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**SIMULACIÓN DE LA PERSISTENCIA DE LA
POBLACIÓN DE HUEMULES (*Hippocamelus
bisulcus*) PARA DISTINTOS ESCENARIOS DE USO
DE SUELO EN LA REGION DE AISEN**

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En Cumplimiento Parcial De Los Requisitos
Para Optar Al Grado De
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Evolutiva

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Por

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Director de Tesis Dr: Cristián Estades M.



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INFORME DE APROBACIÓN

**TESIS DE MAGÍSTER EN CIENCIAS
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Se informa a la Escuela de Postgrado de la Facultad de Ciencias que la Tesis de Magíster presentada por la candidata.

CLAUDIA VIVIANA LÓPEZ ALFARO

Ha sido aprobada por la comisión de Evaluación de la tesis como requisito para optar al grado de Magister en Ciencias Biológicas con Mención en Ecología y Biología Evolutiva, en el examen de Defensa de Tesis rendido el día 14 de Junio de 2007.

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The image shows three handwritten signatures in blue ink over dotted lines. The top signature is the most prominent and appears to be 'V. Marín'. Below it is a signature that looks like 'J. Simonetti', and the bottom one is 'R. Vásquez'. To the right of the signatures is a circular stamp with the text 'FACULTAD DE CIENCIAS' at the top, 'BIBLIOTECA CENTRAL' in the middle, and 'U. DE CHILE' at the bottom.



*Dedicada a todos aquellos seres y situaciones que me ayudaron a
crecer como persona y confiar en mis anhelos.*

*Especialmente a José y Guachón, fieles compañeros
en este camino.*



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INDEX

INTRODUCTION	1
DATA AND METHODS	8
Geographic information sources	9
Telemetry data	9
Landscape layers	10
Cell size	11
Movement data	11
Survival data	12
The model	13
Initialization	14
Submodels	14
<i>Movement sub model</i>	14
<i>Mortality sub model</i>	16
<i>Reproduction sub model</i>	17
Calibration	17
Experiments	18
Scenarios	19
Expression of results	19
Sensitivity analysis	20
RESULTS	22
Model behavior	22
Model Calibration	22



Normal scenario and base condition	23
Effect of initial conditions	23
Future development scenarios	24
Sensitivity analysis	25
DISCUSSION	26
Management implications	32
ACKNOWLEDGMENTS	35
REFERENCES	36
TABLES	44
FIGURES	51
APPENDIX 1: EXTEND MODEL DESCRIPTION	57
APPENDIX 2: MODEL CODE	63

TABLE INDEX



TABLE 1	Landscape layers
TABLE 2	Movement probability matrix
TABLE 3	Survival data.
TABLE 4	Movement pattern
TABLE 5	Movement probabilities modifier due to landscape attributes
TABLE 6	Landscape-related mortality
TABLE 7	Parameters for model based condition
TABLE 8	Parameters used in sensitivity analysis
TABLE 9	Calibration result
TABLE 10	Sensitivity analysis result

FIGURE INDEX

- FIGURE 1 Study area
FIGURE 2 Model diagram
FIGURE 3 Normal scenario
FIGURE 4 Model sensitivity to the initial conditions
FIGURE 5 Effects of the landscape changes on the population dynamic
FIGURE 6 Effects of sensitivity analysis over population trajectories



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RESUMEN

El diseño de planes de conservación a gran escala, para especies en peligro de extinción, está frecuentemente limitado por la falta de información biológica para estas especies, especialmente de cómo ellas responden a los cambios en el paisaje. Una forma en la que esta limitación ha sido superada es con el uso de modelos poblacionales espacialmente explícitos y basados en individuos (SPMI, sigla en inglés). Desarrollamos un SPMI para un ciervo en peligro de extinción, el huemul (*Hippocamelus bisulcus*), del sur de Chile y Argentina. El propósito del modelo fue sintetizar la mayor cantidad de la información biológica disponible de esta especie y proyectar la dinámica poblacional para diferentes escenarios futuros de desarrollo en la región de Aisén. El primer escenario se caracterizó por un aumento del 50% en la densidad de ganado y el segundo por la simulación de la construcción de cinco embalses hidroeléctricos. Un tercero fue el escenario actual, él que mantiene las condiciones presentes de la región. El modelo simuló la localización, edad y estatus general de todos los individuos de una población y del paisaje en el que viven. El paisaje fue caracterizado por nueve capas de información: uso del suelo,

