatric felines (e.g. Hunter et al. 2003, Moisés Gallas & Silveira 2011). However, both articles had only an indirect approach of HLF effects and do not direct inferences of its consequences on felines.

Studies considering felines as target species can help elucidate species-specific or taxonomic patterns, which is important given the ecological functions these species perform within ecosystems. Felids are the top predators in many ecosystems (Ritchie & Johnson 2009) and their extirpation may affect community structure through a process known as mesopredator release. Mesopredator release impacts the ecosystem due to the increase of small predator abundance, the decline of prey populations, and the consequent species extinctions (Prugh et al., 2009).

Felines may occupy partially overlapping niches, competing for resources (Caro & Stoner, 2003; Foster et al., 2010); considering that felines are territorial species, they can compete for the habitat available in a landscape. Habitat loss and fragmentation can favor different species according to the predominant matrix type given that the species differ in their environmental plasticity and their ability to use suboptimum habitat. Thus, we could expect that land cover change alters the

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competitive relationship among sympatric felines. It is a relevant topic for felineconservation planning, but this topic remains unexplored (Figure 3B).

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4.1.3 Characteristics of HLF evaluated

Habitat reduction or subdivision effects on species were the themes most often 247 investigated (Figure 1C). Only a few studies addressed exclusively the effects of human 248 infrastructures on felines, and the least studied topic was habitat loss due to climate 249 250 change (Figure 1C). According to the IUCN Red List (IUCN, 2011), HLF affects all 36 wild felines; for 21 of them, it is a primary threat. Currently, climate change does not 251 252 represent a threat to felid species (IUCN, 2011), but studies focusing on the synergies among climate change and habitat loss for felines are scarce (Figure 3C-E), impairing 253 our comprehension of its consequences (Heller & Zavaleta, 2009). 254

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4.1.4 Methodological approach

There is a clear bias for empirical approaches in the reviewed literature (Figure 1D), but the imbalance among theoretical and empirical publications does not constitute a gap. It is possible to generate good data and generalizations about HLF effects on felines by adopting each type of approach, but it would be interesting to have theoretical approaches providing suggestions to be tested in the field (McGarigal & Cushman, 2002). In this way, theoretical and empirical studies could be considered with two parts of investigation process, the first find pattern and process to be tested by the second.

Theoretical studies can permit manipulations through a variety of conditions helping to understand the species response in a large range of human interferences on the landscape, which could be impossible to perform for ethical or logistical reasons due to the obvious difficulties to do field manipulations on rare large-bodied wide-ranging species. In this way, theoretical approaches could have two main functions on HLF
studies with felines, simulations of species responses in a large-range of environmental
conditions and help to plan empirical studies.

271 As example of manipulative approaches in HLF studies with felines, Reed (2004) investigates the HLF effects on population of many species evaluating the 272 importance of dispersal among subpopulation to long term survival of population. 273 Brook et al. (2002) also investigated HLF effects on a set of species, but in an 274 275 inbreeding depression context, which increase the extinction risk. Tian et al. (2011), by the way, used a more robust field data to investigate the HLF effects on long-term 276 277 survival of the Amur tiger. These are the only manipulative studies among the reviewed articles and all are into theoretical approach of population viability. As described, the 278 objectives of these studies were simulates the species responses in different 279 280 environmental conditions; however, no one used the theoretical approach as a way to plan empirical studies as a strategy to better design field work. (Brook et al., 2002; Reed, 281 282 2004; Tian et al., 2011)

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4.1.5 Differentiation of habitat loss from fragmentation

285 To conduct an efficient separation of the processes of habitat loss and fragmentation, landscape scale studies and true replicas are needed (McGarigal & 286 Cushman, 2002); however, most of the studies reviewed were conducted at the local 287 scale. The distinction of habitat loss from fragmentation should support management 288 289 strategies for species (Fischer & Lindenmayer, 2007; Mortelliti et al., 2011), but only one article tackles the differences between such processes (Tian et al., 2011) (Figure 290 291 3F). Of course, it is difficult to define landscape boundaries and true independent replicas in a real world landscape, especially for species with large dispersion ability 292

293 like felines. Theoretical approaches could allow for the differentiation of habitat loss 294 from fragmentation for some species through modeling of hypothetical landscapes. Many articles discuss the use of movement corridors as a mechanism to maintain 295 296 or reestablish population dynamics (e.g. Carroll & Miquelle 2006, Hetherington et al. 2008, Morrison & Boyce 2009), solving or minimizing the fragmentation problem. 297 Corridors might be a coherent conservation strategy for felids due to the difficulty of 298 299 finding large and connected habitat areas, which is needed to felines conservation 300 (Boitani et al., 2011); however, dispersion corridors could have negative consequences to species conservation, making species susceptible to contagious diseases from 301 302 domestic animals and retaliatory hunting due to human-predator-prey conflicts (Chetkiewicz et al., 2006). Among the reviewed articles, only a few were designed to 303 304 actually evaluate corridor function for felid conservation (Figure 1E). We believe this 305 topic needs more attention from the felid conservationist community to determine 306 whether such statements are truly supported by data, elucidating the real effects of 307 corridors and which species might benefit from such a strategy. 308 A set of specific data are essential for designing corridors and evaluating their efficiency, such as dispersal rates of different sexes and ages, considering also different 309 310 spatial and temporal scales. The spatial data necessary to discuss these issues is relatively frequent among the reviewed publications (Figure 1F), but it was adequately 311 explored for only a few species (Figure 3I and also section 4.1.7 for further details 312 concerning the movement ecology sub-discipline). 313 314 Even the correct definition of processes (habitat loss and fragmentation *per se*)

Even the correct definition of processes (habitat loss and fragmentation *per se*)
was found only in a small number of articles, given that 'habitat fragmentation' was
commonly used to represent both processes (Figure 1G). For many years there was a
confusion regarding HLF concepts and nomenclature until Andrén (1994) provided a

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318 review of habitat loss and fragmentation effects and defined the terminology. This lack
319 of differentiation between processes has been generated, in part, by a delay in the
320 adoption of a widespread scientific terminology by the feline scientific community.

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4.1.6 Knowledge on the sub-disciplines

323 Knowledge about HLF is concentrated in only a few sub-disciplines as habitat selection and patch-landscape configuration account for 56% of all publications (Figure 324 325 4). P. concolor and L. rufus were the focal species in 44% (Figure 3G) of habitat selection studies and had similar responses to HLF, such as the ability to use landscapes 326 327 with some level of anthropogenic disturbance (Johnson et al., 2010; Burdett et al., 2010) (see Appendix B - Table S.B1 for general results of HLF on felines). This trend is also 328 329 observed in the second most studied sub-discipline, patch-landscape configuration 330 (Figure 4), in which three species (*P. concolor, L. rufus*, and *Leopardus pardalis*) comprise 48% of the articles (Figure 3H). 331 332 Knowledge on movement ecology is fundamental to understand spatial 333 dynamics at the landscape level, which is a key aspect to the conservation of largebodied wide-ranging species. This research theme has been well-explored only for Lynx 334 335 *pardinus* through studies of habitat selection on dispersion phases (Palomares et al., 2000), landscape structure (Ferreras, 2001), and matrix heterogeneity effects on 336 dispersion (Revilla et al., 2004). There are also a large number of articles about 337 movement ecology for L. lynx and L. rufus (Figure 3I), but the ecological questions do 338

not address as many issues as in *L. pardinus* studies.

Landscape genetics has been investigated in a large number of species (Figure
3), resulting in interesting conclusions about HLF effects on population genetic
structure (Ernest et al., 2003; Janečka et al., 2008; Schmidt et al., 2011), inbreeding

depression (Björklund, 2003; Johnson et al., 2004; Loxterman, 2011), and their long-343 344 term consequences (Singh & Gibson, 2011; Schnitzler, 2011). Landscape genetics has become more popular than both demographic viability and genetic viability (Figure 3J-345 346 L and Figure 4), which are older conservation issues. Studies concerning HLF impacts on population genetics are relevant because demographic data might be unrealistic from 347 a conservation standpoint, due to their long generation times and lengthy time-lags in 348 population responses (Jackson & Sax, 2010; Krauss et al., 2010); however, not a single 349 350 article measured the time delay of felids in response to HLF (Figure 3M). Additionally, there is difficulty in "putting 'landscape' in landscape genetics" (Storfer et al., 2007), 351 and thus the majority of studies are based on population genetics and make indirect 352 inferences about HLF. 353

Conservation medicine is the only sub-discipline with a higher number of species than publications (Deem et al., 2001; Aguirre & Tabor, 2008). However, the lack of *in situ* data is still considerable (Figure 3N), probably due to the interdisciplinary nature of conservation medicine studies that combines landscape ecology and veterinary approaches.

The least studied disciplines are systematic conservation plan and road ecology 359 (Figure 4). The selection of priority areas can be a difficult task for feline conservation 360 because HLF studies are conducted mainly at the local or landscape scale, whereas site-361 selection studies are commonly carried out at a macroecological scale (Loyola et al., 362 2009; Mortelliti et al., 2010; Rondinini et al., 2011). Consequently, inserting HLF into 363 364 feline site-selection schemes may be a challenge, especially if includes connectivity and dispersal data (Hodgson et al., 2011; Lourival et al., 2011; Crooks et al., 2011); we can 365 366 observe this in our results, as only one species received an adequate approach (Figure 3O). Road ecology studies attempt to quantify the impacts of vehicle collision on 367

animals. Only a few of these studies, however, measure quantitatively the relationship
between traffic, mortality and its consequences for the population (Kerley et al., 2002;
Riley et al., 2006; Schwab & Zandbergen, 2011). Roadkill threatens some felines
(Appendix B - Table S.B1 and Figure 3), but the studies are not focused on these
species (Appendix B - Table S.B1).

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4.2 Allocation of research effort

375 The allocation of research effort is unevenly distributed among felids, in which more than 80% of published studies concerned with only seven species, and 11 species 376 377 have not yet been studied (Figure 3). Conservation priorities did not motivate effort allocation, as threat status and range distribution contraction were unrelated to the 378 379 number of publications (Table 2). As a consequence, five threatened species do not have 380 a single publication pertaining to HLF; if we consider only the studies investigating directly HLF effects, the number of threatened species without scientific publication 381 382 increases to eight (Figure 3). In addition, among the five felines listed as large mammals 383 with high range contraction (Morrison et al. 2007), three of them are poorly studied (Panthera leo, Panthera pardus, and Acinonyx jubatus) (Figure 3). 384

385 We also expected species with larger distributions to have more publications given that their wide distribution could provide field researchers more options for 386 selecting study sites. However, our results did not support this prediction (Table 2). 387 Instead, large bodied felines are more studied (Table 2), suggesting that researcher 388 389 choice may be associated with charismatic characteristics, rather than conservation priorities (see also Brodie 2009). Another explanation could be the ease of studying 390 391 large cats through camera trapping, as larger body sizes have higher chances to be detected by sensors (Karanth et al., 2004), and the coat patterns used to identify 392

393	individuals (Karanth et al., 2006) are most common in large cats (Brodie, 2009).
394	However, camera trapping techniques are used in only a few of the articles reviewed
395	(Figure 1F) and, consequently, cannot be responsible for the difference in effort
396	allocated between large and small cats.
397	As expected, countries with higher economic development possess greater
398	knowledge of HLF effects on their felines than countries with lower economic
399	development (Figure 5). As a consequence, the effort allocation of felid HLF studies is
400	also disproportional across countries (see Appendix B - Figure S.B1 for a map depicting
401	study area locations), in which the majority of research are concentrated in North
402	America and Europe. The studies realized on countries with lower economic
403	development are frequently conducted by researcher from the region; however, it is not
404	rare these studies have as coauthor researches from countries with higher economic
405	development (Figure 6A). Therefore, in general, economically developed countries
406	contribute to the knowledge about HLF on felines, as they also lead research in less
407	developed countries (Figure 6A), and the inverse association is rarely the case (Figure
408	6B-C). This result shows a collaborative relation of researches probable due to the
409	funding provided by developed countries and the gap knowledge of the less developed
410	countries.

4.3 Gap analysis of HLF knowledge on feline

Many felines have a large knowledge gap concerning HLF effects (Figure 3QT). In a general context, only *L. rufus* has been adequately studied, as it has publications
regarding the majority of issues discussed here (Figure 3Q). Conversely, sixteen species
are still without precise information about HLF effects on them. The proportion of
range unstudied decreases the knowledge gap for a few species (Figure 3R); this occurs

(Forrest et al., 2012; Trisurat et al., 2012). However, if we weight the species by threat
status, four species display higher gaps (*Leopardus jacobita, Pardofelis badia, Prionailurus planiceps*, and *Prionailurus viverrinus* – Figure 3S), and thus these species
could be considered the ones with the most urgent need of study. The index value for
few species changes if we weight the gap index by both threat status and proportion of
range studied compared with only threat status, given that, in general (Figure 3T), the
proportion of species range studied is low.

due to theoretical studies regarding large proportion of range distribution of species

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427 **5.** Conclusion

The results of our analyses demonstrate that the knowledge gap concerning HLF 428 effects on felids varies greatly among species. Many species are poorly studied and 429 430 those with a reasonable number of publications are lacking in sub-disciplines and generality of results. Feline research urgently needs larger-scale investigations and 431 432 generalizations to better improve the preservation of biodiversity of this group. A strategy to decrease of gap knowledge on felines could be focus in theoretical 433 approaches of some topics appointed in this study, such as: (i) differentiation of habitat 434 435 loss from fragmentation effects through theoretical scenarios; (ii) selection of priority areas for conservation considering land cover types and configuration on a range 436 distribution scale; and (iii) consequences of habitat loss due to climatic changes that had 437 its effects largely unknown. These studies are not the only ones necessary to understand 438 439 HLF effects on felines and, maybe, they is not even same the most urgent; however, these topics are a good first step to decrease the knowledge gaps concerning HLF 440 effects on felines since they will help discern general patterns and will cover a large 441 portion of a range distribution. 442

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Table 1. Definitions of terms used in this rev	view
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Term	Definition
Process evaluated	
Habitat reduction	Loss in the total area of habitat available to a species
Habitat subdivision	Habitat partition into smaller patches
Human buildings as barrier	Non-natural barriers such as roads, dams, urban
	areas that make animal movement in the landscape
	difficult
Climate change	Reduction of the total area of habitat available to a
	species through the increase of global average
	temperature
Approach	
Review	A survey paper about a particular subject
Empirical	Use of observed data to report a result
Theoretical	A paper that uses a simulated environment and data
	base to investigate a pattern or test a hypothesis
Sub-discipline	
Conservation medicine	Investigates wildlife health in response to
	anthropogenic pressure and habitat conversion
Demographic viability	Investigation of population viability through the
	number of individuals in a population or
	metapopulation
Genetic viability	Investigation of population viability through the
	genetic diversity of a population or metapopulation
Habitat selection	Evaluation of habitat suitability through the

Term	Definition				
	hierarchy of space, which can be based on				
	variegation or contour models				
Landscape genetics	The influence of the landscape on gene flow and				
	spatial genetic variation				
Movement ecology	Concerned with the movement of an organism in a				
	landscape, dispersal ability, and its choice on non-				
	optimal habitats				
Patch-landscape	Measure habitat loss and fragmentation effects on				
configuration	species through the use of fragmentation metrics				
Road ecology	Road network effects on wildlife				
Systematic conservation plan	Selection of priority areas for species conservation				
	through systematic planning				

- Table 2. Results of analysis of covariance performed to identify patterns in the
- allocation of research effort for publications about habitat loss and fragmentation effects
- on felines.

