



# Simulations of populations of *Sapajus robustus* in a fragmented landscape



F. Keesen<sup>a,\*</sup>, A. Castro e Silva<sup>b,\*\*</sup>, E. Arashiro<sup>c</sup>, C.F.S. Pinheiro<sup>b</sup>

<sup>a</sup> Programa de Pós Graduação em Ecologia de Biomas Tropicais, ICEB, Universidade Federal de Ouro Preto, Campus Universitário s/n, Ouro Preto, MG 35400-000, Brazil

<sup>b</sup> Grupo Ciência da Complexidade, Universidade Federal de Ouro Preto, Departamento de Física, Campus Universitário s/n, Ouro Preto, MG 35400-000, Brazil

<sup>c</sup> Instituto de Matemática, Estatística e Física, Universidade Federal do Rio Grande, Campus Carreiros, Av. Itália, km 8, Rio Grande, RS 96203-900, Brazil

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## ABSTRACT

The study of populations subject to the phenomenon of loss and fragmentation of habitat, transforming continuous areas into small ones, usually surrounded by anthropogenic matrices, has been the focus of many researches within the scope of conservation. The objective of this study was to develop a computer model by introducing modifications to the renowned Penna model for biological aging, in order to evaluate the behavior of populations subjected to the effects of fragmented environments. As an object of study, it was used biological data of the robust tufted capuchin (*Sapajus robustus*), an endangered primate species whose geographical distribution within the Atlantic Rain Forest is part of the backdrop of intense habitat fragmentation. The simulations showed the expected behavior based on the three main aspects that affects populations under intense habitat fragmentation: the population density, area and conformation of the fragments and deleterious effects due to the low genetic variability in small and isolated populations. The model showed itself suitable to describe changes in viability and population dynamics of the species crested capuchin considering critical levels of survival in a fragmented environment and also, actions in order to preserve the species should be focused not only on increasing available area but also in dispersion dynamics.

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## 1. Introduction

Fragmentation and subsequent habitat loss is considered one of the major causes of biodiversity depletion in natural environments (Fahrig, 2003; Gibson et al., 2011; Vitousek et al., 1997). Effects of habitat fragmentation on populations will vary depending on species with different life story strategy (Robinson et al., 1995; Ewers and Didham, 2006; Ferraz et al., 2007; Koprowski, 2005; Srinivasiah et al., 2012). Features such as large body size (Gehring and Swihart, 2003; Lomolino and Perault, 2007), specialized ecological requirements (Dale et al., 1996) and extensive home range (Crooks, 2002; Gerber et al., 2012) resulted in lowering the viability of populations subjected to loss and habitat fragmentation. Besides these effects take a role on entire structure of the community, such as changing patterns of richness and abundance

depending on the size and degree of isolation of the fragments (Laurance, 1997; Laurance et al., 2002, 1998).

Some species of vertebrates, such as primates, are especially sensitive to loss and fragmentation of habitat. A recently published study showed that the diversity and abundance of primates was directly proportional to the size of the reserves (Pontes et al., 2012). The work of Chiarello and de Melo (2001) observed that the population density of three species of primates endemic to the Atlantic rainforest was directly correlated with the size of the fragments studied, leading to the conclusion that the species population viability may be compromised in the medium and long term in small fragments. Cristóbal-Azkarate and Arroyo-Rodríguez (2007) observed differences in diet, living area and population size of *Alouatta palliata* in fragmented areas of Mexico.

For the Atlantic rainforest biome, only 8.5% of its original area still resists and is heavily fragmented (SOS Mata Atlântica, 2013), resulting in a great number of species considered endangered of extinction. Nearly two thirds of the 26 endangered species of primates in Brazil take place in the Atlantic Forest (MMA, 2014). Concerning *Sapajus*, formerly genus *Cebus* (Alfaro et al., 2012), three out of the four endemic species of the Atlantic rainforest are considered endangered (*S. xanthosternos*, *S. flavius* and *S. robustus*). From

\* Corresponding author.

\*\* Principal corresponding author.

E-mail addresses: [fkeesen@gmail.com](mailto:fkeesen@gmail.com)

(F. Keesen), [alcides@iceb.ufop.br](mailto:alcides@iceb.ufop.br) (A. Castro e Silva), [earashiro@furg.br](mailto:earashiro@furg.br) (E. Arashiro), [felipe@iceb.ufop.br](mailto:felipe@iceb.ufop.br) (C.F.S. Pinheiro).

this, *Sapajus robustus* is among the 10 most endangered primates on the Atlantic rainforest, being the third most endangered of the Cebidae in Brazil. Probably abundant in the past, the main threats to the populations of this species are habitat destruction and intense hunting pressure (IUCN, 2016; MMA, 2014).

In order to simulate the population dynamics of the species of primate *S. robustus* subject to the effects of habitat fragmentation, a computational model, whose bases were structured from acknowledged Penna model for biological aging (Penna, 1995) was developed. The Penna model is based on the “Mutation Accumulation” (Medawar, 1952) theory, which states that the pressure of natural selections decreases with age. That way, bad mutations or deleterious alleles would be harmless in early stages of life when the selection is strong, however, in old ages, when selection is weak, the sum of the effects of all mutations could cause dangerous outcomes in the organism. Only the individuals that bypass this first stage (the strong selection) and reach the sexual maturity are able to transmit their genes. Those genes start to accumulate in the population by genetic drift, leading to age evolution.