ecotonos de bosques, hidrografía, pendiente, altitud, exposición, caminos, centros poblados y densidad de ganado. Los individuos se movieron en celdas de 500x500 m cada una semana, siguiendo un algoritmo de movimiento obtenido de datos de telemetría. Probabilidades de muerte debidas a la edad y a las características del paisaje, se aplicaron individualmente, cada semana. La reproducción ocurrió estacionalmente. Debido a la incertidumbre en el tamaño y localización de la población actual en la región, fueron considerados cuatro tamaños iniciales (100 a 1.200) y tres patrones de distribución espacial inicial. Cada simulación fue de 50 años y para cada escenario se realizaron 20 repeticiones. A pesar de la alta sensibilidad del modelo a parámetros como la probabilidad de muerte semanal y la escala de percepción del paisaje, hubo una tendencia general de crecimiento poblacional, lo que concuerda con datos no formales sobre esta especie. La mayoría de las simulaciones que partieron con 100 individuos tendieron a la extinción de la población, esto sugiere la existencia de tamaño crítico para la viabilidad. Los dos escenarios futuros evaluados tuvieron un bajo impacto en la dinámica y persistencia de la población, pero la no consideración de algunos factores asociados a estos escenarios (ej. Cambios en el uso del suelo vecino a los embalses), puede hacer que se esté subestimando el impacto real sobre la especie. El efecto del tamaño y localización inicial de la población sobre la persistencia reflejan la importancia de estos datos básicos para el manejo y la recuperación de esta especie.

SIMULATION OF HUEMUL (*Hippocamelus bisulcus*) POPULATION PERSISTENCE FOR DIFFERENT LAND USE SCENARIOS IN AISEN REGION

ABSTRACT

The design of large-scale conservation plans for endangered animal species is often limited by the lack of biological information, particularly on how they respond to landscape changes. One way in which this limitation has been mitigated is with the use of spatially explicit population models based on individuals (SPMI). We developed a SPMI for the endangered Huemul deer (*Hippocamelus bisulcus*) of southern Chile and Argentina. The goal of the model was to synthesize most available information on the species and to project the population trajectories under different future development scenarios in the Aisén region of Chile. The first scenario was characterized by a 50% increase in livestock density and the second simulated the building of five hydroelectric reservoirs. A third “normal” scenario maintained present conditions in the region. The model simulated the location, age and general status of all individuals in the population and the landscape in which they lived. The latter was characterized by nine different layers: land use, forest ecotones, hydrography, slope, aspect, altitude, roads, towns and livestock density. Individuals moved between 500x500m cells in 1-week time steps following a movement algorithm derived from telemetry data. Age-dependent and landscape-related mortality probabilities were applied weekly to each individual.

Reproduction took place seasonally. Due to uncertainty regarding the actual population size in the region four initial population sizes (100 up to 1.200) and three spatial aggregation patterns were used. Each simulation comprised a period of 50 years, and for each scenario a total of 20 replicates were conducted. Although the model was very sensitive to parameters such as weekly mortality rate and individual landscape perception scale, the general trend was that of a positive population growth, which agrees with anecdotal information on the species. The fact that most simulations starting with 100 individuals resulted in the extinction of the population suggests the existence of a population viability threshold. Both studied potential scenarios had minimal impacts on population persistence and dynamics, but failure to incorporate all elements associated to such scenarios (e.g. land use changes in the vicinity of reservoirs) may have underestimated their real effect on the species. The important effect that initial population size and spatial aggregation had on persistence highlights the relevance that population estimates may have on building the basis for the species management and recovery.