Effect	Degree of	F
	Freedom	
Intercept	1	2.31
IUCN threat status	4	2.18
Body size	1	10.78*
Range size	1	< 0.01
Total habitat area	1	0.38
Proportion of habitat in the range	1	0.29
Error	27	

* p < 0.05





Figure 1. Proportion of published articles (N=162) classified according to the study 664 approaches. (A) Articles that evaluate indirectly or directly the effects of habitat loss 665 666 and fragmentation (HLF) on felines; those studies with a clear objective and variables focused on HLF processes or consequences were considered as direct inferences about 667 668 HLF on felines. (B) Number of target species investigated in the study (focal taxa). (C) Studies which evaluate the influences of human infrastructures (roads, dams, buildings, 669 670 and other physical barriers - HC) and their effects on habitat destruction (HD), and 671 habitat loss due to climatic changes (CC) on felines. (D) Methodological approach to investigating HLF effects. (E) Inference about dispersion corridors for the conservation 672 of felines in fragmented landscapes. "No inference": no reference made to this issue; 673 "Indirect inference": mentioned the importance but did not test it; "Evaluate the 674 importance": made direct inferences about dispersion corridors. (F) Methods of data 675 676 sampling. (G) Studies that differentiate conceptually habitat loss from habitat fragmentation. NA represents articles in which this differentiation is unnecessary 677 because, based on its objectives, it is not relevant. 678



Figure 2. Relative growth of knowledge about HLF effects on felids over time, taking

into account the increase of publications in all areas of science indexed on ISI Web of

682 Science for the year.

Puma yagouaroundi - Puma concolor - Prionailurus viverrinus*- Prionailurus rubiginosus*- Prionailurus planiceps*- Pardofelis temminckii - Pardofelis temminckii - Pardofelis badia*- Pardofelis badia*- Panthera uncia*- Panthera tigres*-	• • •	•	0	0		•	0	٥		°			0	
Panthera pardus -		•	·											$\bigcirc \bigcirc \circ \circ \circ \bigcirc$
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Panthera leo*-	۰	۰	•							٥	\bigcirc	\bigcirc		0000
Otocolobus manul -														$\bigcirc \bigcirc \circ \circ \circ$
Neofelis nebulosa*-														0000
Neofelis diardi*														$ \circ\circ\circ\circ $
Lynx rufus -	0	\bigcirc	\bigcirc		(\bigcirc	\bigcirc	0	\bigcirc	0		\bigcirc	\bigcirc	• • · ·
Lynx pardinus*-	\bigcirc	\bigcirc	0		4	0	0	0	0	0	\bigcirc			\circ \cdot \circ \cdot
Lynx lynx -	\bigcirc	\bigcirc	0		(0	0	\bigcirc		0				00
Lynx canadensis-	0	٥	•			0	0					\bigcirc		$\bigcirc \circ \cdot \cdot$
Leptailurus serval-														$\bigcirc \bigcirc \circ \circ \circ$
Leopardus wiedii-		0			1	0	۰							$\bigcirc \bigcirc \circ \circ \circ$
Leopardus tigrinus*		٠				•								$ \bigcirc \bigcirc \bigcirc \bigcirc \bigcirc \bigcirc \bigcirc \bigcirc]$
Leopardus pardalis -	0	\circ			(0	\bigcirc							$\circ \circ \cdot \circ$
Leopardus jacobita*-														0000
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Felis silvestres-	۰	٥	0			٠	۰							00
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Acınonyx jubatus*		•								0				
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Figure 3. Chart of habitat loss and fragmentation (HLF) effects on felines, which depict the knowledge state of species. The knowledge of species is expressed by the number of publications that evaluate directly the effects of HLF; number of articles was linearly transformed to standardize it in each topic listed, varying from zero (without circle) to one (largest circle). The topics of knowledge considered were: (A) one feline as the target species; (B) competitive relationship between sympatric felines; (C) effects of

habitat destruction; (D) human infrastructures (roads, dams, buildings, and other 690 physical barriers); (E) habitat loss due to climatic change; (F) differentiation between 691 the effects of habitat loss and fragmentation; (G) habitat suitability studies; (H) patch-692 landscape configuration; (I) movement ecology; (J) landscape genetics; (K) 693 demographic viability; (L) genetic viability; (M) time delay of response to habitat loss 694 and fragmentation; (N) conservation medicine; (O) systematic conservation plan; (P) 695 road ecology. These topics were summarized into indexes (Q-T) that express the gap of 696 697 knowledge (GK) concerning HLF effects, which also vary from zero (smallest circle maximum knowledge) to one (largest circle – maximum knowledge gap). (Q) Basic GK 698 index based on topics cited in Figure 3. (R) GK weighted by the proportion of range 699 700 distribution unstudied. (S) GK weighted by values hierarchically distributed to represent threat status (Least Concern -0.2; Near Threatened -0.4; Vulnerable -0.6; Endangered 701 702 -0.8; Critically Endangered -1.0). (T) GK weighted by both the proportion of range 703 distribution unstudied and threat status. *Threatened species.



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Figure 4. Number of publications in sub-disciplines considered in this study. HS –

habitat suitability studies; PLC – patch-landscape configuration; ME – movement

ror ecology; LG – landscape genetics; DV – demographic viability; GV – genetic viability;

708 CM – conservation medicine; SCP – systematic conservation plan; RE – road ecology;

and NC - non-classified.



Figure 5. Comparison of research effort between countries with low annual Gross 711 National Income *per capita* (GNI - ≤ 10 times the income needed to live at the poverty 712 line), medium GNI (> 10 and \leq 30 times), and high GNI (> 30 times). The research 713 effort of countries was represented by: (A) the proportion of felines studied, considering 714 the national feline richness (Kruskal- Wallis test: $\chi^2 = 12.56$, p < 0.01; Nemenyi test for 715 716 low and high classes: p = 0.01; and (B) the proportion of the range distribution studied (Kruskal- Wallis test: $\chi^2 = 10.98$, p < 0.01; Nemenyi test for low and high classes: p = 717 718 0.04). In both cases, the countries with intermediary GNI (between 10 and 30 times) is not different from the countries with low and high GNI. 719



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Figure 6. Economic power of the country of residence for authors that researched the 721 effects of habitat loss and fragmentation on felines. Firstly, the papers were classified 722 723 into three groups, according to the Gross National Income per capita (GNI) of the 724 country in which the study area is located: GNI lower than 10 (A), between 10 and 30 (B), and higher than 30 (C) times the annual income needed to live at the poverty line. 725 726 The economic power of the authors was expressed by the same categories in the graphics abscissas (low, medium, and high respectively) according to the GNI of the 727 countries in which they reside. Dark gray represents the nationality of first author and 728 light gray represents the nationality of the author from the most developed country. 729

Appendix A – Search words used to investigate habitat loss and fragmentation effects on felines and publications found.

- Habitat loss and fragmentation key words: fragmentation OR "habitat fragmentation" OR "habitat loss" OR "habitat destruction" OR "habitat alteration" OR "human alteration".
- Taxonomical groups of felines: mammal OR mammalia OR Carnivore OR felid OR feline OR Felidae
- Search string to felid studied and list of publications on habitat loss and fragmentation effects to each species.

Species	Search string	References
Acinonyx jubatus	"Acinonyx jubatus" OR "hunting leopard" OR	Reed, 2004
	cheetah	
Caracal aurata	"Caracal aurata" OR "Profelis aurata" OR "Felis	N/A
	aurata" OR "African golden cat" OR "golden cat"	
Caracal caracal	"Caracal caracal" OR "Felis caracal" OR caracal OR	N/A
	"African caracal" OR "Asian caracal" OR "desert	
	lynx"	
Felis chaus	"Felis chaus" OR "jungle cat" OR "reed cat" OR	N/A
	"swamp cat"	

Species	Search string	References
Felis margarita	"Felis margarita" OR "sand cat" OR "sand dune cat"	N/A
Felis nigripes	"Felis nigripes" OR "black-footed cat" OR "small-	Blaum et al., 2007
	spotted cat"	
Felis silvestres	"Felis silvestres" OR ""wildcat"	Virgós, 2001; Virgós et al., 2002; Mata et al., 2005; Ascensão
		& Mira, 2006; Klar et al., 2008, 2009, 2012; Santos et al.,
		2008; Meinig & Boye, 2009; Say et al., 2012
Leopardus colocolo	"Leopardus colocolo" OR "Felis colocolo" OR	Carvalho et al., 2009; Medina-Vogel, 2010; Moisés Gallas &
	"Oncifelis colocolo" OR "pampas cat" OR "Chilean	Silveira, 2011; Pereira et al., 2011
	pampa cat"	
Leopardus geoffroyi	"Leopardus geoffroyi" OR "Oncifelis geoffroyi" OR	Canepuccia et al., 2008; Andrade-Núñez & Aide, 2010;
	"Felis geoffoyi" OR "geoffoy's cat"	Medina-Vogel, 2010; Moisés Gallas & Silveira, 2011; Pereira
		et al., 2011; Lantschner et al., 2012
Leopardus guigna	"Leopardus guigna" OR "Oncifelis guigna" OR "Felis	Acosta-Jamett et al., 2003; Acosta-Jamett & Simonetti, 2004;
	guigna" OR "kodkod" OR "guiña" OR "Chilean cat"	Farias & Jaksic, 2011

Species	Search string	References			
Leopardus jacobita	"Leopardus jacobita" OR "Oreailurus jacobita" OR	Medina-Vogel, 2010			
	"Felis jacobita" OR "Oreailurus jacobitus" OR				
	"Andean mountain cat" OR "Andean Cat" OR				
	"Mountain Cat"				
Leopardus pardalis	"Leopardus pardalis" OR "Felis pardalis" OR	Bisbal, 1993; Estrada et al., 1994; Medellin & Equihua, 1998;			
	"ocelot"	Chiarello, 1999; Mora et al., 2000; Cuarón, 2000; Jacson et			
		al., 2005; Dillon & Kelly, 2007; Dotta & Verdade, 2007,			
		2011; Janečka et al., 2008, 2007; Whiteman et al., 2007;			
		Michalski & Peres, 2007; Lyra-Jorge et al., 2008, 2010;			
		Cáceres et al., 2010; Sampaio et al., 2010; Thornton et al.,			
		2010; D. H. Thornton et al., 2011			
Leopardus tigrinus	"Leopardus tigrinus" OR "Felis tigrinus" OR	Bisbal, 1993; Chiarello, 1999; Coelho et al., 2008; Moisés			
	"oncilla" OR "little spotted cat" OR "little tiger cat"	Gallas & Silveira, 2011; Dotta & Verdade, 2011			
	OR "tiger cat"				

Species	Search string	References
Leopardus wiedii	"Leopardus wiedii" OR margay OR "tree ocelot"	Bisbal, 1993; Estrada et al., 1994; Medellin & Equihua, 1998;
		Chiarello, 1999; Cuarón, 2000; Andrade-Núñez & Aide,
		2010; Dotta & Verdade, 2011; D. Thornton et al., 2011; D. H.
		Thornton et al., 2011
Leptailurus serval	"Leptailurus serval" OR "Caracal serval" OR "serval"	N/A
Lynx canadensis	"Lynx canadensis" OR "canada lynx"	Carroll et al., 2001; Schwartz et al., 2003; Hoving et al., 2005;
		Koehler et al., 2008; Murray et al., 2008; Bayne et al., 2008;
		Dunne & Quinn, 2009
Lynx lynx	"Lynx lynx" OR "Felis lynx" OR "Eurasian lynx"	Schadt, Revilla, et al., 2002; Schadt, Knauer, et al., 2002;
		Kramer-Schadt et al., 2004, 2005, 2011; Niedziałkowska et
		al., 2006; Zimmermann et al., 2007; Breitenmoser et al., 2007;
		Hetherington et al., 2008; Meinig & Boye, 2009; Schmidt et
		al., 2009, 2011; Hepcan et al., 2009; Basille et al., 2009;
		Mortelliti et al., 2010; Huck et al., 2010

Species	Search string	References
Lynx pardinus	"Lynx pardinus" OR "Felis pardinus" OR "Iberian	Rodríguez & Delibes, 1992, 2002, 2003, 2004; Ferreras et al.,
	lynx" OR "lynx pardinus" OR "pardel lynx" OR	1992, 2001, 2004; Gaona et al., 1998; Palomares et al., 2000;
	"Spanish lynx"	Palomares, 2001; Ferreras, 2001; Fernández et al., 2003;
		Johnson et al., 2004; Revilla et al., 2004; Santos et al., 2008;
		Revilla & Wiegand, 2008; Medina-Vogel, 2010; Rodríguez et
		al., 2011
Lynx rufus	"Lynx rufus" OR "Felis rufus" OR "bobcat" OR "bay	Lomolino & Perault, 2000; Velázquez et al., 2001; Crooks,
	lynx"	2002; Tigas et al., 2002; Hunter et al., 2003; Riley et al., 2003,
		2006; Cain et al., 2003; Hilty & Merenlender, 2004; Reed,
		2004; Constible et al., 2006; Hilty et al., 2006; George &
		Crooks, 2006; Riley, 2006; Millions & Swanson, 2007; Preuss
		& Gehring, 2007; Markovchick-Nicholls et al., 2008; Tucker
		et al., 2008; Medina-Vogel, 2010; Roberts et al., 2010;
		Johnson et al., 2010; Ordeñana et al., 2010; Ruell et al., 2012;

Species	Search string	References
		Lee et al., 2012; Linde et al., 2012
Neofelis diardi	"Neofelis diardi" OR "Sunda clouded leopard" OR "	N/A
	enkuli clouded leopard" OR "Sunda islands clouded	
	leopard" OR "Sundaland Clouded Leopard"	
Neofelis nebulosa	"Neofelis nebulosa" OR "clouded leopard"	Laidlaw, 2000; Lau et al., 2010
Otocolobus manul	"Otocolobus manul" OR "Felis manul" OR "manul"	N/A
	OR "Pallas's Cat"	
Panthera leo	"Panthera leo" OR "lion" OR "African Lion"	Brook et al., 2002; Björklund, 2003; Reed, 2004; Alexander et
		al., 2010; Singh & Gibson, 2011; Schnitzler, 2011
Panthera onca	"Panthera onca" OR "jaguar"	Bisbal, 1993; Medellin & Equihua, 1998; Ortega-Huerta &
		Medley, 1999; Chiarello, 1999; Cuarón, 2000; Whiteman et
		al., 2007; Michalski & Peres, 2007; McCain & Childs, 2008;
		Carvalho et al., 2009; Sampaio et al., 2010; Conde et al.,
		2010; Haag et al., 2010; Vynne et al., 2011; Colchero et al.,

Species	Search string	References
		2011; D. Thornton et al., 2011
Panthera pardus	"Panthera pardus" OR "Felis pardalis" OR "leopard"	Fleury & Brown, 1997; Pattanavibool & Dearden, 2002;
		Johnsingh & Negi, 2003; Ngoprasert et al., 2007; Lau et al.,
		2010; Svengren & Björklund, 2010; Trisurat et al., 2012
Panthera tigres	"Panthera tigres" OR "tiger"	Fleury & Brown, 1997; Wikramanayake et al., 1998; Laidlaw,
		2000; Lynam et al., 2001, 2006; Kerley et al., 2002;
		Pattanavibool & Dearden, 2002; Kawanishi et al., 2003;
		Kinnaird et al., 2003; Linkie et al., 2003; O'Brien et al., 2003;
		Johnsingh & Negi, 2003; Reed, 2004; Carroll & Miquelle,
		2006; Goodrich et al., 2008; Chauvenet et al., 2010; Lau et al.,
		2010; Lynam, 2010; Wibisono & Pusparini, 2010; Loucks et
		al., 2010; Xiaofeng et al., 2011; Tian et al., 2011; Mondal &
		Nagendra, 2011; Trisurat et al., 2012
Panthera uncia	"Panthera uncia" OR "Uncia uncia" OR "snow	Forrest et al., 2012

Species	Search string	References
	leopard"	
Pardofelis badia	"Pardofelis badia" OR "Felis badia" OR "Catopuma	N/A
	badia" OR "bay cat" OR "Bornean bay cat" OR	
	"Bornean marbled cat" OR "Borneo bay cat"	
Pardofelis marmorata	"Pardofelis marmorata" OR "Felis marmorata" OR	Trisurat et al., 2012
	"marbled cat"	
Pardofelis temminckii	"Pardofelis temminckii" OR "Catopuma temmincki"	Lau et al., 2010
	OR "Felis temmincki" OR "Asiatic golden cat" OR	
	"golden cat" OR "temminck's cat"	
Prionailurus bengalensis	"Prionailurus bengalensis" OR "Felis bengalensis"	Rhim & Lee, 2007; Izawa et al., 2009; Lau et al., 2010;
	OR "rusty-spotted cat" OR "leopard cat"	Trisurat et al., 2012
Prionailurus planiceps	"Prionailurus planiceps" OR "Felis planiceps" OR	N/A
	"flat-headed cat" OR "flat headed cat"	
Prionailurus rubiginosus	Prionailurus rubiginosus	N/A

Species	Search string	References
Prionailurus viverrinus	"Prionailurus viverrinus" OR "Felis viverrinus" OR	N/A
	"fishing cat"	
Puma concolor	"Puma concolor" OR "Felis concolor" "puma" OR	Bisbal, 1993; Beier, 1993, 1995; Smallwood, 1994; Estrada et
	"mountain lion" OR "cougar" OR "deer tiger" OR	al., 1994; Fleury & Brown, 1997; Chiarello, 1999; Cuarón,
	"red tiger"	2000; Sweanor et al., 2000; Hoctor et al., 2000; Velázquez et
		al., 2001; Buergelt et al., 2002; Dickson & Beier, 2002; Ernest
		et al., 2003; Hunter et al., 2003; Daily et al., 2003; Hilty &
		Merenlender, 2004; Dickson et al., 2005; Hilty et al., 2006;
		Whiteman et al., 2007; Markovchick-Nicholls et al., 2008;
		Lyra-Jorge et al., 2008, 2010; Land et al., 2008; Morrison &
		Boyce, 2009; Medina-Vogel, 2010; Cáceres et al., 2010;
		Sampaio et al., 2010; Burdett et al., 2010; Mazzolli, 2010;
		Ordeñana et al., 2010; Vynne et al., 2011; Castilho et al.,
		2011; Dotta & Verdade, 2011; Schwab & Zandbergen, 2011;

Species	Search string	References
		Loxterman, 2011; D. Thornton et al., 2011; Miotto et al.,
		2011; Lantschner et al., 2012
Puma yagouaroundi	"Puma yagouaroundi" OR "Herpailurus yaguarondi"	Bisbal, 1993; Estrada et al., 1994; Medellin & Equihua, 1998;
	OR "Herpailurus yagouaroundi" OR "jaguarundi"	Chiarello, 1999; Cuarón, 2000; Daily et al., 2003; Sampaio et
		al., 2010; Moisés Gallas & Silveira, 2011; Dotta & Verdade,
		2011; Pereira et al., 2011; D. Thornton et al., 2011; D. H.
		Thornton et al., 2011

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Appendix B – Species specific results about effect of habitat loss and fragmentation

Table S.B1 - Current threat status of felines and knowledge on HLF (N= 162 scientific publications). Species vulnerability was expressed considering threat status according to the IUCN Red List (IUCN 2011). Complete list of publications in Appendices A.