In this work we have developed a new version of sexual Penna model on a lattice with the introduction of a “identification genome” to take into account the effects of inbreeding, also simulating different space configurations. It was named here as “Fragmented Penna Model”.

This paper is organized as follows: Section 2: modeling context; Section 3: results and discussions; Section 4: conclusion and future perspectives.

## 2. Modeling context

### 2.1. Penna model of aging – sexual version

The sexual version of Penna model (Penna and Stauffer, 1995) is a computer model based in accumulation of mutation theory. This model has successfully explained the semelparous senescence of Pacific salmon (Penna et al., 1995), the control mechanism of menopause in parental care on sexual populations (Moss de Oliveira et al., 1999), the process of sympatric speciation (Oliveira et al., 2003), the effects of temperature over population dynamics (De Oliveira et al., 2008), the emergence of chaotic behavior (Bernardes et al., 1998; Castro e Silva and Bernardes, 2001) and recent simulations have shown some results regarding population stability and carrying capacity (Piñol and Banzon, 2011). The first works with sexual version of Penna model was carried by Bernardes (1996) and Stauffer et al. (1996). Sousa et al. (2000) simulated inbreeding depression through mutation accumulation theory. These authors tested, among other things, the effect of the influence of environmental conditions on reproduction and its consequences in population aging – longevity and catastrophic senescence. More recently, the Penna sexual model has been used not only as a mathematical perspective, but also considering simulation applied to the biological insect control (de Souza et al., 2009). Another adaptations using species characteristics, environmental factors and others were performed as well (Magdoń and Maksymowicz, 1999; Kim et al., 2012).

In the sexual version, each individual is represented by two “alleles” or *chronological genomes* given by “bit” strings formed by two sequences of “0s” and “1s”. These sequences have a length of a computer word (usually 32 or 64 bits) that represents the organism’s life span. The bits in these words are time ordered in “years”, and a bit “1” in a given position represents a bad mutation that will lead to a disease in that related year. The disease will be expressed taking into account if the “1s” appears in both alleles (homozygous) or if the bad mutation is dominant. The diseases are accumulative, and the organism dies at the age when  $T$  diseases are expressed. The whole population is aged structured and when sexual maturity is

reached, couples are formed randomly among males and females with age greater than  $R$ . The reproduction is done with crossing-over recombination of the parents words, and  $m$  mutations are introduced in random positions of the  $B$  offsprings *chronological genomes*. The gender of the descendants is chosen between male or female with 50% chance. In order to simulate a carrying capacity of the environment,  $K$ , preventing an unrealistic growth of the population, each individual can die with a probability given by the Verhulst factor, namely  $V = N(t)/K$ , where  $N(t)$  is the number of individuals at time.

### 2.2. Biological parameters of the model

The present model was built considering the inherent biological parameters *Sapajus robustus* species from published studies (Table 1). Given the taxonomic conflict around the old genus *Cebus*,<sup>1</sup> this species was considered for many years as a subspecies of *Cebus apella* (Torres de Assumpção, 1983) or, as a subspecies of *C. nigrurus*. That brings a lack of unique ecological data for the species. Thus, information that refer to genus, prioritizing those alluding to *Sapajus nigrurus* were used. This species is phylogenetically close to *S. robustus*, and has its geographical distribution in the Atlantic Forest Biome (Alfaro et al., 2012; Rylands et al., 2005)

The species is distributed geographically in an area of intense interference on landscape by human activities, with extensive fragmented areas, and subject to various uses and occupations of the soil, which places it in a situation of greater vulnerability than *S. nigrurus*.

All the information on the ecology and reproduction of the species, considered essential to feeding and dynamics of the model (Table 1), were then raised. Every significant aspect to the understanding of social structure and behavioral information were also assessed for information and indirect validation of the model.

### 2.3. Fragmented Penna model

In order to simulate the *Sapajus robustus* behavior in fragmented environment, some adaptations were made in the Penna model. The first is the introduction of the correct set of parameters (Table 1). In this case,  $R=7$ , lifespan=32,  $B=1$  and  $T=5$ . The second one is the environment. In the original Penna model there is no definition of the environment, or “space” where the dynamics takes place. There is just one environmental parameter, the carrying capacity  $K$ .

In the fragmented model, the simulations are done in square lattices of size  $L=N \times N$ , with one individual for cell. In the initial condition of the dynamic ( $t=0$ ) the cells are filled randomly with equal amount of males and females, following a density  $\rho(0)$ . Each cell is labeled according to the sexual status of its individual at present time: (–1) for young males, (–2) sexually mature males, (1) young females, (2) sexually mature females, (3) pregnant and (4) parental care. It is important to note that, even if we do not take into account dispersion and sexual preferences, males and females have different reproductive stages during its lifetime. Pregnant females and females in parental care are unable to reproduce while those states does not occur in males. The use of so many states are, in this case, necessary to perform a more realistic simulation of this species reproductive behavior.

The simulation can be summarized as follows. Each time step is considered one year, in this period there are the steps of migration, reproduction, birth and death. At each time step first

<sup>1</sup> Silva (2001) elucidated the taxonomy of the genus *Cebus*, *C. robustus* revalidated as a species. More recently the species was separated into another genus: *Sapajus* (Alfaro et al., 2012).

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