INTRODUCTION

One of the greatest challenges for conservation biology is providing solutions for endangered species in modern landscapes, where much prime habitat has been altered and many species occur mostly in small nonviable populations (Palomares et al. 1999; With & King 1999; Schadt et al. 2002b). These human dominated landscapes are characterized by a high level of habitat disturbance and fragmentation which have been identified as major factors behind the decline of threatened species (Soulé 1986; Forman 1996; With & King 1998; Wiegand et al. 2004b).

Landscape changes can alter population dynamics due to changes in the availability and spatial distribution of resources important to the species (Morrison et al. 1992, Wiens et al. 1993; Fahrig & Merriam 1994), changes in species interactions (Ewers & Didham 2005) and the alteration of population dispersion patterns (Sutherland 1996; With & King 1999). Successful dispersal of individuals and establishment of populations in new areas are key factors in the dynamics of spatially structured populations as they influence the vulnerability of a population to local extinction (With & King 1999; King & With 2002; Revilla et al. 2004). Therefore, the degree of landscape connectivity and the availability of good quality sites (Wiegand et al. 1999) are two elements that strongly influence population persistence (Handson 1991).

The design of animal conservation plans at large scales is often limited by the lack of relevant biological information on the species (Schadt et al. 2002; Kramer-Schadt et al. 2004; Wiegand et al. 2004*b*), in particular empirical information on how species respond to landscape structure (Turner et al. 1995; Lima & Zollner 1996). This limitation is particularly severe in developing countries where the lack of resources restricts the potential for even basic ecological research.

One way in which these limitations have been mitigated is with the use of simulation models. This approach to research is being increasingly used in applied ecology and in particular in conservation biology (Wiegand et al. 2003). The use of “spatially explicit population models based on individuals (SPMI)” has been useful in understanding how landscape structure influences dispersion of individuals in the landscape and in studying interactions between habitat configuration and demographics (Bart 1995; Dunning, et al. 1995; Wiegand et al. 1999; Kramer-Schadt et al. 2005; Melbourne et al. 2004; Wiegand et al. 2004*a*). This has allowed managers to anticipate and minimize the impact of landscape changes (Ahearn et al. 2001; Cramer & Portier 2001).

Individual based models describe population dynamics by simulating the behavior of each individual in a population (Wiens et al. 1993). They integrate the life-history information and behavioral rules on dispersal and habitat selection in a meaningful way because the basic modeling unit, the individual, is also the biological unit of observation (Wiegand et al. 1999). The rules are extracted directly from the species’ biological

information (Wiegand et al. 1999; Kramer-Schadt et al. 2004b; Revilla et al. 2004), and much of the model output is directly comparable to field data, and can be analyzed in that way (Wiegand et al. 2004a). Spatially explicit population models often use geographical information systems to compile maps on habitat quality allowing a better understanding of the influence of landscape change over population dynamics (Wiegand et al. 2004a).

Some important advantages are that these models allow the integration of empirical biological information of differing quality (Schadt et al. 2002a; Schadt et al. 2002b; Wiegand et al. 2003). The latter can be particularly useful in developing countries, where most of the available information for some species comes from observers such as park rangers or settlers who are in direct contact with the species and their habitat.

Mechanistic modeling of populations can also help to identify variables of particular interest to the system and thus prioritise future research (Wiegand 2004a), and to efficiently manage human and economic resources for the generation of effective conservation plans (Palomares et al. 1999; Schadt et al. 2002b; Kramer-Schadt et al. 2004). These simulation models can also help to overcome some of the fundamental problems involved in obtaining reliable empirical data at the large temporal and spatial scales required for the study of the effect of landscape changes on populations (Gu et al. 2002; Hargrove & Pickering 1992).