Species	IUCN	Summary of main results
Acinonyx jubatus*	VU ¹⁺	NA
Caracal aurata*	NT ¹⁺	NA
Caracal caracal*	LC^1	NA
Felis chaus*	LC^1	NA
Felis margarita*	NT^{1+}	NA
Felis nigripes*	VU^{1+}	• Negatively affected by increase of shrub cover.
Felis silvestres	$LC^{1,2}$	• Stable populations in the most part of its distribution;
		• Negatively affected by human activities and
		settlement, construction of dams, and roads.
Leopardus colocolo*	NT ¹⁺	• In Goiás state (Brazil) is not found fragments larger
		than 10 times its home range;
		• Infection by domestic animals parasites.
Leopardus geoffroyi	NT ¹⁺	• Grassland are unsuitable, but can use areas of eucalypt
		plantation;
		• Habitat loss in rain station;
		• Infection by domestic animals parasites.
Leopardus guigna*	VU^{1+}	• High habitat requirement: large patches of dense shrub
		cover and distant of roads;

Species	IUCN	Summary of main results
		• Many metapopulation in Chile are threatened.
Leopardus jacobita*	EN^1	• Infection by parasites
Leopardus pardalis	LC^1	• Threats: local loss of genetic diversity, diseases from
		domestic animals, and road kill;
		• Use of eucalypt and sugar-cane matrix as corridors.
Leopardus tigrinus*	V U ^{1,2}	• It can use small patches since it has good
		environmental quality;
		• Infection by parasites.
Leopardus wiedii*	NT ^{1,2}	• Populations are declining;
		• It is observed more frequently in core areas of
		fragments.
Leptailurus serval*	LC^1	NA
Lynx canadensis	LC^1	• Avoid open areas and roads;
		• Peripheral populations have lower genetic diversity.
Lynx lynx	LC^1	• Its distribution is largely fragmented, resulting in a
		population marginalized, demographically unviable,
		more susceptible to disease, with low and sub-structured
		genetic diversity;
		• Reconnection of unviable population is difficult due to
		small size of adjacent patches and human construction
		working as barrier.
Lynx pardinus	CR^{1+2}	• It is restricted to two populations;
		• Threats: range contraction due to HLF; low genetic

Species	IUCN	Summary of main results
		variability leading to inbreeding depression; increase of
		mortality rate due to road kills, trapping, and shooting;
		and contagion by domestic animals diseases;
		• Populations cannot be reconnected due to urban areas
		and roads working as barrier.
Lynx rufus	LC^{1+}	• It can cross highways, but it increases mortality rate;
		• It uses anthropogenic land covers, but as less suitable
		habitat;
		• It presents domestic animals diseases in transitional
		areas of natural and anthropogenic land cover.
		• It responds positively to increase in patch size and
		habitat interspersion, but negatively to irregular patch
		shapes and increase in edge habitats;
		• Its populations are genetically structured due to roads,
		but still have high diversity.
Neofelis diardi*	VU^1	NA
Neofelis nebulosa*	VU^1	• High habitat area requirement.
Otocolobus manul*	NT^1	NA
Panthera leo	VU^1	• Inbreeding depression and local extinction due to
		habitat loss;
		• High index of infection by parasites.
Panthera onca	NT^{1+}	• Low tolerance to habitat loss, fragmentation, and
		anthropogenic land cover;

Species	IUCN	Summary of main results
		• Isolated populations in Atlantic Forest and Cerrado
		biome (Brazil);
		• Native vegetation is an important predictor of its
		occurrence.
Panthera pardus*	NT^{1+}	• Its population is subdivided by fragmentation and
		roads.
Panthera tigres	EN^{1+}	• Moderately tolerant to human disturbance, but its
		abundance can be reduced in anthropogenic areas due to
		its high ecological requirements;
		• Populations divided by anthropogenic pressure, such
		as roads, infrastructure, and agriculture;
		• Unviable populations.
Panthera uncia*	EN^1	• Climatic changes can reduce about 30% of snow
		leopard habitat in the Himalaya.
Pardofelis badia*	EN^{1+}	NA
Pardofelis marmorata*	VU^{1+}	NA
Pardofelis temminckii*	NT^{1+}	NA
Prionailurus bengalensis*	LC^{1+}	• Moderately tolerant to degraded habitat;
		• Threats: Habitat loss, competition with introduced
		species, and road kill.
Prionailurus planiceps*	EN^{1+}	NA
Prionailurus rubiginosus*	VU^{1+}	NA
Prionailurus viverrinus*	EN^{1+}	NA

Species	IUCN	Summary of main results
Puma concolor	LC ^{1+,2}	• It has a high environmental plasticity that makes it
		capable to use landscapes with some level of
		anthropogenic influence and to cross areas with roads
		and bridges;
		• Threats: increase of mortality by road kill, sub-
		structuration of genetic variability among fragments,
		inbreeding depression, edge effects, and contagion by
		domestic animals diseases.
Puma yagouaroundi*	LC^{1+}	• It is moderately tolerant to anthropogenic land cover
		and use edge fragments, but mainly habitat of better
		quality;
		• Infection by parasites.

^{*} Poorly studied species

¹ HLF is considered a threat to species

² Road kill is considered a threat to species

⁺ The main threat to species



Continuation Figure S.B1



Figure S.B1 - Distribution of felines with at least one publication (in gray) and location where scientific studies about habitat loss and fragmentation have been conducted studies (red point).

CAPÍTULO 2

Esse capítulo foi submetido para a revista Journal of Nature Conservation, portanto, segue as normas de formatação da mesma. Atualmente, o artigo está avaliado como *Major Review* (Anexo 2).

- 1 The jaguar's patches: the decline of jaguar populations
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14 The jaguar's patches: the effects of fragmentation on jaguar populations

15

16 **1. Abstract**

Habitat loss and fragmentation have serious consequences for population extinction risk, so 17 we investigated the effects of these processes on jaguar (Panthera onca) populations across 18 19 the species' distribution range. We employed theoretical simulations of population dynamics, making use of real and hypothetical landscapes, which permitted us to measure the effects of 20 21 landscape configuration on persistence probability and to disentangle the effects of habitat loss and fragmentation on jaguar populations. Jaguar persistence probability was related to 22 habitat configuration in real landscapes. However, habitat configuration was correlated with 23 24 the amount of total habitat, rendering it difficult to differentiate the processes of habitat loss and fragmentation. The hypothetical landscapes helped us to understand the different effects 25 of these two processes. Our findings show that fragmentation affects jaguar long-term 26 persistence more than habitat loss, because jaguars had a higher persistence probability in 27 landscapes comprised of a continuous habitat patch than in landscapes with the greater 28 29 quantity of habitat but composed of several separate patches. Given the increase in habitat fragmentation and the current threat status of the jaguar, conservation initiatives need to take 30 account of the results presented in this study for the development of jaguar conservation 31 32 strategies.

33

34 Keywords

35 Critical threshold, habitat loss, habitat fragmentation, *Panthera onca*, population viability36 analyses

37 **2. Introduction**

The effects of habitat loss and fragmentation on species persistence are a central 38 topic in conservation biology (Lenore Fahrig, 1997, 2003). Habitat loss and fragmentation 39 reduce and subdivide the available habitat (Andrén, 1994; Lenore Fahrig, 2003), thereby 40 41 altering the colonization rates of patches (Belisle, Desrochers, & Fortin, 2001). Even though 42 habitat loss and fragmentation occur simultaneously in real landscapes, they are two different processes, both of which affect wildlife populations. The majority of studies on this theme 43 44 have frequently investigated the integrated effects of both processes because they are 45 inevitably correlated in real landscapes (Smith, Koper, Francis, & Fahrig, 2009). Despite inherent difficulties, it is critical to differentiate the effects of each process in order to better 46 47 guide wildlife management strategies, permitting a more efficient use of limited conservation resources (Lindenmayer & Fischer, 2007; Smith et al., 2009). 48

Estimates of persistence probability provide useful insights for wildlife managers 49 planning species conservation in a world where habitat destruction and degradation rates are 50 soaring (Caughley, 1994). Habitat alteration may be perceived differently by species 51 52 (Lindenmayer & Fischer, 2007), and so a species-specific approach is essential for measuring 53 the effects of habitat loss and fragmentation. Population viability analysis (PVA) has become a useful tool for investigating the effects of habitat loss and fragmentation on species, given 54 55 that it may evaluate persistence probability in relation to a variety of environmental threat 56 scenarios according to species-specific parameters (Brook, Tonkyn, O'Grady, & Frankham, 2002). 57

58 Our research focused on the effects of habitat loss and fragmentation on the long-59 term persistence of jaguar (*Panthera onca*, Linnaeus 1758) in landscapes distributed 60 throughout its range. Historically, this species was distributed from the southern United States 61 to Argentina, but its geographic range has been reduced to less than 60% of its original extent

due to human pressures (Morrison, Sechrest, Dinerstein, Wilcove, & Lamoreux, 2007). The
jaguar is ranked15th among the large-bodied mammals with greatest geographic range
contraction in the last 500 years due to anthropogenic effects (Morrison et al., 2007). Today,
the jaguar is listed as Near Threatened (IUCN, 2013), but this status may soon be revised to
reflect further declining populations (IUCN, 2013).

The current habitat configuration of landscapes is a result of past habitat loss and 67 fragmentation (Villard & Metzger, 2013); thus, present-day habitat configuration can be 68 69 considered as a pattern generated by the synergistic effects of both processes (habitat loss and 70 habitat fragmentation). Therefore, we mapped known jaguar populations across its distribution range and then investigated how the current landscape configuration could 71 72 determine jaguar persistence probability. To better understand the consequences of habitat loss and fragmentation for jaguars, we created hypothetical landscapes to investigate the non-73 linear relationship of habitat configuration and species persistence based on the simplest 74 75 landscapes features, i.e. the total habitat area and the number of patches. For that, we modeled 76 jaguar population dynamics in landscape scenarios for (i) a controlled number of patches 77 while reducing the total habitat area, and (ii) a controlled total habitat area while increasing 78 the number of patches. This approach allowed us to disentangle the effects of habitat loss and fragmentation on jaguar populations. 79

Habitat loss and fragmentation are the main threats to jaguar populations (IUCN, 2013). On this perspective, we measured the viability of jaguar populations at a landscape level, generating a map of threatened populations. We also evaluated the amount of habitat necessary to maintain a viable population and the extent of habitat fragmentation a jaguar population can support while maintaining a high persistence probability. This gave us a general insight into the importance of increasing total habitat area and connecting isolated fragments to ensure the long-term persistence of jaguar populations in the landscapes.

87 **3.** Methods

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89 **3.1. Study Area**

To conduct jaguar PVAs (see below) we selected 28 study areas for which jaguar 90 density estimates were available and had been measured in a similar way. We used as a 91 92 reference the review of Maffei et al. (2011), where authors reported jaguar densities for 49 study areas distributed across 14 countries. However, the studies considered in that review 93 94 used different density estimation methods and sampling designs, so we selected sites where 95 density was estimated by capture-recapture methods, using two camera-traps at each sampling station as the census technique. The 28 study areas used in our investigation were located 96 97 throughout nine countries, with density estimations varying from 1.12 to 11.56 jaguars/100 km² (Supplementary Material A). 98

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3.2. Landscape scenarios

PVAs were performed in real landscapes to evaluate the effect of landscape 101 102 configuration on jaguar persistence probability, but also in a set of hypothetical landscapes to disentangle the effects of habitat loss and fragmentation. The real landscapes were delimited 103 by establishing a 10,000 km² buffer around the central point where the density studies were 104 105 conducted. A landcover map (Bontemps, Defourny, Bogaert, Kalogirou, & Perez, 2011) was created using a binary classification; we categorized native vegetation cover as suitable for 106 jaguars and anthropogenic landcover as unsuitable. This level of generalization was adopted 107 108 because jaguars present significant environmental plasticity in terms of their use of vegetation 109 types (Colchero et al., 2011), making this a good generalization of jaguar habitat use at a broad environmental grain. It is known that jaguars occupy anthropogenic vegetation 110 (Colchero et al., 2011; Figel, Durán, & Bray, 2011), but it is unclear from studies on habitat 111

suitability if jaguars use these areas or simply traverse them. Additionally, jaguar mortality probably increases in anthropogenic vegetation, justifying our classification of it as unsuitable for jaguars. The number and size of habitat patches were estimated for each landscape in the jaguar habitat map. Patches larger than 100km² were included in our PVA because we considered that these patches adequately function as stepping stones and since it is a reasonable size for a jaguar home range (Cavalcanti & Gese, 2010; Cullen Jr., 2006).

The hypothetical landscapes were designed with a controlled structure to measure the 118 119 effects of habitat area and subdivision. The simulations started considering a landscape with the maximum of structural integrity, i.e. a patch of 10,000 km². In order to model the effects 120 of habitat loss, the total area was reduced gradually, by blocks of 1,000 km², until only 1,000 121 km^2 remained, and then to 500 km^2 and finally to 100 km^2 . In order to model the effects of 122 123 habitat fragmentation, the total area of habitat was kept constant (i.e. the same amount of 124 habitat used in the habitat loss simulations), but it was divided into a number of scenarios where we gradually increased the number of patches. The first scenario had two patches, the 125 second had four patches of equal size, continuing progressively by steps of four up to 28 126 127 patches. The patches were of equal area without reducing the total area, and so each patch had equivalent relevance to population persistence. 128

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3.3. Population Viability Analysis

The software VORTEX version 9.99 (Lacy, 2012) was used to simulated the population dynamics of jaguars and estimate persistence probability for 200 years. VORTEX is a Monte Carlo simulation that considers a set of factors affecting a population, including: deterministic forces (e.g. trends in carrying capacity); demographic, environmental and genetic stochasticity; and catastrophes (Lacy, 2000). We chose VORTEX due to its spatiallyimplicit approach, which was necessary for our study because the literature concerning the

137 jaguar lacks information about dispersal rates and mortality in different landcover types and138 areas.

Most of the life history data were obtained from the 'Brazilian Action Plan for 139 Jaguars' because it compiles the most up-to-date biological data on the species (de Paula, 140 Desbiez, & Cavalcanti, 2010) (Table 1). These data represent an actual, but non-specified, 141 142 jaguar population (de Paula et al., 2010), so the population might be derived from anywhere within the species distribution. The differences among the populations modeled in our study 143 144 only concerned the landscapes where they are located, so the differences among PVAs in this 145 study related only to landscape features. We designed the (meta)population structure based on the simplest landscape features, i.e. patch number and area. The number of patches in the 146 147 landscape determined whether the dynamics were best modeled by a population or a metapopulation. The total area of the patches determined initial population size, which was 148 149 calculated as a product of area and jaguar density. Due to the spatially-implicit approach, the total habitat area and the number of patches were integrated into the PVA indirectly; the 150 151 number of patches was used as a surrogate for the number of populations and the total amount 152 of suitable habitat was a surrogate for population size.

153 We assumed that carrying capacity was equal to the initial population size, which 154 was a conservative approach because there is no information about the temporal change in 155 carrying capacities of these studies areas. There is also no information about jaguar dispersal rates or mortality in the different landcover types. Therefore, we chose a generalized 156 157 approach, whereby the movement of migrants between fragments was considered symmetric, 158 i.e. individuals could move in either direction between patches at the same rate. The total 159 number of migrants was estimated as a function of the number of subadults in the population because, typically, at this life-history stage, felines are looking to establish a territory 160 161 (Funston, Mills, Richardson, & van Jaarsveld, 2003). The proportion of subadults was

determined as a proportion of the dynamic sites (*sensu* Gotelli, 1991) that can be occupied in
the metapopulation. Since a subadult competitively excludes another individual from its *site*,
the excluded jaguar (which can be an adult or another subadult) can compete for another *site*in the metapopulation. Therefore, the number of subadults defined the proportion of
dispersers, but the dispersers could be any jaguar in the population.

167 Of the estimated life-history parameters for jaguars, the percentage of males in the breeding pool and mortality were those having the greatest degree of uncertainty. The 168 169 percentage of males in the breeding pool is difficult to estimate. An accurate estimate would 170 require long-term demographic study, using expensive techniques, such as genetic analysis 171 and GPS monitoring. Mortality too is a complex parameter that varies according to sex, age 172 and location (Ferreras et al., 2004), as well as anthropogenic factors (Inskip & Zimmermann, 173 2009). We modeled PVAs based on the best preserved landscape in our study area (jaguar density of 11.56 jaguars/100 km² and 10,000 km² of available habitat), with different values 174 for the percentage of males in the breeding pool and jaguar mortality to take into account the 175 uncertainty of these parameters. The proportions of males in the breeding pool used in the 176 177 models were 100%, 80% and 70% while, for mortality rates, we used 10%, 30% and 50% (for 178 both sexes and every age class). These values were attributed randomly into the 500 PVA 179 models.

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181 **3.4. Statistical Analysis**

To investigate the synergistic effects of habitat loss and fragmentation on jaguar
population viability, we used landscape metrics as a measure of landscape configuration. We
calculated landscape metrics using the Fragstats software program (McGarigal & Marks,
185 1994) on a landcover map (Bontemps et al., 2011), with our classification of

186 suitable/unsuitable habitat for jaguars. The selected metrics included: the proportion of native

cover in the landscape (PLand); largest patch index (LPI); landscape shape index (LSI); patch
number (PN); cohesion; mean size of patches (Area-MN); and the standard deviation of patch
area (Area-SD) (Table2). These various landscape metrics might capture the same process,
resulting in over-parameterization of the statistical analysis. Thus, we conducted a principal
components analysis (PCA) to remove redundant parameters (Legendre & Legendre, 1998),
and the associated principal component scores were used to represent the landscape
configuration.

194 The real landscapes studied could be spatially structured throughout the jaguars' 195 distribution and may depict spatial autocorrelation, so we adopted the use of spatial filters as a covariable to address this problem. Spatial filters consist of synthetic variables added into 196 197 analyses with the objective of expressing the geographic relationships among landscapes (Dray, 2011; Patuelli, Griffith, Tiefelsdorf, & Nijkamp, 2010). They capture orthogonal 198 199 variation in spatial structure at different scales without inserting redundant parameters (Diniz-Filho & Bini, 2005). Spatial filters are eigenvectors from a principal coordinates analysis of 200 neighbor matrices (Borcard & Legendre, 2002), calculated through the truncated distance 201 202 matrix W

$$W = (w_{ij}) = \begin{cases} 0 \to i = j \\ 0 \to d_{ij} > t \\ \left[1 - (d_{ij} / 4t)^2\right] \to d_{ij} \le t \end{cases}$$

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where *wij* is each one of the elements and *t* is the truncation distance. The spatial filters were
generated by the Spatial Analysis Macroecology software (SAM) (Rangel, Diniz-Filho, &
Bini, 2010) based on the geographical distance between landscape centroids.

207 Model selection was performed to evaluate the best model explaining the relationship 208 between persistence probability, landscape configuration and spatial filters. This was 209 accomplished through the use of the Akaike Information Criterion corrected for small sample

210 size (AICc) (Burnham & Anderson, 2004), which permits a hierarchical ordination of models 211 according to their descriptive power and complexity (Burnham & Anderson, 2004). We 212 expected to generate a non-linear pattern of species responses to habitat loss and 213 fragmentation (Swift & Hannon, 2010), so we used a logistic adjustment for our models to be 214 more consistent with theory. We also included a model composed only of a linear coefficient 215 to evaluate if a random solution explained the persistence probability better than the proposed 216 variables. We considered models with AICc values lower than two as complementary 217 explanations of pattern (Burnham & Anderson, 2004), since the null model was not among 218 the best solutions.

To measure the amount of habitat necessary to maintain a viable population of 219 220 jaguars, and the extent of fragmentation a jaguar population can support while maintaining its 221 viability, we performed a piecewise linear regression with the hypothetical landscape data. 222 Piecewise analysis estimates the tipping point at which system alteration generates qualitative changes in population persistence probability, i.e. from viable to unviable. This tipping point 223 is known as the critical threshold and it is defined as an abrupt and non-linear alteration in a 224 225 given variable occasioned by small changes in the original system (Leonore Fahrig, 2001; 226 Scheffer et al., 2009). Mathematically, piecewise analyses adjust more than one regression line through data variation, and the "breakpoint" (or the place where the lines converge) is 227 228 considered the critical threshold (Toms & Lesperance, 2003). We calculated the critical threshold using the SiZer package (Sonderegger, 2011) in R software (R Core Team, 2013). 229 230 The sensitivity of our base population viability model was investigated using a 231 regression tree (Cutler et al., 2007; Harper, Stella, & Fremier, 2011), which permits the 232 evaluation of multiple uncertain parameters and their nonlinear interaction (Harper et al., 2011). The regression tree structures data through hierarchical and binary partitions (splits) to 233 create groups (nodes) of higher homogeneity, reflecting parameter importance, up to an 234
235 undivided group of populations (leaves) (Rejwan, Collins, Brunner, Shuter, & Ridgway, 236 1999). The evaluation of node numbers in the regression tree was accomplished by a cross-237 validation procedure, which calculates the true prediction error in the addition of nodes (Breiman, 2001). A random forest was performed to evaluate the relative importance of each 238 239 parameter in the PVA estimations (Cutler et al., 2007), which indicated the variable that needed to be more accurately estimated (Harper et al., 2011). The random forest analysis was 240 carried out using 1000 random trees through bootstrap sampling (Breiman, 2001). We used 241 242 the rpart (Therneau, Atkinson, Ripley, & Ripley, 2011) and randomForest (Liaw & Wiener, 243 2002) packages to conduct the regression tree and random forest analyses in R software (R Core Team, 2013). 244

245

246 **4. Results**

The landscape metrics used to calculate the configuration of real landscapes were correlated (Figure 2), so we selected only the first principal component of the PCA, according to a broke-stick method, which described 58% of the landscape metrics variation. The variables PLand, LPI, Area-MN, Area-SD and cohesion were positively correlated with the principal component, while PN and LSI were negatively correlated.

252 Two out of the 64 competitive models were considered the best (i.e. AICc < 2) in 253 explaining the persistence probability of jaguars in the landscape, the null model not being amongst them (Table 3 and Supplementary Material B). The principal component condensing 254 255 the landscape configuration appeared in both models (Table 3), evidencing the homogenous 256 effect of landscape configuration, which could be observed due to the low variance in the 257 coefficient value and the low standard error of the competitive models (Figure 3). Spatial filters three and five also appeared in the best models, but had large standard errors associated 258 with them, obscuring their importance in predicting persistence probability (Table 3). 259

260 Therefore, we considered only the principal component summarizing landscape configuration261 as an efficient predictor of jaguar persistence probability.

262 The habitat loss critical thresholds varied widely among jaguar populations, attaining values ranging from 230 km² to 5,841 km² (Figure 1A). These values were strongly correlated 263 264 with jaguar density (Figure 4 A) due to the direct effects of initial population size on 265 persistence probability. Variation in the order of decimal degrees generated changes of more than 100 km² in the critical threshold. However, the fragmentation critical threshold was more 266 267 sensitive to changes in the landscape than the habitat loss critical threshold. The tolerance of jaguar populations to fragmentation was not sufficient to determine fragmentation critical 268 thresholds; the piecewise linear regression calculated the critical thresholds when the 269 270 metapopulation had a persistence probability close to zero (tipping points have a negative slope –Supplementary Material C). In only a few cases did the populations have a high 271 persistence probability after the first subdivision, even in landscapes with 10,000 km² of 272 suitable habitat (Figure 5 and Supplementary Material C). 273

As a complementary result, we calculated a habitat critical threshold with a 97.5% 274 275 confidence interval, to have a conservative estimate of ensuring long-term jaguar persistence. When populations had a density greater than 4.13 jaguars/100 km², jaguar population viability 276 suffered an abrupt and stable change following a small reduction of habitat, which resulted in 277 278 almost uniform residuals and an inadequate fit of the piecewise-regression to bootstrap samples. This mathematical artifact generated a relationship between density and the critical 279 threshold similar to a parabola, in which the estimated density decreases to 4.13 jaguars/100 280 281 km² and thereafter starts to increase (Figure 4 B). Of course, there is no biological sense to this pattern since the area needed to maintain a jaguar population must decrease with higher 282 density. Thus we considered it acceptable, from a conservation perspective, to consider the 283 threshold estimated at 4.13 jaguars/100 km² for populations with greater densities. Based on 284

that, the jaguar habitat critical threshold varied from 3,000 km² to 7,000 km² (Supplementary
Material A).

287 The real landscapes evaluated were able to support a jaguar population only in two out of the 28 sites investigated (Figure 1B; Supplementary Material A), based on 95% 288 persistence probability after 200 years (Table 1). Both of these viable populations are located 289 290 in Guatemala and exhibit high jaguar density and a landscape with almost 100% native 291 vegetation. Many other high density populations were unviable (Figure 1B and 292 Supplementary Material A). These landscapes frequently had a total area that was larger than 293 the habitat loss critical threshold, but the area was divided into a number of patches that were also larger than the fragmentation critical threshold, which resulted in unviable populations. 294 295 Therefore, the main threat to the long-term persistence of the jaguar populations studied 296 seemed to be habitat fragmentation.

The sensitivity analysis showed that 82% of the predictors' variance could be explained by random forest. The regression tree was composed of six nodes, all defined by female mortality (Figure 6). Therefore, the PVA model was sensitive to poorly-estimated parameters, especially adult female mortality (Figure 7). The final node showed the populations with higher persistence probability, which were those with a female mortality rate lower than 20% from birth to sexual maturity (i.e. three years of age) (Figure 6). Thus, low mortality in female jaguars may be seen as a surrogate of population persistence probability.

304

305 **5. Discussion**

Our study investigated the effects of habitat loss and fragmentation on the
persistence probability of jaguar populations. To do that, it is first necessary to perceive
habitat loss and fragmentation as processes that have a known spatial pattern on landscape
configuration. We observed a strong correlation between the selected landscape metrics used

to measure the spatial configuration of our real landscapes. This finding is a product of the
large amount of jaguar suitable habitat in the landscapes (Average PLand = 77.7%), which
homogenized the landscape configuration as predicted by percolation theory (landscapes
composed of an amount of suitable habitat greater than 65% are structurally connected)
(Bascompte & Sole, 1996; K. A. With, 1997).

As expected, persistence probability was related to the proportion of jaguar suitable 315 habitat in the landscapes (Table 3). According to percolation theory predictions, we expected 316 317 that the landscapes composed of habitat aggregated into one single patch had a larger 318 proportion of suitable habitat than landscapes with two or more patches. The landscapes 319 analyzed in the current study supported this general prediction (\overline{X} PLand_{metapopulation}=65%; \overline{X} PLand_{population}=87%; t-value = 2.18; DF = 26; p = 0.04). Therefore, the relationship we found 320 321 between total habitat available and persistence probability expresses more than a simple 322 metric for the predictability of an ecological process. The increase in availability of suitable habitat acts directly on landscape connectivity, thereby altering population structure 323 (Bascompte & Solé, 1996). 324

There are several empirical examples of habitat configuration affecting species 325 persistence in the landscape (see review of Villard & Metzger, 2013). The general findings 326 327 indicate that habitat configuration abruptly reduces species richness at the landscape scale when the amount of suitable habitat is around 10–30% (Andrén, 1994; Estavillo, Pardini, & 328 da Rocha, 2013; Lenore Fahrig, 2003), which is the threshold for conversion from a 329 330 fragmented to a relictual landscape (McIntyre & Hobbs, 1999). However, the amount of suitable habitat and its configuration establishes a complex relationship, whereby habitat 331 configuration could potentially reduce the effects of habitat loss, which is species-dependent 332 333 since habitat perception is a species-specific attribute (Villard & Metzger, 2013).

334 The hypothetical landscapes used in our study helped us to understand the complex 335 relationship between landscape configuration and species persistence based on the simplest 336 landscapes features, i.e. total habitat area and number of patches. We observed that an increase in patch number generated a stronger reduction in jaguar persistence probability than 337 a decrease in the amount of suitable habitat. Therefore, we can confirm that fragmentation is 338 more detrimental than habitat loss for jaguar populations. Other theoretical studies have given 339 similar predictions (Lenore Fahrig, 2003; K. With, Cadaret, & Davis, 1999), but our results 340 341 differ from those of empirical studies (Mortelliti et al., 2011, 2012; Tian et al., 2011; Villard 342 & Metzger, 2013).

The low persistence probability of jaguar populations in fragmented landscapes is 343 344 probably linked to an increase in overall mortality, arising by impediments to dispersal. We established a stable proportion of migrants and survivors between patches in our models, so 345 346 total mortality increased with an increase in the number of patches. The effects of mortality were reinforced by our sensitivity analysis, especially for female mortality, since the PVA 347 estimates were sensitive to this parameter. Jaguar mortality can vary widely among 348 349 populations because it is strongly influenced by extrinsic factors (Azevedo, 2008; Polisar et 350 al., 2003). However, it seems reasonable that female mortality at the reproductive stage is 351 important because a relationship between the total number of females in the reproductive pool 352 and growth rate is expected for a polygenic species. Even though this parameter is quite 353 relevant for jaguar ecological studies, there is no information about the variability and 354 intensity of jaguar mortality in terms of sex, age or matrix type. This resulted in persistence 355 probabilities that were sensitive to poorly-estimated parameters. However, an increase in 356 mortality during dispersal in a fragmented landscape can be expected, as we assumed in our models even with the different rates we used. Thus, while our results might vary in intensity 357 358 with better model paramaterization, the overall findings would not change.

359 *Conservation implications*

Our approach permitted us not only to summarize the effects of habitat loss and 360 361 fragmentation on jaguar persistence probability, but also to generate a diagnostic of jaguar 362 conservation status because all the results discussed here have strong applicability from a conservation perspective. According to our results, we can confirm that jaguar conservation is 363 364 in a precarious situation, given that only two of the 28 evaluated populations had a high probability of persistence. Over recent years, the species has become more dependent on 365 366 protected areas (Riley, 2006), but currently few such areas can support demographically-367 viable jaguar populations (Sollmann, Torres, & Silveira, 2008). Thus, our results provide an important contribution to jaguar conservation because the habitat loss critical thresholds can 368 369 be used to predict the necessary size of protected areas (L. Traill, Bradshaw, & Brook, 2007; 370 L. W. Traill, Brook, Frankham, & Bradshaw, 2010).

371 Even with our growing dependence on protected areas for species conservation, many are not fulfilling their conservation function because they do not support long-term 372 viable populations (Sollmann et al., 2008). We can highlight Iguaçu National Park (INP) and 373 374 its surrounding areas as a significant example because it supports one of the few remaining 375 southern jaguar populations located in an area with large suitable habitat fragments 376 (Altrichter, Boaglio, & Perovic, 2006; Mazzolli, 2009). However, the jaguar population in this 377 landscape is highly vulnerable to extinction (Persistence Probability < 0.01, Mean time to extinction = 58.7 years), even though the landscape comprises $9,200 \text{ km}^2$ of native vegetation 378 cover in a practically single and large patch. The unviability of this population might be due 379 380 to the low number of individuals it harbors, since it had the lowest density of all the locations 381 evaluated in this study. Due to the time lag of species' responses to environmental alterations, especially those species of significant longevity (Krauss et al., 2010) such as jaguars, the 382 mean time to extinction can be higher than those estimated. Nevertheless, INP still has one of 383

the most threatened jaguar populations. The areas surrounding INP suffer from severe hunting
pressures (Azevedo, 2008), which decrease jaguar population density both directly by
poaching and indirectly by prey reduction.

Currently, the implementation of dispersal corridors is the main strategy 387 388 recommended by researchers and conservation managers to bolster threatened jaguar populations and to connect protected areas (Rabinowitz & Zeller, 2010; Rodríguez-Soto, 389 Monroy-Vilchis, & Zarco-González, 2013). Our study provides theoretical evidence of low 390 391 jaguar persistence probability under metapopulation dynamics (Figure 5). Thus, the 392 establishment of dispersal corridors needs to be carefully planned, given that the negative consequences of metapopulation dynamics can be worse than those for populations that 393 394 remain isolated (Brito & Fernandez, 2002). A corridor can force species to cross less-suitable habitats (Franklin & Lindenmayer, 2009). For top-predators such as jaguars, this can 395 396 exacerbate retaliatory hunting in response to the intensification of jaguar predation on 397 domestic animals (Inskip & Zimmermann, 2009), which would probably occur in these 398 contexts.

399 Therefore, our results raise the question of how to manage jaguar populations in fragmented landscapes. Perhaps jaguar conservation planning should emphasize strategies 400 401 that increase population size by decreasing human-wildlife conflicts and increasing habitat 402 quality. Decreasing human-wildlife conflict will depend on multiple factors because it has an 403 ecological, social and probable regional context (Zanin et al. unpublished data). Increasing 404 habitat quality is also a complex task because it will involve landscape management - though 405 the field of restoration ecology is rapidly advancing, which will be of assistance in this area. 406 Of course, jaguar conservation is far more complex than the connectivity between two areas, as has been suggested by researchers (Rabinowitz & Zeller, 2010; Rodríguez-Soto et al., 407 2013), but it seems to be of fundamental significance for long-term jaguar conservation. 408

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Figure 1. Maps of the jaguar populations used in our study according to (A) the area
requirement (in km²) needed to maintain viable populations (also called the habitat loss
critical threshold) and (B) their persistence probabilities in 200 years based on actual
landscape configurations. Dark gray indicates original jaguar distribution range and light gray
the current distribution.