SPMIs have been a powerful tool in the assessment of species conservation plans and the influence of land use on species survival (Ahearn et al. 2001; Cramer & Portier 2001; Schadt et al. 2002a; Schadt, et al. 2004b; Kramer-Schadt et al. 2004; Wiegand et al. 2004a). They also have been used to determine important biological parameters related to population persistence and landscape composition (Wiegand et al. 1998; Revilla et al. 2004),

The huemul (*Hippocamelus bisulcus*) is a medium sized deer endemic to southern Chile and Argentina. Prior to the colonization by Europeans (1800 a.c.), huemules were distributed between the 34° to 53°S in Chile and between the 40° to 52°S in Argentina (Aldridge & Montecinos 1998; Smith-Flueck 2000). Nowadays, the majority of the Chilean population is concentrated south of the Aisén region (44°S). A few isolated populations persist in Nevados de Chillán (36°30'S, Bío Bío region) (Aldridge & Montecinos 1998).

Due to the strong decrease in its geographical distribution, the huemul has been classified as an endangered species (IUCN, 1990-present). The cited causes of its decline have been habitat destruction, illegal hunting, disease from domestic animals, and dog attacks (Povilitis 1984; Simonetti 1995; Aldridge & Montecinos 1998; Frid 2000; Smith-Flueck 2000).

In Chile, most information regarding the huemul is in the hands of the National Park Service (CONAF). This information includes census data and a radio telemetry study

both conducted in the Tamango National Reserve. Other studies include general biology and reproductive strategies (Povilitis 1983; Povilitis 1984; Smith-Flueck 2000), mortality patterns (Smith-Flueck & Flueck 2001), sexual segregation and habitat selection (Povilitis 1998; Frid 1994; 1999; 2000; Smith-Flueck 2000), home range (Povilitis 1984; Aldridge & Montecinos 1998), group size (Povilitis 1983; Frid 1994; 1999; Smith-Flueck 2000) and interactions with cattle (Povilitis 1989; Frid 2000).

Huemules have home ranges that vary from 36 to 450 hectares (Aldridge & Montecinos 1998; Gill et al. 2008). Habitat selection depends on age and phenology (Frid 1994; Smith-Flueck 2000), but in general, during the summer the species prefers grassland, wetlands or periglacial areas, whereas during the winter they use forests and open areas in the same proportion. They also prefer low altitude with north to north-eastern facing slopes (Aldridge & Montecinos 1998; Frid 1992; Smith-Flueck 2000). During the breeding season females seek protected areas with greater slope, altitude or high vegetation and they also move farther away from the group. During heat season, males cluster in open areas and fights are frequent but mortality is low (Povilitis 1984; Smith-Flueck 2000). Observed group size is six or seven individuals (Smith-Flueck 2000), but the basic group structure is an adult male and female with the newborn calf (Povilitis 1983). The effect of cattle on huemul survival has been less well studied, although research has shown that huemules tend to avoid areas where cattle are present (Povilitis 1989; Frid 2000). Although knowledge of huemul biology is more detailed than that of most of the other Chilean mammals, previous to this study, this information had not

been compiled for the purpose of making population forecasts or understanding the relationship between landscape structure and survival.

The goal of the present study was twofold. First we tried to synthesize all available information for the species with the help of a spatially-explicit individual-based simulation model. Second, using the model we explored the population trajectories of the species under two future development scenarios for the Aisén region in southern Chile. The first scenario is characterized by a significant increase in livestock densities due to potential government incentives (CORFO, 2007; INDAP, 2007). Even though there are not studies that detail the impact of the coexistence of bovine livestock and huemul populations in the Aisén region, observations of changes in habitat use patterns due to the presence of livestock (Frid 2000), the transmission of diseases (Povilitis 1984, Simonetti 1995), and several records of attacks by dogs associated with livestock (park rangers, pers. comm.), suggest that this factor can have an important effect on huemul survival. Although competition for food has not been documented, this common effect of livestock on large wild herbivores (Kie et al. 1991; Loft et al. 1991; Loft et al. 1993), and it is reasonable to assume that such an effect might exist on huemules as well.

The second scenario is the building of five hydroelectric dams that will create two reservoirs in Baker river and three in Pascua river. Both of these areas are documented huemul habitat (Vila et al. 2004). Although the environmental impact assessment of these projects did not address the effects that such reservoirs might have on big mammals, there is a potential for a reduction in landscape connectivity as these large

flooded areas may disrupt the capacity of huemules to move freely. Huemules have been seen swimming distances of up to 80 m without problems but the potential for drowning over longer distances may cause them to avoid large reservoirs.

DATA AND METHODS

The simulation was conducted over an area of 41,184 km² located in the Aisén Region of southern Chile (latitude 46°30'S to 49°00'S, Fig. 1). This area encompasses most of the known huemul population in Chile. The region has a diverse geomorphology due to a high tectonic, volcanic and glacial activity (Faúndez et al. 2002). Climate is considered extreme, with an average precipitation over 1500 mm (a significant proportion as snow) and an average annual temperature of 9°C (Burgos et al. 1991). Settlement has concentrated in the valleys and coastal areas.

Dominant vegetation types are *Nothofagus* forests, deciduous scrub and steppes. Deciduous forests (dominated by *N. pumilio*) are located on high hillsides of the Andes, with an altitude between 900 and 1200 m high, whereas evergreen forests (dominated by *N. betuloides*, with presence of *Drimys winteri* and *Podocarpus nubigena*) are located between 100 and 900 m altitude, mostly on the east side of Northern Ice Field (Fig. 1) and the west side of the Andes Mountains (Luebert & Plischoff 2004).

Deciduous scrub is dominated by *N. antarctica*, and is located at the upper vegetation limit (800 m), in peri-glacial areas and at the ecotone between forests and steppes, mainly in low hillsides of the east side of the Andes (Luebert & Plischoff 2004). Steppes

are *Festuca palllescens*, *Acaena splendens* and *Mulinum spinosum* (Luebert & Pliscoff 2004).

Geographic information sources

Land use information was obtained from the National Native Forest Inventory (scale 1:100,000; CONAF-CONAMA-BIRF, 1999). Information on towns and roads came from the Aisén Regional Development Plan (scale 1:50,000; SEREMI MINVU, 2004). Hydrology and elevation (contour) maps were obtained from digital 1:50,000 charts (Instituto Geográfico Militar, 2002)

Information on livestock density was obtained from the 2005 Livestock Regional Census (Servicio Agrícola y Ganadero, Aisén Region, unpublished data). For the study area this census included 740 points associated to different properties but only 67% of the latter were georeferenced. Data for each point included numbers of cows, horses, goats, sheep y camelids, but for the analysis they were transformed into Animal Units (AU) (Holecheck et al. 1995, Herve & Balochi 1995, see “landscape layers”).

Telemetry data

Telemetry data used for the development of the movement algorithm was obtained from the project “Investigación sobre la ecología del huemul (*Hippocamelus bisulcus*) como contribución a su conservación en el sur de Chile” (see acknowledgments). The data set

used included the location of 15 individuals (11 in Tamango National Reserve and La Baguala areas, and 4 in Candonga a forest private land close to Río Castillo National Reserve) from September 2000 to November 2002, with a total of 475 locations and an average (SD) interval of 9.96 (SD=14.9) days between points.

Landscape layers

Geographic information was used to create eight landscape layers: land use, ecotones (between forests and other land uses), hydrography, slope, aspect, altitude, roads, towns and livestock density (Table 1). Although most data were treated as vectors during processing, during simulation all layers were expressed in a raster format using a 500 x 500 m grid (see “Cell size”).

Ecotone layer was built by creating an influence area of 250 meters both sides from the edge of forest polygons (land use map). Slope, altitude and aspect layers were obtained from a Digital Elevation Model (DEM), built from the contour map. Because towns were represented as points they were transformed into areal data assigning an influence area of 2000 ha to cities and 300 ha to smaller towns.

A livestock density layer was built using a model to transform the point data on AU into an areal expression of livestock abundance. For that purpose the model distributed all the AUs associated to a point among the neighboring cells considering three restrictions: a habitat-specific carrying capacity (0.5 UA/ha for grasslands, steppes and other

herbaceous habitats, and 0.25 UA/ha for forests and shrub lands, Scheu et al. 1998, Cruces et al. 1999), topography (slope < 50% and altitude < 800 m) and continuity (i.e. all AU for a point were distributed in a single continuous patch).