585 Figure 2. Principal components selected by the broken-stick method in a principal

586 components analysis, which shows the correlation between landscape metrics. LPI – large

587 patch index, PLand – proportion of native vegetation in the landscapes, Area-MN – size of

588 patch, Area-SD – standard deviation of patch area, PN – patch number, and LSI – landscape

shape index.



590

591 Figure 3. Variation in coefficients (A) and standard error (B) of the explanatory variables

592 employed to describe jaguar persistence probability: a = coefficient of non-linear regression;

593 PC = first principal component condensing landscape configuration; SF (1-5) = spatial filters

594 capturing differing spatial structures of selected landscapes.



596 Figure 4. Relationship between jaguar density and the habitat loss critical threshold (HCT).

597 (A) Habitat critical threshold estimated to maintain a jaguar population with a high

persistence probability. (B) Habitat critical threshold with a 97.5% confidence interval (97.5%

599 CI). The log transformed HCT ranged from 5.3 to 8.9, which is equivalent to a range of 230 to 5.041 km^2

600 5,841 km².



602 Figure 5. Persistence probability (SP) of metapopulations relative to jaguar density (JD) in

landscapes composed of two patches, each of $5,000 \text{ km}^2$.



Figure 6. Illustration of the regression tree and the relationships between parameters used to
estimate jaguar persistence probability. The final node indicates the probability values along
with the number of observations ("n"). FM is female mortality. There is only one pathway
(delimited by the square) that leads to viable populations (high persistence probability).



Figure 7. Sensitivity of jaguar persistence probability estimates for each variable in the global



Table 1. Biological and statistical parameters used in the jaguar population viability analysis.

Parameter	Value
Number of interactions	1000
Number of years	200
Extinction	Only 1 sex remains
Inbreeding	Yes (Default)
EV concordance in persistence and	Yes (Default)
reproduction	
Reproductive system	Polygynous
Age of first offspring for females	3
Age of first offspring for males	4
Maximum age of reproduction	10
Maximum number of progeny per year	4
Sex ratio at birth (% males)	50
Alle parameter, A	0.5
Steepness parameter, B	2
% adult females breeding	(P0((P0-PK)*((N/K) ²)))*(N/(A+K))
EV in % breeding	12.5
EV in % breeding	Specific
Adult females producing	
1 young	5%
2 young	40%
3 young	30%

613 EV - environmental variation; SD - standard deviation.

Parameter	Value
4 young	25%
Mortality rates in females	
Age 0-1	34 ± 10
Age 1-2	17 ± 8
Age 2-3 (Subadult)	19 ± 5
Age 3-4 (Adult)	20 ± 5
Mortality rates in males	
Age 0-1	34 ± 10
Age 1-2	17 ± 8
Age 2-3 (Subadult)	35 ± 5
Age 3-4 (Subadult)	30 ± 5
Age 4-5 (Adult)	30 ± 5
Males in breeding pool	90%
Age distribution	Stable
SD carrying capacity	5% of N(0)
Migration rate	20%
Dispersers surviving	90%

615	Table 2. Fragmentation metrics used in this study. Abbreviations used in the fragmentation
616	metrics formulae: N - patch number (unit); a_{ij} - area of ij patch (m ²); A - total area in the
617	landscape (m ²); max a_{ij} - patch with the largest area (m ²); p_{ij} - perimeter of patch ij (unit of
618	cells); min p_{ij} - minimum perimeter if patch was maximally aggregated (unit of cells); Z -
619	total number of cells in the landscape.

Metric	Formula
Proportion of landscape with natural vegetation	$\frac{\sum_{j=1}^{N} a_{ij}}{A} \cdot 100$
Largest patch index	$\frac{\max(a_{ij})}{A} \cdot 100$
Landscape shape index	$\frac{p_{ij}}{\min p_{ij}}$
Patch number	Ν
Cohesion	$\left[1 - \frac{\sum_{j=1}^{N} p_{ij}}{\sum_{j=1}^{n} p_{ij} \sqrt{a_{ij}}}\right] \cdot \left[1 - \frac{1}{\sqrt{Z}}\right]^{-1} \cdot 100$
Mean size of patch	$\frac{\sum\limits_{j=1}^{N}a_{ij}}{N}$
Standard deviation of patch area	$\sqrt{\frac{\sum_{j=1}^{N} \left[a_{ij} - \left(\frac{\sum_{j=1}^{N} a_{ij}}{N}\right)\right]^{2}}{N}}$

Table 3. Models with AICc values lower than four describing jaguar persistence probability

based on landscape configuration and spatial structure (complete list in Supplementary

622 Material B). PC - first principal component condensing landscape configuration; SF (1-5) -

Variables in the model	Δ AICc	AICc	Residual	Degrees of
		Weighted	Standard Error	freedom
PC, SF3	0.00	0.24	0.25	25
PC, SF3, SF5	1.93	0.09	0.25	24
PC, SF2, SF3	2.17	0.08	0.25	24
PC	2.53	0.07	0.27	26
PC, SF3, SF4	2.80	0.06	0.25	24
PC, SF1, SF3	2.94	0.05	0.25	24
PC, SF2, SF5	3.08	0.05	0.26	24
PC, SF5	3.26	0.05	0.26	25

623 spatial filters capturing the different spatial structures of selected landscapes.

Supplementary Material A

Jaguar populations studied on the basis of the effects of habitat loss and fragmentation on population dynamics. Locations were selected based on density studies with similar sampling designs (for a review of density studies, see Leonardo Maffei et al. 2011). N – number of jaguars estimated in the landscape through multiplying total habitat area and jaguar density; SP – persistence probability; MTE – mean time of extinction (in years); N pop – number of population in the landscape; CT – habitat loss critical threshold; and $CT_{97.5\%}$ – habitat loss critical threshold calculated with a confidence interval of 97.5% by a bootstrapping method.

Study site	Reference	Ν	SP	MTE	N Pop	СТ	CT _{97.5%}
Iguazú, Argentina	Paviolo, De Angelo, Di Blanco, & Di Bitetti	99	0.00	59	1	5841	7221
	(2008)		0.01				
Palmar (Ravelo) - Kaa-Iya, Bolivia	Montaño, Maffei, & Noss, 2007; Romero-	63	0.00	25	2	5743	7203
	Muñoz (2008)						
Yasuní-Waorani, Ecuador	Espinosa, S (unpublished data)	63	0.00	21	3	4721	6497
La Gloria-Lechugal, Guatemala	Moreira et al. (2007)	132	0.01	67	1	4341	6100
Ravelo, Kaa-Iya, Bolivia	Cuéllar, Dosapei, Peña, & Noss (2003)	105	0.00	30	2	3460	5025

Study site	Reference	N	SP	MTE	N Pop	СТ	CT _{97.5%}
Emas National Park, Brazil	Silveira (2004)	18	0.00	13	4	3334	5016
Golfo Dulce/Golfito, Costa Rica	Но (2008)	29	0.00	14	5	3334	5016
Morro do Diablo, Brazil	Cullen Jr. (2006)	8	0.00	11	1	3055	4211
Guanacos - Kaa-Iya, Bolivia	Cuéllar, Segundo, Castro, & Noss (2004)	105	0.00	28	3	3046	5022
Fazenda Santa Fé, Brazil	Jaguar Conservation Fund (unpublished data)	52	0.00	19	5	2504	5001
Serra da Capivara National Park,	Silveira et al. (2009)	251	0.20	83	1	2553	4654
Brazil							
Rios Tuichi & Hondo – Madidi,	Silver et al. (2004)	188	0.00	35	4	2349	4985
Bolivia							
Estación Isoso - Kaa-Iya, Bolivia	Romero-Muñoz, Maffei, Cuéllar, & Noss	222	0.00	37	4	2352	4228
	(2010)						
Tucavaca - Kaa-Iya, Bolivia	L Maffei, Julio, Paredes, Posiño, & Noss	309	0.31	86	1	2140	3929
	(2004)						

Study site	Reference	Ν	SP	MTE	N Pop	CT	CT _{97.5%}
Bosawas, Nicaragua	Polisar (2006)	282	0.26	84	1	2051	4014
Mountain Pine Ridge	Kelly (2003)	340	0.00	42	4	1797	3167
San Miguelito, Bolivia	Arispe, Rumiz, & Venegas (2005)	205	0.00	36	4	1599	3167
Cerro Cortado - Kaa-Iya, Bolivia	L. Maffei, Barrientos, Mendoza, Ity, & Noss	394	0.53	90	1	1218	3167
	(2003)						
Fireburn, Belize	Miller (2006)	191	0.00	39	2	1234	3167
El Encanto, Bolivia	Arispe, Rumiz, & Venegas (2007)	543	0.81	93	1	1185	3167
Tikal, Guatemala	García et al. (2006)	617	0.89	93	1	1061	3167
San Cristovan, Costa Rica	Amit (2007)	98	0.00	25	5	1060	3167
Corcovado, Costa Rica	Salom-Pérez, Carrillo, Sáenz, & Mora (2007)	103	0.00	26	5	1033	3167
Chiquibul, Belize	Silver et al. (2004)	606	0.00	49	4	1015	3167
Los Amigos, Peru	Carrillo-Percastegui, S; Tobler M.; and	920	0.00	64	2	310	3167
	Powell, G. (unpublished data)						
Rio Azul, Guatemala	Miller and Miller (unpublished report)	1037	0.99	94	1	230	3167

Study site	Reference	N	SP	MTE	N Pop	СТ	CT _{97.5%}
FazendaSete, Brazil	Soisalo & Cavalcanti (2006)	321	0.39	88	1	298	3167
Carmelita-AFISAP, Guatemala	McNab et al. (2008)	993	0.99	96	1	542	3167

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Supplementary Material B

Models used to test the predictive power of landscape configuration and spatial structure for jaguar population persistence probability. The models were ordinated according to their descriptive power and complexity. PC is the first principal component from the principal component analysis condensing landscape configuration. SFs (1-5) are spatial filters capturing the different spatial structures of the selected landscapes.

 X7 ' 11		A A I C	AICc	Cumulative
variables			Weighted	Weight
PC, SF3	8.33	0.00	0.24	0.24
PC, SF3, SF5	10.26	1.93	0.09	0.33
PC, SF2, SF3	10.49	2.17	0.08	0.41
PC	10.86	2.53	0.07	0.48
PC, SF3, SF4	11.12	2.80	0.06	0.53
PC, SF1, SF3	11.27	2.94	0.05	0.59
PC, SF2, SF5	11.41	3.08	0.05	0.64
PC, SF5	11.58	3.26	0.05	0.69
PC, SF4	12.50	4.17	0.03	0.72
PC, SF1	12.69	4.36	0.03	0.74
PC, SF2	12.80	4.48	0.03	0.77
PC, SF2, SF3, SF5	13.02	4.69	0.02	0.79
PC, SF2, SF3, SF4	13.12	4.79	0.02	0.81
PC, SF4, SF5	13.33	5.01	0.02	0.83
PC, SF1, SF3, SF5	13.40	5.07	0.02	0.85
PC, SF3, SF4, SF5	13.51	5.18	0.02	0.87

			AICc	Cumulative	
Variables	AICc	Δ AICc	Weighted	Weight	
PC, SF1, SF5	13.53	5.21	0.02	0.89	
PC, SF1, SF2, SF3	13.76	5.44	0.02	0.90	
PC, SF2, SF4, SF5	14.27	5.94	0.01	0.91	
PC, SF1, SF4	14.34	6.02	0.01	0.92	
PC, SF1, SF3, SF4	14.40	6.07	0.01	0.94	
PC, SF1, SF2, SF5	14.45	6.13	0.01	0.95	
PC, SF1, SF2, SF3, SF4	14.91	6.58	0.01	0.96	
PC, SF2, SF4	15.00	6.68	0.01	0.96	
PC, SF1, SF4, SF5	15.13	6.81	0.01	0.97	
PC, SF1, SF2	15.35	7.02	0.01	0.98	
PC, SF2, SF3, SF4, SF5	16.45	8.12	0.00	0.98	
PC, SF1, SF2, SF3, SF5	16.59	8.26	0.00	0.99	
PC, SF1, SF3, SF4, SF5	16.96	8.63	0.00	0.99	
PC, SF1, SF2, SF4	17.49	9.16	0.00	0.99	
PC, SF1, SF2, SF3, SF4, SF5	17.51	9.19	0.00	1.00	
PC, SF1, SF2, SF4, SF5	17.62	9.29	0.00	1.00	
SF3	21.17	12.85	0.00	1.00	
Null Model	21.54	13.22	0.00	1.00	
SF3, SF4	22.09	13.76	0.00	1.00	
SF1, SF3	22.27	13.95	0.00	1.00	
SF1	22.98	14.65	0.00	1.00	
SF4	23.56	15.24	0.00	1.00	

Variables		Δ AICc	AICc	Cumulative
	AICc		Weighted	Weight
SF3, SF5	23.58	15.26	0.00	1.00
SF2, SF3, SF4	23.89	15.56	0.00	1.00
SF2, SF3	23.91	15.58	0.00	1.00
SF5	24.00	15.67	0.00	1.00
SF2	24.03	15.70	0.00	1.00
SF1, SF3, SF4	24.48	16.15	0.00	1.00
SF3, SF4, SF5	24.62	16.29	0.00	1.00
SF1, SF4	24.62	16.30	0.00	1.00
SF1, SF3, SF5	24.98	16.65	0.00	1.00
SF1, SF2, SF3	25.22	16.89	0.00	1.00
SF1, SF5	25.51	17.18	0.00	1.00
SF1, SF2	25.58	17.26	0.00	1.00
SF4, SF5	26.24	17.91	0.00	1.00
SF2, SF4	26.25	17.92	0.00	1.00
SF2, SF3, SF5	26.38	18.05	0.00	1.00
SF2, SF5	26.70	18.38	0.00	1.00
SF1, SF2, SF3, SF4	27.10	18.78	0.00	1.00
SF2, SF3, SF4, SF5	27.16	18.83	0.00	1.00
SF1, SF3, SF4, SF5	27.55	19.22	0.00	1.00
SF1, SF2, SF4	27.55	19.23	0.00	1.00
SF1, SF4, SF5	27.57	19.24	0.00	1.00
SF1, SF2, SF3, SF5	27.95	19.63	0.00	1.00

Variables	AICc	Δ AICc	AICc	Cumulative
			Weighted	Weight
SF1, SF2, SF5	28.43	20.10	0.00	1.00
SF2, SF4, SF5	29.18	20.85	0.00	1.00
SF1, SF2, SF3, SF4, SF5	30.63	22.31	0.00	1.00
SF1, SF2, SF4, SF5	30.80	22.47	0.00	1.00
Supplementary Material C

Graphs generated by the piecewise linear regression and used to calculate the fragmentation critical thresholds. All scenarios failed to maintain viable jaguar metapopulations, so the analysis outcome presents a negative slope. Consequently, the critical thresholds indicated when metapopulation persistence probability became zero, which was not the focus of our study. The values within the graphs are the landscape total area for each simulation.

Scenarios to jaguar density = 1.12 (100 km²) 1.0 1.0 100 km² 500 km² 1 000 km² 0.8 0.8 -0.8

0.2

4

0.0 -

0 4 8 12 16 20 24 28

Number of Patches

0.2

0.0

δ 4

8 12 16 20 24 28

Number of Patches



0.2 -

0.0

5 4

8 12 16 20 24 28

Number of Patches

0.2

6 4

8 12 16 20 24 28

Number of Patches

1.0 -

0.2 -

0.0

4 8 12 16 20 24 28

Number of Patches

8 12 16 20 24 28

Number of Patches





Scenarios to jaguar density = 1.92 (100 km²)

















Scenarios to jaguar density = 4.13 (100 km²)



Scenarios to jaguar density = 5.24 (100 km²)



Scenarios to jaguar density = 5.66 (100 km²)





Scenarios to jaguar density = 7.48 (100 km²)









4 8 12 16 20 24 28

Number of Patches

0.2 -

0.0 -

6

4 8 12 16 20 24 28

Number of Patches

0.2 -

0.0

6

4 8 12 16 20 24 28

Number of Patches

0.2 -

0.0

5

4 8 12 16 20 24 28

Number of Patches

Scenarios to jaguar density = 11.56 (100 km²)

0.2 -

0.0

Ъ

12 16 20 24 28

0.0

4

8

Number of Patches

4 000 km²

12 16 20 24 28

10 000 km²

4 8 12 16 20 24 28

Number of Patches

0.2 -

0.0

CAPÍTULO 3

Esse capítulo segue as normas de formatação da revista Molecular Ecology.

1	Landscape genetics of American felids: from regional to local scales
2	
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19 Landscape genetics of American felids: from regional to local scales

20

21 **1.** Abstract

22 Human induced changes in landscapes can modify environmental permeability, which affects gene flow and the genetic structure of species. We investigated such changes in 23 24 the genetic structure of puma and jaguar populations, from the regional to the local 25 scale. In order to address this issue, we first tested the hypotheses of isolation by 26 distance, isolation by effective distance, and isolation by resistance. We used individuals pairwise distance analyses to calculate landscape isolation and correlated 27 28 these measures with genetic distances. Then, we evaluated the genetic structure through cluster analysis, delineating species populations and subpopulations. We found that 29 30 jaguars and pumas are not a uniform and panmictic population. At the regional scale, 31 spatial trends in allele frequencies for both species generated clinal patterns. However, 32 their genetic structures differed at the local scales, both in terms of the numbers of 33 subpopulations and their limits. Therefore, we observed two levels of genetic structuring (clines and clusters), occurring simultaneously, but at different scales. These 34 35 patterns were generated according to isolation by distance because the landscape could 36 be considered pristine, due to its low complexity. Lower genetic structuring was 37 expected for jaguar because they have greater movement ability in pristine areas. However, it is known that pumas have greater movement ability plasticity in 38 anthropogenic vegetation, so we suggest new studies comparing the genetic structure 39 40 for both jaguars and pumas in areas with a higher degree of habitat loss and 41 fragmentation.

42

- **Key words:** clinal pattern; isolation by distance; spatial principal component analysis;
- 44 discriminant analysis of principal components; *Panthera onca*; *Puma concolor*.

45 **2. Introduction**

46 Gene flow is a mechanism that ensures gene movement among populations, which homogenizes allele frequencies (Slatkin 1985). Gene flow is of critical 47 48 importance for a wide array of demographic and evolutionary processes, such as the regulation of local adaptation, polymorphism, effective population size, genetic drift, 49 50 selection and speciation (Lenormand 2002; Bolnick & Otto 2013). Species dispersal 51 abilities play an important role on a given population's genetic structure, as it is a 52 mechanism for gene transfer among populations and subpopulations (Lenormand 2002; François & Durand 2010). Since landscape permeability affects dispersal success, it has 53 54 a major impact on gene flow (Baguette & Van Dyck 2007; Pérez-Espona et al. 2012). Human-induced landscape changes can produce discontinuities in the 55 56 environment and modify its permeability due to alterations of the composition and 57 configuration of the landscape (Ewers & Didham 2006; Fischer & Lindenmayer 2007). Such changes may modify the genetic structure of species because they inhibit natural 58 59 patterns of gene flow and alter the distribution of genetic variation, thereby restricting dispersal and isolating populations (Guillot et al. 2005; Vandergast et al. 2007; Walker 60 et al. 2008). Susceptibility to human-induced landscape changes is related to species 61 62 ecological plasticity (Davidson et al. 2009; Thornton et al. 2011), so it is expected that 63 species with high ecological plasticity are less affected (or sometimes even favored) by landscape changes than species with strict environmental requirements (Ryall & Fahrig 64 65 2006; Villard & Metzger 2013). Therefore, comprehending how landscape alterations 66 affect species' spatial genetic structure is fundamental to their conservation and should guide the design of management strategies (Eizirik et al. 2001; Schmidt et al. 2011; 67 68 Loxterman 2011).

Here, we investigated the genetic structure of the largest felids of the Americas, 69 70 the puma (*Puma concolor*, Linnaeus, 1771) and the jaguar (*Panthera onca*, Linnaeus 1758). Pumas and jaguars have a continental distribution (IUCN 2013), suggesting both 71 72 species exhibit high environmental plasticity. However, their historical distribution has largely been reduced by human-induced landcover changes (Morrison et al. 2007). 73 74 Currently, pumas and jaguars are not listed as globally threatened, but both species 75 display a general trend of population declines (IUCN 2013). Studies at smaller scales 76 have diagnosed habitat loss and fragmentation as a threat to both species, generating isolated (Haag et al. 2010; Andreasen et al. 2012) and unviable populations (Reed 2004; 77 78 Hostetler et al. 2012; Galetti et al. 2013). These effects seem to be more severe in jaguars than in pumas (IUCN 2013) because jaguars are less tolerant of anthropogenic 79 80 alterations in their environment (De Angelo et al. 2011).

81 Due to their large distributional range and the wide scale of potential genetic responses, our study tested how dispersal capacity influences the local and regional 82 83 genetic structure of pumas and jaguars. We investigated the spatial genetic structure at the regional scale by searching for a clinal pattern for both species. To do this, we 84 measured the strength of the signal of isolation by distance in the structuring of genetic 85 86 variation *sensu* (Wright 1943). We also estimated the relative importance of landscape and environmental variables on gene flow, testing both the hypotheses of isolation by 87 effective distance sensu (Adriaensen et al. 2003) and isolation by resistance sensu 88 (McRae 2006). 89

Afterwards, we examined genetic structuring at a smaller scale, looking for
genetic clusters and delineating populations and subpopulations. Here, we examined the
difference in genetic structure (here measured as the number of clusters) between both
species. Current theory predicts that dispersal capacity is positively correlated with

94	body size (Whitmee & Orme 2013), so we expected jaguars to be able to disperse over
95	longer distances than pumas. As a consequence, genetic structuring should be lower in
96	jaguars. However, pumas have greater environmental plasticity, making them more
97	efficient at moving across human-modified landscapes (Dickson et al. 2005; De Angelo
98	et al. 2011). Consequently, pumas might have greater dispersal capacity in
99	anthropogenic landscapes than jaguars. Therefore, we have two predictions according to
100	the level of anthropogenic influence on the landscape: (i) we expect a larger number of
101	clusters for jaguars in anthropogenic landscapes; and (ii) a larger number of clusters for
102	pumas in pristine landscapes.
103	
104	3. Methods
105	
106	3.1. Sample collection and laboratory procedures
107	Our study area is located in Mexico between longitudes 107° 52' 12"W and 86°
108	31' 48" W and latitudes 24° 27' N and 14° 28' 48" N (Figure 1), covering more than 50%
109	of the country and comprising 27 states. The study area still contains a large proportion
110	of pristine habitat, composed of grasslands, scrublands, temperate forests, and lowland,
111	medium and montane forests (Bontemps et al. 2011). The study area also contains
112	anthropogenic landcover, especially agriculture and urban areas (Bontemps et al. 2011).
113	Fecal samples were collected from nine opportunistically-selected locations within the
114	
	study area (Figure 1). As a result, the sampling locations were not equidistant from each
115	other, varying from 60 km to 1900 km apart.
115 116	other, varying from 60 km to 1900 km apart. The genomic data was obtained from fecal DNA extracted from feces collected
115 116 117	study area (Figure 1). As a result, the sampling locations were not equidistant from each other, varying from 60 km to 1900 km apart. The genomic data was obtained from fecal DNA extracted from feces collected between 2005 and 2012. Fecal DNA is a non-invasive technique that has been

119	2006; Perez et al. 2006; Mondol et al. 2009; Borthakur et al. 2010). The samples were
120	collected through actively searching along dirt roads and trails. The location of each
121	fecal sample was georeferenced using a GPS and it was stored in silica gel until genetic
122	analyses were conducted.
123	The DNA was extracted using a GuSCN/silica method (Boom et al. 1990; Frantz
124	et al. 2003), and then purified and concentrated by ultra-filtration using Microcon-30
125	(Millipore). Species identification was performed according to Roques et al. 2011.
126	Individual genotyping was conducted using an optimized set of different microsatellite
127	markers for each species. For jaguars, we used 11 domestic cat microsatellite markers
128	(Fca024, Fca126, F115a, Fca176,Fca026, Fca082b, Fca077, Fca090, Fca043, Fca547b,
129	and Fca566b; Menotti-Raymond et al. 1999); whereas, for pumas, we used 12
130	microsatellite markers, eight of which were originally described for pumas (Kurushima
131	et al. 2006) and four for cats (PcoA208, PcoA216, PcoA339, PcoB003, PcoB010,
132	PcoB210, PcoC108, PcoC112, Fca077, Fca82b, Fca126, and Fca547b). For a detailed
133	description of these methods, see Roques et al. (2014) and Villela et al. (unpublished
134	data).
135	
136	3.2. Distance models

We adopted individual-based analyses to measure the degree of isolation in terms of puma and jaguar genetic structuring. We constructed a distance matrix from all possible pairwise combinations of individuals. This approach organized the data according to the similarity of the genetic profile of each individual to those of all other individuals tested. For individuals having more than one record, we randomly selected one of its locations to be used in the pairwise distance analyses.

We calculated the classical Euclidian distance to test the hypothesis of isolation by distance, which consisted of the shortest distance between pairs of individuals. We developed cost and resistance models to test both of our hypotheses. The cost models adopted least-cost route analysis, which estimates efficient movement routes and costs in landscapes (Adriaensen *et al.* 2003). The resistance models were a random walk prediction of species movements generated from a connectivity measure based on circuit theory (McRae 2006).

150 We selected a set of variables to express landscape components that could affect jaguar and puma movement and, consequently, gene flow. Variable selection was based 151 152 on studies of habitat suitability and animal movement for both jaguars and pumas, trying to select studies conducted in areas as similar as possible to our study area. For 153 154 jaguars, we constructed the cost and resistance models based on the studies of Conde et 155 al. (2010) and Colchero et al. (2011), which highlighted the effects of distance to roads, 156 human population density and landcover. For pumas, the variables selected for the cost 157 and resistance models were road density, landcover, and elevation (Dickson et al. 2005; 158 Burdett et al. 2010 - more details of the variables and models are given in the 159 Supplementary Material, Appendix A).

160 We used Geographic Information System data of landcover (Bontemps et al. 161 2011), roads, human population density and elevation (Diva-GIS, 2014) to construct the cost and resistance models for each species. The continuous variables (distance to roads, 162 population density and elevation) were transformed into permeability maps through the 163 164 model function that described the species relationship to the variable (Supplementary Material, Appendix A). The landcover map is a categorical expression of the landscape, 165 166 so we linearized the angular coefficients of the species suitability models and attributed the transformed values according to the cover type. Previous jaguar studies had 167

observed differences in the movements of males and females (Conde *et al.* 2010;
Colchero *et al.* 2011), so we constructed different GIS raster maps to express the
differing permeability of the landscape for each sex.

171 Despite having information about species movements in the landscape from previous studies, it was not clear which landscape features might affect gene flow. 172 173 Therefore, we applied a multifactorial approach, assuming that all combinations of 174 variables could potentially explain gene flow patterns, with each combination of 175 variables representing a hypothesis of landscape permeability. For jaguars, which exhibit sex-biased permeability, the multifactorial approach was conducted with five 176 177 sets of variables: (i) average sex permeability for each variable, i.e. we assumed that gene flow was symmetric of both sexes; (ii) female- and (iii) male-specific permeability 178 179 rasters, i.e. we supposed an asymmetric sex-biased effect whereby only one gender was 180 responsible for gene flow; (iv) minimum permeability based on the barrier principle, so the lower permeability for one sex was sufficient to restrict gene flow; and the 181 182 alternative (v) maximum permeability, whereby the higher permeability of one sex was sufficient to permit gene flow. These cost and resistance models were analyzed in R 183 184 software (R Core Team 2013) using the gdistance package (van Etten 2012); the final 185 output of these analyses being pairwise estimates of effective distance and resistance 186 between individuals.

187

188

3.3. Isolation pattern among individuals

We used Spatial Principal Component Analyses (sPCA) to summarize the genetic diversity and, at the same time, to reveal spatial structure. As for classical Principal Component Analysis (PCA), sPCA is an ordination method for variable reduction, but it has the advantage of optimizing the data variance for principal components scores as well as encompassing spatial structure (Jombart *et al.* 2008).
Therefore, when applied to allelic frequency data, the genetic variability among
individuals is summarized into a few uncorrelated components, which maximizes the
genotypic variance, and spatial information is also taken into account (Jombart *et al.*2008). Moreover, the use of sPCA to explore genetic data does not require populations
to be in Hardy–Weinberg equilibrium or linkage equilibrium, since it is not based on a
genetic model (Jombart *et al.* 2008).

200 This approach requires the generation of a connection network to define the neighboring sites, transforming the PCA into a spatially explicit method. We used a 201 202 distance-based neighborhood graph with 100 km as a threshold of maximal distance 203 between connected individuals (a reasonable average of species home-ranges) (Cullen 204 Jr. 2006; Cavalcanti & Gese 2009). This type of connection network is recommended 205 for data with an aggregated distribution (Jombart et al. 2008), such as our records. 206 Spatial structure was detected by conducting Moran's I test (Moran 1948, 1950), which 207 may assume positive or negative values. Therefore, the sPCA eigenvalues can reveal 208 two types of spatial pattern: positive Moran's I (global structure) and negative Moran's I (local structure) (sensu Thioulouse et al. 1995). A pattern of global spatial structure 209 210 occurs when the allelic frequencies among neighbors are more similar than that of a 211 random distribution, whereas a local spatial structure occurs when the allelic frequencies among neighbors are more dissimilar than for a random distribution 212 (Jombart et al. 2008). 213

The selection of principal components was done graphically, balancing the genetic variability and spatial structure summarized in the principal components. The criterion of percentage variability explained by eigenvalues that is common in a classical PCA cannot be applied in a sPCA because the principal components also

express the product of spatial autocorrelation. Therefore, we considered the abrupt
decrease in information contained in the eigenvalues as a threshold to select principal
components (Legendre & Legendre 1998). Due to the subjectivity of our criterion, the
global and local tests (Jombart *et al.* 2008) were applied to confirm the presence of a
spatial pattern in the axes. These analyses were done in R software (R Core Team 2013)
using the *adegenet* package (Jombart & Ahmed 2011).

224 The principal components selected were used to calculate the pairwise genetic 225 dissimilarity between individuals, which consisted of a Euclidian distance of individuals' score. Genetic dissimilarity was correlated with landscape distances to 226 227 evaluate the pattern of gene flow, following a causal modeling framework (Cushman 2006). The causal modeling framework is an efficient method to identify paths of gene 228 229 flow in complex landscapes, allowing landscape permeability hypothesis to be tested 230 (Cushman & Landguth 2010; Cushman et al. 2013). Correlations were carried out by 231 means of a Mantel test in the vegan package (Oksanen 2012) in R (R Core Team 2013). 232

252

233

3.4. Genetic clustering analysis

Bayesian cluster analyses were performed to investigate population structure in 234 235 the data set, i.e. to assign individuals into clusters. It has been recommended to confirm 236 genetic structure patterns using both non-spatial and spatial approaches (Chen et al. 2007; Frantz et al. 2009), so we employed both the STRUCTURE (non-spatial; 237 Pritchard et al. 2000; Falush et al. 2003) and TESS (spatial; Chen et al. 2007; Durand et 238 239 al. 2009) software packages to identify populations. Both of these software packages use Markov Chain Monte Carlo algorithms to identify k populations without a priori 240 241 group definition. They also have the option of applying an admixture model, which 242 permits efficient classification of individuals into a population even if the source

population has not been sampled (Durand *et al.* 2009). The main difference between the
two algorithms applied by these packages is that TESS assumes geographical continuity
of allele frequencies, which would make neighboring sites more similar than distant
sites (François *et al.* 2006). This feature allows TESS to detect clines and/or clusters,
making it the most efficient Bayes algorithm to be applied to scenarios with data on the
effects of isolation by distance (François & Durand 2010).

249 We ran admixture models in STRUCTURE and TESS, using 10,000 iterations 250 after a burn-in period of 100,000 iterations, for k = 2 - 9, with 10 independent runs for each k. For the non-spatial model, the logarithm of the probability of the data (LnP(D); 251 252 Pritchard *et al.* 2000) and Δk (Evanno *et al.* 2005) were plotted against k to identify the plateau of the curve and, consequently, to estimate the number of clusters (François & 253 254 Durand 2010); for the spatial model, this relationship was determined using the 255 deviance information criterion (DIC; Spiegelhalter et al. 2002). The CLUMPP software 256 (Jakobsson & Rosenberg 2007) was used to average the admixture proportions of 257 individuals over the 10 replicates of the most likely k. 258 These Bayesian methods are efficient for assigning individuals into populations, but they may fail to identify subdivisions within populations (Jombart & Ahmed 2011). 259 260 Thus, a classical statistical analysis may detect fine-scale changes in genetic 261 configuration more efficiently because it is not based on models of population genetics. We performed a Discriminant Analysis of Principal Components (DAPC) to investigate 262 if the two species showed a finer substructure than that of population. Discriminant 263 264 Analysis (DA) is a method that sorts individuals into pre-defined clusters, focusing on increasing between-group variability while reducing within-group variation (Legendre 265

266 & Legendre 1998). It has limited use in genetic studies because DA demands a higher

267 number of sampling units than variables (Legendre & Legendre 1998), which is rarely

268	the case in genetic data. DAPC uses PCA as a prior step to DA, condensing the data and
269	thereby satisfying the DA requirements (Jombart & Ahmed 2011). We used the
270	sampling areas as a priori individual clusters and made a graphical interpretation of
271	individuals' ordination and assignment to define the final subpopulations. DAPC was
272	performed using the adegenet package (Jombart & Ahmed 2011) in R software (R Core
273	Team 2013).