Cell size

Cell size was set to be slightly smaller than the size of a “small” home range for an individual (Wiegand et al. 2004a). Because the Huemul home ranges vary from 40 to 400 ha (Smith-Flueck 2000), a cell of 500 x 500 m (25 ha) was chosen. Therefore, with this grain most home ranges were composed of two to eight cells, allowing for the description of landscape effects over movement pattern (Krammer-Schat et al. 2005). A basic assumption of this model is that individuals functionally perceive their environment as being homogeneous inside a given cell (Wiegand et al. 1999).

Movement data

Telemetry data was used to obtain the probability of individuals moving from a cell to another during a 1-week period, considering land use of both the departure and arrival cells (see movement sub model). Data on individual locations were interpolated in order to generate spatial locations in 1-week intervals. Only real locations separated by less than 13 days were interpolated, this processes generated 662 registers in total, 378 for R.N. Tamango, 183 for La Baguala and 101 for Candonga. The movement probability matrix (MPM in Table 2, see movement sub model) was built with interpolated data.

Available information allowed for the estimation of movement probabilities for only five land use categories (those present in the area where telemetry data was obtained). Probabilities for other land uses were estimated from the literature (Povilitis 1984;1986; Aldridge & Montecinos 1998; Frid 1994; 1999; 2000; Smith-Flueck 2000).

Movements to and from Argentina were made possible only through “passes” connecting areas with suitable habitat in both countries (Vila et al. 2004) and with altitudes lower than 1200 m. Annually, the program balanced the movements among countries by introducing the same number of individual immigrants as there were emigrants.

Survival data

No formal studies on survival have been conducted for the species. However, park rangers have been monitoring huemul populations for more than fourteen years and have recorded the deaths of several known individuals. With that data along with the known maximum longevity for the species (14 years) age-specific annual mortality rates were estimated (Table 3). This mortality included different causes such as: natural mortality, hunting and dog attacks.

The model

The main purpose of the model was to describe the dynamics and, particularly, the viability of huemul populations under different development scenarios in the Aisén region. The model simulates the movements, reproduction and deaths of individuals during a 50-year period through three sub models: movement, mortality and reproduction (Fig. 2). There are two basic matrices in the model: the first is a collection of individuals (the population) and their attributes and the second, a raster representation of the landscape.

All individuals are characterized by the following state variables: identity number, sex, age, and spatial location. Age is assigned randomly (3-14 years, uniform distribution) to all individuals at the beginning of the simulation. Newborns are 0 years old. Age is increased by one at the end of the year. Spatial location of individuals is determined by the movement sub model (see Sub models), or during the initialization process (see Initialization). Family group formed each year with a maximum number of three, one male and two female. Individuals less than one year old are considered fawns. Males one to two years old are considered juveniles, and males more than two years old and females more than one year old are referred to as adults. Twins are not allowed by the model.

Randomness in the model operates at two hierarchical levels, seasonality and individual behavior. Seasonality includes the simulation of processes and events related to change

in a seasonal fashion, such as reproductive behavior and general movement and habitat selection patterns. The processes are male rut, reproductive season, winter movement and birth season. Movement patterns are represented by a normally distributed function composed by biological information from the literature (Aldridge y Montecinos, 1998; Smith-Flueck, 2000), and are calculated every year with a random variation of initial week and length of period to include some differences, in climate condition that exist between years (Table 4). Individual behavior includes movement and mating decisions.

Initialization

Initial population size and general location pattern of individuals are parameters that are defined before the beginning of the simulation. At initialization individual state variables are assigned values. Following the general location pattern (see Experiments) individuals are located randomly in grid cells containing appropriate habitat conditions (excluding lakes, rivers, ice, roads, towns, and livestock). Family groups are formed by grouping individuals at 8 kilometers distances or less.