275

3.5. Descriptive statistics of genetic clusters

To measure the genetic diversity of the identified groups (populations and 276 277 subpopulations), we calculated the allele richness and rarefied allele richness (using the Hp-Rare software - Kalinowski 2005), and the observed (H_o) and expected 278 279 heterozygosity (He) under Hardy-Weinberg assumptions (using the FSTAT software -280 Goudet 2002). The significance of Hardy-Weinberg equilibrium was evaluated through 281 a Bonferroni correction of P-values (Rice 1989). We estimated inbreeding for each 282 subpopulation to measure the degree of substructure, which may be driving the subpopulations into more divergent groups. Therefore, we calculated F_{IS} over 283 subpopulations and loci using the FSTAT software (Goudet 2002) with 10,000 284 permutations. The degree of population differentiation was measured by F_{ST} and R_{ST} 285 286 using the SPAGeDi software (Hardy & Vekemans 2013). 287

288 **4. Results**

We could identify a total of 205 samples for each species. For pumas, a total of 158 samples belonging to 67 individuals were genotyped. For jaguars, a total of 151 samples belonging to 34 individuals were genotyped (Table S4). For both species, the cost and resistance models produced landscape distances strongly correlated with

Euclidian distances (average Pearson correlation between landscape distance and Euclidian distance; Puma - r = 0.98, p < 0.01; Jaguar - r = 0.99, p < 0.01). Therefore, the least-cost and resistance distances were not informative about landscape permeability and species movement. Thus, we assumed that the environment was pristine for both species because we did not detect high contrast of suitability on the landscape. Consequently, we only used Euclidian distances in the subsequent analyses to test the isolation-by-distance hypothesis.

300 We only selected the first eigenvalue from each sPCA because there was a strong decrease in eigenvalues thereafter (Figure 2a and b), they summarized a 301 302 significant amount of the genetic variance (Variance ≈ 0.4) and captured the spatial 303 structure (Figure 2 c and d). The global test confirmed the evidence of a global spatial 304 pattern indicated by a positive eigenvalue score (Global Test; Puma = 0.06, p < 0.01; 305 Jaguar= 0.09, p < 0.01), whereas there was no support for a local spatial pattern (Local 306 Test; Puma = 0.03, p = 0.18; Jaguar = 0.05, p = 0.62). Therefore, we only used the first 307 principal component to calculate pairwise genetic distances between individuals. The 308 Mantel tests evidenced a correlation between genetic distance and the logarithm of Euclidian distance (Figure 3), revealing a gradual and continuous change in genetic 309 310 composition according to spatial distance, which is characteristic of a clinal pattern at a 311 regional scale. Thus, we corroborated the hypothesis of isolation by distance for both pumas and jaguars. 312

We observed differing numbers of clusters according to the curve plateau of the Bayesian methods used. STRUCTURE inferred six populations for pumas and three for jaguars when we interpreted the Δk scores (Figure 4a and b), while LnP(D) scores also suggested six populations for pumas, but only two for jaguars (Figure 4c and d). The DIC score estimated by TESS identified three and four as the most likely k for pumas

318 and jaguars, respectively (Figure 4e and f). However, STRUCTURE was inefficient in 319 assigning either puma or jaguar individuals into genetic clusters; plots of its assignment proportion estimates showed a continuous and unbroken allele frequency distribution, 320 321 making it impossible to define subclusters (Figure 5a-f, top plots). In contrast, TESS presented more consistent individual assignments (Figure 5a-f, bottom plots), allowing 322 us to distinguish boundaries between genetic clusters. We identified a clear 323 324 discontinuity in assignment proportions in the region of El Carmen, making this a clear 325 boundary between two populations for both species (Figure 5a-f, bottom plots). The F_{ST} and R_{ST} values confirmed the significant genetic differentiation between puma 326 327 populations (F_{ST} = 0.07, p < 0.01; R_{ST} = 0.13, p < 0.01) and jaguar populations (F_{ST} = 0.15, p < 0.01; $R_{ST}=0.17$, p=0.01). Thus, we could conclude that the number of clusters 328 329 suggested by these curve plateau approaches (i.e. Δk , LnP(D) and DIC score) are all 330 overestimated.

In the DAPC clustering method, we selected the principal components to 331 332 accumulate 80% of the total variation, which consisted of 21 eigenvalues for puma and 333 13 eigenvalues for jaguar. The final ordination was done with the first two discriminant functions because we observed a strong reduction in explanatory power after the second 334 function (Figure 6). The assignment efficiency of DAPC was higher for pumas than for 335 336 jaguars (average assignment probability: Puma = 0.75 and Jaguar = 0.62). Therefore, we did an additional analysis to evaluate if the higher efficiency for pumas could reveal a 337 biological pattern to be further explored, or if it was only a mathematical artifact due to 338 339 having sampled a higher number of individuals of this species and, thus, disproportionately having greater statistical power. We evaluated the assignment 340 341 efficiency of DAPC by means of 10,000 random subsamples of 34 pumas, i.e. the same sample size for jaguars in our study. The higher assignment efficiency for pumas was 342

observed even for the smaller dataset (Figure 7), giving us the first evidence of strongergenetic structuring in pumas compared to jaguars.

We confirmed the structure of the populations, but the subpopulations 345 346 corresponded only partially to the *a priori* groups (Figure 8). In the DAPC, El Carmen was considered a different cluster for both species, but jaguars from El Carmen were 347 348 more isolated than pumas (Figure 8). El Eden and Zapotal can be considered the same 349 subpopulation for both species (Figure 8). However, we note a transitioning of the 350 genetic configuration for pumas, akin to a gradient (best visualized in the assignment proportions of Figure 8), revealing genetic structuring at a small spatial scale. This same 351 352 pattern is also observed for pumas from Petcacab, Cojolite, Calakmul and Caobá (Figure 8a) and for jaguars from Petcacab, Caobá, Calakmul and Ocotones (Figure 8b); 353 354 these four areas respectively defining other subpopulations of pumas and jaguars. For 355 pumas, we also identified Selva de Ocone and Ocotones as subpopulations (Figure 8a). 356 Therefore, we assumed a total of five subpopulations for pumas and three for jaguars 357 (Table 2), which corroborates our hypothesis of stronger spatial structure for pumas in a pristine environment (as suggested by permeability models). 358

We adopted the DAPC clusters to carry out diversity estimates. All loci were 359 360 polymorphic for both species; the numbers of alleles in subpopulations ranged from 20 361 to 76 for pumas and from 29 to 57 for jaguars (see Table S4 and S5 for estimates by locus). Following a rarefaction procedure, the average allele richness over loci ranged 362 from 1.67 to 4.00 for pumas and from 2.57 to 2.79 for jaguars (Table 1). No locus 363 364 showed linkage disequilibrium after Bonferroni correction for multiple comparisons. In addition, following Bonferroni correction, there was no evidence of inbreeding in 365 366 subpopulations for either species (Table 1). However, pumas exhibited higher variation

in genetic diversity (ranging from 0.56 to 0.76) compared to jaguars (ranging from 0.62
to 0.70) (Table 1).

369

370 **5. Discussion**

The overall genetic variation showed that the study area does not represent a uniform and panmictic population for pumas and jaguars. At a regional scale, pumas and jaguars exhibited similar patterns, showing a clinal trend in allele frequencies from El Carmen to El Edén (François & Durand 2010). At the same time, their genetic structures differed at the local scale because they showed differences in the number of subpopulations. Therefore, we note that both levels of genetic structure investigated (clines and clusters) acted simultaneously, but at different scales.

378 The study area exhibited low landscape heterogeneity and complexity, so our 379 results do not support the isolation by effective distance or resistance hypotheses. The 380 absence of landscape population structuring is probably due to two features of our study 381 area. The first is the low complexity of the landscape configuration; the study area 382 comprises a large and connected block of native vegetation extending from El Edén to Los Ocotones. The second is the limited variability in permeability among the landscape 383 384 features. The detectability of landscape effects on genetic structure is correlated with the 385 extent to which landscape features limit animal movement and gene flow. It is also correlated with animal perceptions of the boundaries between landscape elements 386 (Jaquiéry et al. 2011; Cushman et al. 2011, 2013). Therefore, genetic differentiation due 387 388 to landscape alteration is stronger for species with lower environmental plasticity because the boundaries between landscapes elements will affect them more strongly 389 390 (Cushman et al. 2013).

391 Our results showed a clinal pattern for both species, indicating that vegetation 392 was not a genetic barrier. It is known that genetic processes act within different time 393 scales compared to landscape change (Wagner & Fortin 2013; Ewers et al. 2013), so it 394 is possible that the spatial genetic structure of puma and jaguar will change over generations. The time it takes for a species to respond to landscape changes is called 395 396 'relaxation time' in the ecological literature and it seems to be positively correlated with 397 longevity and dispersal ability (Hylander & Ehrlén 2013), suggesting a long relaxation 398 time for jaguars and pumas.

Both species could be divided into two populations, with the fragmented area 399 400 between Los Ocotones and El Carmen as a boundary. However, this fragmented area 401 also represents a sampling gap in our study, so this population division is probably gradual as suggested by the clinal pattern found. Such clinal patterns can confuse the 402 403 determination of populations and their boundaries, even using software that adopt 404 spatial approaches, making it difficult to differentiate genuine clusters from sampling 405 artifacts (Dyer & Nason 2004; Frantz et al. 2009). However, assignment statistics can 406 be quite revealing in terms of uncovering patterns of isolation by distance.

Pumas are structured into a larger number of subpopulations than jaguar in our 407 408 study area, corroborating our hypothesis of a stronger influence of landscape effects on 409 isolation by distance in pumas due to low landscape complexity. Our prediction was associated with the generalized theory of dispersal ability for species (Whitmee & Orme 410 411 2013), so we had expected that jaguar would have a greater movement potential in 412 pristine areas due to its larger body size. However, jaguars are known to have lower ecological plasticity than pumas in anthropogenic habitats, so such habitats should 413 414 structure jaguar populations into more clusters due to a reduced dispersal success. 415 Therefore, we recommend that new studies be carried out comparing the genetic

416 structuring of jaguars and pumas in areas with a higher degree of habitat loss and417 fragmentation.

In our study, we observed that the clusters and clinal patterns detected were 418 419 mainly generated due to isolation by distance. In landscapes with a low degree of fragmentation, animal movements approach a random walk pattern, thereby structuring 420 421 the genetic configuration at a local scale (François & Durand 2010). This pattern can 422 extend across larger distances, generating isolation by distance pattern from regional- to 423 species-distribution scales (François & Durand 2010). Isolation by distance is one of the most tested patterns in population genetics and evidence for it has been presented for 424 425 many species, including other carnivores with large dispersal ability (Paetkau et al. 1999; Castilho et al. 2011; Loxterman 2011). 426

427 In a conservation context, we observed that no subpopulation of either species 428 presented a signal of inbreeding depression and the genetic diversity indices are similar 429 to those of other feline populations (Loxterman 2011; Miotto et al. 2011; Andreasen et al. 2012; Dutta et al. 2013). However, fragmentation of the habitat between these 430 populations represents a potential future risk for these species by driving loss of genetic 431 diversity due to a reduction in gene flux and population viability (Flather & Bevers 432 433 2002; Ovaskainen & Hanski 2003; Cushman et al. 2006, 2013). Species conservation is 434 not only related to maintenance of genetic diversity and avoiding inbreeding depression, 435 it is also necessary to secure evolutionary and demographic processes. Therefore, the 436 current scenario should not be viewed as a reason not to enact management strategies. 437 Instead, it should be seen as an opportune time to evaluate the future consequences of recent human-induced changes and, if necessary, to design appropriate conservation 438 439 plans to avoid further genetic erosion.

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441	6.	References
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	656	Table 1.	Genetic	diversity	estimates	for pun	na and	jaguar	subpo	pulations.	AR	-rarefied
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allelic richness averaged over loci; Ho – observed heterozygosity; He – expected

	AR	Ho (SD)	He (SD)	Fis
Puma concolor				
El Edén and Zapotal	3.22	0.61 (0.08)	0.65 (0.11)	0.12
Petcacab, Cojolita, Calakmul and Caobá	3.29	0.65 (0.11)	0.66 (0.11)	0.06
Selva el Ocone	2.50	-	-	-
Ocotones	1.67	0.69 (0.33)	0.55 (0.24)	-0.22
El Carmen	4.00	0.71 (0.11)	0.76 (0.11)	0.12
Panthera onca				
El Edén and Zapotal	2.79	0.62 (0.26)	0.58 (0.23)	-0.06
Petcacab, Caobá, Calakmul and Ocotones	3.24	0.70 (0.19)	0.66 (0.17)	-0.03
El Carmen	2.57	0.64 (0.20)	0.59 (0.16)	-0.03







- 662 (4) Ejido Caoba; (5) Calakmul; (6) La Cojolita; (7) Selva El Ocone; (8) Los Ocotones;
- and (9) El Carmen. Dashed line is the limit of our study area used for cost and
- resistance models and gray color represents native vegetation cover.



Figure 2. Selection of principal components of the Spatial Principal Components
Analysis (sPCA) for puma (left) and jaguar (right). Upper graphs (a and b) are
eigenvalues expressing the explanatory power of the principal components. Lower
graphs (c and d) display the genetic variance and spatial autocorrelation (measured by
Moran's Index) contained in each principal component. For both species, the first
principal component is the only one that captures spatial structure and substantial
genetic variation, which corresponds to the outlier point in both graphs c and d.



Figure 3. Correlations between genetic and logarithm of Euclidian distance for puma (a)

675 and jaguar (b).



Figure 4. Number of genetic clusters (k) estimated by STRUCTURE (a-d) and TESS (e and f) for pumas (left panels) and jaguars (right panels). Δk and average log likelihood LnP(D) results show k =6 for pumas (a and c, respectively) as the best fit of the data for the highest level of hierarchical genetic structure; for jaguars, the best fit was k = 3 (b) and k = 2 (d) for Δk and LnP(D) respectively. The deviance information criterion (DIC) scores computed by the TESS admixture model indicated k = 3 for pumas (e) and k = 4 for jaguars (f). The intervals represented in figures c-f are the standard deviations.



Figure 5. Bar plots showing the assignment proportions of individuals for

686 STRUCTURE (top) and TESS (bottom). Left-hand-side panels are puma-assigned

groups for k = 2 (a), k = 3 (b), and k = 6 (c). Right-hand-side panels are jaguar-assigned

groups for k = 2 (d), k = 3 (e), and k = 4 (f). Numbers along the bottom of (c) and (f)

689 indicate the sampling location of individuals (see Figure 1).



690

691 Figure 6. Eigenvalues expressing the explanatory power of the linear discriminant

692 function of the Discriminant Analysis of Principal Component analysis for puma (a) and

693 jaguar (b).





Figure 7. Proportion of pumas correctly assigned into 10,000 random subsamples to



697 Component analysis due to differences in sample size for puma and jaguar. Dashed line

698 marks the average assignment proportion for jaguar, which was often lower than the

average assignment proportion of puma subsamples (Mean = 0.80).



Figure 8. Summary of Discriminant Analysis of Principal Component results. Genotype
ordination for pumas (a) and jaguars (b) are given in the left-hand-side panels, showing
differentiation into groups (points and circle of the same color) and between group
variation (distance of one group centroid to another). The right-hand-side panels show
the assignment proportions of individuals for each sampling location (numbers along
bottom; see Figure 1 legend for spatial location).

Appendix A. Raster creation representing landscape permeability for jaguars and pumas

Jaguar

We used three variables to calculate the permeability of the landscape for jaguars: distance to roads, human population density and landcover. These variables were selected based on the studies of (Conde *et al.* 2010; Colchero *et al.* 2011). These studies uncovered sex-biased differences in habitat use and movement, so we constructed different permeability rasters for each sex.

Distance to roads

Firstly, we created a raster of distance to road (in kilometers) through the function map calculator of ArcGIS using road shapefiles from Mexico, Guatemala and Belize (Diva-GIS 2014). Then, we applied the logistic function representing the model of habitat selection reported by (Colchero *et al.* 2011) using the map calculator in ArcGIS:

Female = Exp([Road Distance] * 0.776) / (1 + Exp ([Road Distance] * 0.776))Male = Exp ([Road Distance] * 0.305) / (1 + Exp ([Road Distance] * 0.305))

Human population density

We converted the raster of human population (Diva-GIS 2014) into a human population density (HPD) function and calculated the model function of (Colchero *et al.* 2011):

Female = Exp([HPD] *(-2.386)) / (1 + Exp([HPD] *(-2.386)))

Male = Exp([HPD] * 0.219) / (1 + Exp [HPD] * 0.219)

Landcover

We used coefficients of the models of Conde *et al.* (2010) to express transformed landcover type suitability; to mirror other variables used in the distance models, they were linearly transformed to vary from zero to one. The transformation was done taking account of the range of variation of both sexes and capturing the differences between females and males (Table S1). We attributed the linear scores to the landcover map (Bontemps *et al.* 2011) based on the similarity of cover types described in the landcover map of Conde *et al.* (2010) (Table S2).

Pumas

We also used three variables in the distance models for pumas: road density, topography and landcover. Unfortunately, we did not find studies of habitat selection and movement for pumas in our study area, so the variables were selected according to studies conducted in different environments. We assumed that the hierarchical relationship of habitat preferences is the same, independently of region. These other puma studies did not evaluate sex-biased habitat selection, so we created only one permeability raster for each variable.

Road density

We adapted the results of Dickson *et al.* (2005), who state that "*total paved road density was about 21% lower on cougar travel paths* (4.20*m/km2*, x=0.10 +/- 0.20*m/km2* [*SD*]) compared to available paths (5.30*m/km2*, x=0.12 +/-0.22m/km2; t= -2.16, P=0.04, n=44)". Thus, we assumed a road resistance of 21% (79% permeability). However, tracks facilitate puma movement: "density of dirt roads was slightly higher on paths used by cougars (62.50m/km2 x=1.42 +/-1.04m/km2)

compared to available paths (59.17m/km2, x=1.34 +/-0.78m/km2; t=1.48, P=0.15, n=44). Buffered movement segments intersected dirt roads in all but 2 sessions, during which no dirt roads were available. All tracked individuals encountered or used dirt roads (368 occasions during 41sessions)" (Dickson *et al.* 2005). Therefore, tracks do not impede puma movement, but instead facilitate movement 5.63% more than for native landcover. These values of permeability (79% and 105.63%) were linearly transformed to vary from zero to one, resulting in scores of 0.75 and 1 for tracks and roads, respectively.

Landcover

The model coefficients of (Burdett *et al.* 2010) were used as a measure of landcover suitability. As for the other variables, the coefficients were linearly transformed to vary from zero to one (Table S3) and the resulting scores were attributed to the landcover map (Bontemps *et al.* 2011) based on the similarity of cover types (Table S2).

Topography

We converted the altitude raster (Diva-GIS 2014) through the function described in (Burdett *et al.* 2010) using the map calculator tool of the ArcGIS software: Puma Topography = Exp([Altitude] * 12.11) / (1 + Exp([Altitude] * 12.11))

Vegetation Type	Coefficient	Linear transformation
Female		
Agriculture-cattle	-2.784	0.075
Secondary vegetation	-3.034	0.000
Short forest	0.021	0.917
Tall forest	-0.364	0.802
Male		
Agriculture-cattle	-0.270	0.830
Secondary vegetation	-0.834	0.660
Short forest	-0.563	0.742
Tall forest	0.297	1.000
Swamps	-0.492	0.763

Table S1. Linearly transformed scores from (Conde *et al.* 2010) describing permeability of landcover type for jaguars.

 Table S2. Attribution of linear scores to landcover types in the (Bontemps *et al.* 2011)

 landuse map.

Vegetation Type	Jaguar	Jaguar	Puma
	(female)	(male)	
Rainfed croplands	0.075	0.830	0.199
Mosaic Croplands/Vegetation	0.075	0.830	0.199
Mosaic Vegetation/Croplands	0.075	0.830	0.199
Closed to open broadleaved evergreen or	0.802	1.00	0.199
semi-deciduous forest			
Closed broadleaved deciduous forest	0.802	1.000	1.000
Open broadleaved deciduous forest	0.802	1.000	1.000
Closed needleleaved evergreen forest	0.802	1.000	1.000
Closed to open mixed broadleaved and	0.802	1.000	1.000
needleleaved forest			
Mosaic Forest-Shrubland/Grassland	0.917	0.742	1.000
Mosaic Grassland/Forest-Shrubland	0.917	0.742	0.251
Closed to open shrubland	0.917	0.742	0.251
Closed to open grassland	0.917	0.742	0.251
Sparse vegetation	0.000	0.660	0.000
Closed to open broadleaved forest, regularly	0.000	0.763	0.000
flooded (fresh-brackish water)			
Closed broadleaved forest, permanently	0.000	0.763	0.199
flooded (saline-brackish water)			
Closed to open vegetation, regularly flooded	0.000	0.763	0.251

Table S3. Linearly transformed scores from (Burdett et al. 2010) describing

Vegetation Type	Coefficient	Linear
Barren	-0.870	0.035
Coastal scrub	-0.250	0.251
Grassland	-0.970	0.000
Riparian	1.900	1.000
Oak woodland	0.650	0.564
Exurban	-0.400	0.199
Suburban/Urban	-0.800	0.059

permeability of landcover type for puma.

Location	Puma	Jaguar
El Edén	36 (6:7)	37 (6:0)
El Zapotal	57 (5:8)	51 (7:0)
Petcacab	14 (2:5)	18 (4:1)
Ejido Caoba	12 (1:3)	14 (3:1)
Calakmul	27 (3:6)	20 (6:1)
La Cojolita	3 (1:1)	0 (0:0)
Selva El Ocone	1 (0:1)	0 (0:0)
Los Ocotones	23 (2:1)	1 (1:0)
El Carmen	31 (7:7)	10 (2:2)

Table S4. Number of identified scats collected in each sampling location for pumas and jaguars (males:females indicated in brackets).

Loci	El Edén and Zapotal				Petcacab, Cojolita, Calakmul and Caobá								Selva el Ocone							Ocotones						El Carmen							Global Da				
	N	Α	AR	PA	Ho	He	Fis	Ν	А	AR	PA	Но	He	Fis	Ν	Α	AR	PA	Ho	He F	Fis l	ΝA	AR	PA	Но	He	Fis	N	A AR	PA	Но	He	Fis	N	А	Ho	He
Fca077	26	6	2.49	0.42	0.54	0.56	0.07	23	3	2.60	0.65	0.52	0.59	0.11	1	2	1.00	0.00	-	-	-	3 1	1 2.00	0.00	0.00	0.00	- 0	14	8 4.65	3.11	0.71	0.84	0.15	67	11	0.55	0.57
Fca126	26	6	3.20	0.65	0.69	0.62	<-0.01	23	6	2.86	0.54	0.52	0.50	0.04	1	1	2.00	0.00	-	-	-	2 2	2 1.00	0.04	1.00	0.50	0-1.00	14	5 3.46	0.73	0.64	0.72	0.11	66	7	0.56	0.55
Fca547b	23	5	3.16	0.83	0.70	0.71	0.06	21	6	3.28	0.70	0.62	0.67	0.21	1	1	2.00	0.00	-	-	-	3 2	2 1.00	0.00	1.00	0.50	0-1.00	4	2 3.00	0.00	0.8	0.50	-0.33	52	6	0.57	0.6
Fca82b	23	7	4.47	1.13	0.74	0.86	0.17	21	7	4.12	0.63	0.71	0.80	0.11	1	1	2.00	0.00	-	-	-	3 2	2 1.00	0.08	0.33	0.33	3 0.00	13	8 4.60	1.85	0.77	0.81	0.05	61	11	0.51	0.65
PcoA208	26	5	2.58	0.53	0.54	0.56	0.03	23	4	2.67	0.14	0.56	0.60	0.09	1	2	4.00	0.00	-	-	-	34	4 2.00	1.09	0.67	0.83	3 0.20	14	7 4.36	1.61	0.93	0.80	-0.16	67	9	0.77	0.7
PcoA216	26	6	3.08	0.64	0.54	0.56	0.10	20	5	2.85	0.53	0.70	0.58	-0.11	1	2	2.00	0.37	-	-	-	3 2	2 2.00	0.34	0.67	0.50	00.00	14	8 3.83	2.00	0.57	0.76	0.25	64	10	0.64	0.65
PcoA339	24	8	4.26	1.51	0.62	0.79	0.28*	23	9	4.21	1.42	0.83	0.77	-0.02	1	1	4.00	0.00	-	-	-	3 3	3 1.00	1.35	1.00	0.8	8-0.33	14	8 4.23	2.37	0.78	0.85	0.17	65	14	0.62	0.74
PcoB003	21	6	2.94	0.09	0.57	0.62	0.11	22	5	3.37	0.31	0.55	0.64	0.18	1	2	2.00	0.07	-	-	-	2 2	2 2.00	0.05	1.00	0.50	0-1.00	10	7 4.55	1.80	0.70	0.87	0.34	56	8	0.73	0.73
PcoB010	24	7	3.57	0.85	0.50	0.71	0.48**	20	7	4.26	0.88	0.7	0.82	0.29	1	2	3.00	0.00	-	-	-	3 3	3 2.00	1.10	1.00	0.67	7 -0.50	14	7 4.50	2.17	0.78	0.79	0.06	62	12	0.74	0.80
PcoB210	26	7	3.59	0.39	0.65	0.75	0.15	23	7	3.96	0.16	0.87	0.78	-0.1	1	2	2.00	0.52	-	-	-	3 2	2 2.00	0.14	0.33	0.67	7 0.50	13	9 4.70	2.41	0.77	0.87	0.1	66	11	0.72	0.79
PcoC108	24	3	2.10	0.15	0.54	0.47	-0.16	23	2	1.99	0.00	0.61	0.50	-0.18	1	2	2.00	0.00	-	-	-	3 2	2 2.00	0.00	0.67	0.50	0-0.33	13	3 2.25	0.32	0.61	0.57	0.23	64	4	0.65	0.56
PcoC108	24	6	3.22	0.00	0.71	0.67	-0.02	23	6	3.37	0.00	0.70	0.71	0.03	1	2	4.00	0.72	-	-	-	34	4 2.00	0.04	0.67	0.92	2 0.27	10	4 3.87	0.71	0.50	0.8	0.41	61	6	0.69	0.79

Table S5. Measures of diversity at 12 microsatellite loci in the five puma subpopulations identified in the study.

Sample size (N), allelic richness (A), rarefaction of allelic richness (AR), private alleles (PA), observed (Ho) and expected (He) heterozygosities,

and inbreeding coefficient (Fis).

Allele richness and private alleles calculated with the HP-Rare software based on seven genes.

* p<0.01

** p< 0.001

Loci			El	Edén a	ind Zap	otal		Р	etcac	ab, Cao	obá, Ca	lakmul	and O	cotones				El C	Carmen	L			Glo	bal Dat	a
	N	А	AR	PA	Но	He	Fis	Ν	А	AR	PA	Но	He	Fis	Ν	Α	AR	PA	Но	He	Fis	Ν	А	Ho	He
FC24	11	3	2.64	0.02	0.85	0.60	-0.36	14	3	2.39	0.00	0.56	0.58	0.13	4	2	2.00	0.20	0.8	0.50	-0.50	29	3	0.69	0.56
FC26	12	3	2.60	0.85	0.92	0.59	-0.55	13	5	2.97	0.54	0.94	0.64	-0.43	3	2	2.00	0.32	0.8	0.50	-0.33	28	5	0.83	0.58
FC43	13	2	1.99	0.00	0.54	0.52	-0.04	17	4	2.56	0.21	0.65	0.59	-0.09	3	2	2.00	0.63	0.3	0.67	1.00	33	4	0.39	0.56
FC77	13	5	3.58	0.30	0.77	0.8	-0.03	15	6	3.78	0.44	0.70	0.78	0.15	4	3	3.00	0.14	0.8	0.71	-0.06	32	6	0.73	0.75
FC82	13	1	1.00	0.00	0.00	0.00	-	17	2	1.62	0.00	0.23	0.21	-0.10	4	2	2.00	0.38	0.8	0.50	-0.50	34	2	0.33	0.23
FC90	11	3	2.21	0.02	0.50	0.39	-0.16	14	5	3.60	1.29	0.81	0.73	-0.07	4	3	2.88	0.24	0.8	0.67	-0.12	29	5	0.66	0.59
FC115	12	7	4.35	2.25	0.54	0.83	0.40	17	12	4.77	2.67	0.76	0.85	0.10	4	3	3.00	2.00	0.8	0.71	-0.06	33	16	0.67	0.81
FC126	12	4	2.86	0.56	0.85	0.62	-0.34	16	4	2.85	0.55	0.65	0.62	-0.01	4	2	1.88	0.88	0.3	0.3	0.00	32	6	0.57	0.50
FC176	12	3	2.47	0.06	0.61	0.56	-0.03	14	5	3.45	0.75	0.73	0.74	0.03	4	3	2.75	1.07	0.50	0.46	-0.09	30	6	0.60	0.59
FC547	13	4	3.05	0.09	0.54	0.70	0.27	16	5	3.73	0.90	0.87	0.78	-0.17	4	4	3.75	1.91	0.8	0.8	0.00	33	7	0.72	0.74
FC566	13	5	3.96	0.83	0.77	0.80	0.04	14	6	3.93	0.81	0.82	0.79	0.01	4	3	3.00	1.01	0.8	0.8	0.00	31	7	0.77	0.78

Table S6. Measures of diversity at 11 microsatellite loci in the three jaguar subpopulations of the study.

Sample size (N), allelic richness (A), rarefaction of allelic richness (AR), private alleles (PA), observed (Ho) and expected (He) heterozygosities,

and inbreeding coefficient (Fis).

Allele richness and private alleles calculated with the HP-Rare software based on seven genes.

No loci exhibited significant Fis values.

DISCUSSÃO GERAL

Em nossa pesquisa, estudamos aspectos referentes ao efeito da perda e fragmetação de habitat sobre felinos, testando hipóteses ecológicas relacionadas ao tema e investigando aspectos socio-ambientais relevantes para a conservação das espécies. Compreender os efeitos da perda e fragmentação do habitat sobre os felinos consiste em um aspecto relevante não apenas para o grupo em questão, mas também para todo o ecossistema onde ocorrem, devido a função ecológica exercida por eles (Ritchie & Johnson, 2009). A extinção de predadores de topo de cadeia alimentar, função ecológica amplamente desenvolvida pelos felinos, gera uma série de eventos em cascata com graves consequências para ambiente. O primeiro desses eventos é o crescimento populacional de mesopredadores que, por sua vez, leva as populações de pequenos predadores e presas ao declíneo ou até mesmo a extinção (Prugh et al., 2009).

Apesar da importância, observamos que existe uma grande lacuna de conhecimento sobre o tema, mesmo sendo os felinos um dos grupos taxonomicos mais estudados (Brodie, 2009). Algumas espécies agregam um número considerável de artigos científicos (*Puma concolor*, *Panthera tigris*, *Lynx pardinus*, *Lynx lynx* e *Lynx rufus*) e mesmo para essas há lacuna de conhecimento, pois os trabalhos são frequentemente redundantes quanto às perguntas ecológicas que visam responder. No entanto, verificamos que as pressões sofridas pelas espécies de felinos são distintas, mesmo consistindo em um grupo relativamente homogêneo quanto aos traços ecológicos. Os efeitos da perda e fragmentação encontrados nos mais de 100 artigos revisados variam de acordo com o tipo de resposta avaliada. Variações de resultado como essa não são uma particularidade do grupo ou das áreas de estudos, pois são observadas frequentemente em outros trabalhos (Baguette & Van Dyck, 2007; Lord & Norton, 1990). Tais padrões consistem em um importante constatação ecológica e com consequências para a conservação (Baguette & Van Dyck, 2007; Lord & Norton, 1990).

O contraste entre os resultados encontrados no capítulo 2 e 3 elucidam a variação dos efeitos ou intensidade dos processos de acordo com a abordagem usada, pois observamos que a principal ameaça às populações de onça-pintadas estão no nível demográfico. Dentre as populações estudadas no capítulo 2 (N = 28), apenas duas tiveram uma combinação adequada de número de indivíduos e estrutura da paisagem que assegurassem a persistência no longo prazo. Em contrapartida, observamos que a diversidade genética da onça-pintada parece não ter sito afetada pela perda e fragmentação em várias localidades do México. É esperado um efeito mais intenso da perda e fragmentação sobre respostas demográfica que genéticas para qualquer espécie, pois existe um 'tempo de resposta' diferente para tais mudanças (Wagner & Fortin, 2013). Esse tempo de resposta está positivamente relacionado à capacidade de dispersão e ao tempo de vida das espécies, que são particularmente altos para os felinos. Dessa forma, podemos esperar grandes tempos de resposta dos felinos à perda e fragmentação de habitat e, consequentemente, que os impactos das alterações antrópicas sobre a estrutura e diversidade genética dessas espécies são frequentemente subestimados.

Subestimados ou não, os efeitos da perda e fragmentação sobre os felinos são inquestionáveis. As altas taxas de conversão de hábitat nos países de maior riqueza de felinos demonstra a ameaça crescente sobre essas espécies (ver mapa da introdução geral). Nesse contexto, faz-se necessário também um rápido avanço científico, pois muitas são as perguntas ecológicas sem respostas acerca do tema, que permitiriam suporte científico às estratégias de conservação a serem adotadas.

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ANEXOS

Anexo 1

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Anexo 2

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