Submodels

Movement sub model: This sub model defines the location of individuals through time based on a “movement probability matrix (MPM)” containing the relative probabilities of weekly movements among grid cells with different land uses (see “movement data”) plus a series of modifiers derived from seasonality, sedentariness and landscape features.

Seasonality effect refers to changes in general movement pattern associated to seasons. Sedentariness is composed of three factors: maximum distance of weekly movements, male attraction to mates, and home range tendency. Maximum distance of weekly movement defines the maximum number of cells that an individual can move in one week. Male attraction defines the male tendency to move close to his present mate(s). Home range tendency is defined by the tendency of an individual to move towards a “gravity center” and it is governed by two parameters: “memory span” referring to the number of previous spatial locations that are saved in memory to calculate the gravity center, and “gravity” that defines the influence of the gravity center on the future position.

Landscape attributes, movement probabilities are eventually modified by information regarding landscape features such as ecotones, hidrography, slope, altitude, aspect, roads, towns and livestock and conspecific density (Table 5). The effects of most of these variables on huemul movement were estimated from biological information on the species (Povilitis 1984;1986; Aldridge & Montecinos 1998; Povilitis 1989; Frid 1994; 1999; 2000; Smith-Flueck, 2000). The effects of livestock and conspecific density were estimated from literature on other deer species (Kie et al. 1991; Loft et al. 1991; Kie et al. 1996; Abbott et al. 1997; Kie et al. 2002).

The movement algorithm starts when an individual randomly chooses an arrival cell. It then assesses the probability of moving to such cell by multiplying the probability in the MPM times the probabilities of the modifiers. The algorithm then compares such

probability with a random number that is the result of multiplying n uniformly distributed random numbers between 0 and 1, with n being the number of modifiers used in the algorithm. If this latter number is smaller, it executes the movement. Otherwise the individual chooses another cell. This procedure is repeated a maximum of five times, after which the individual stays in the origin cell. The algorithm is applied to all individuals, with the exception of fawns, that move along with their mothers.

Because huemules are known to swim, the model allowed individuals to pass through cells containing lakes or rivers. However individuals were not allowed to “stay” in such cells. For that purpose, each time an individual entered a cell covered by water, it increased its movement speed, performing up to five movements in a normal 1-week time step. After that, if the individual still remained in a water cell, it drowned. Besides, each time an individual was present in a water cell an additional death probability was applied (see “mortality sub model”).

Mortality sub model: each week, deaths could happen due to three factors. First, age-specific annual mortality rates at weekly scale (WMR). Second, there is a landscape-related mortality rate that takes values greater than 0 when individuals are in a cell with a river, lake, livestock, road or town (Table 6). Third, males face an additional source of mortality when they fight for females. We used a low probability (0.1%) due to studies that indicate that fights leading to death or serious injury are rare. Clutton Brock (et al. 1979) found two cases of injury in a total sample of 107 observed fights of *Cervus*

elaphus. For the huemul the observed fights present a low level of injury with those individuals that didn't have death as the direct cause.

Reproduction sub model: this sub model is invoked when males enter into rut. Then they search for a female in estrous present within a maximum search distance of 8 km (max-dist). Secondly, males move towards the female and they face the landscape-related mortality their route. If they survive, they assess a fighting probability with other males. If there are not other males in the female's cell or if the individual wins the fight, mating occurs.

Calibration

Parameters used in the movement sub model (maximum distance of weekly movements, male attraction to mates, home range tendency, memory span and gravity) were subjected to calibration using telemetry data from 12 individuals from the Tamango National Reserve. The procedure compared the position of the virtual deer over the simulation period with those from the telemetry database. The proportion of matching locations was used as an index parameter performance. The extent of home ranges was used as a control given that home ranges should fall between the size ranges reported in the literature (25 - 444 ha, Povilitis 1983, 1984; Gill et al. 2008). For all parameters except maximum distance of weekly movement, values ranging between 0.1 and 0.9 were tested. For every parameter combination a total of 50 simulations were run. For maximum distance of weekly movement, the model assumed that juvenile or single

males and pregnant females can move up to 1000 m (2 cells) per week, this was based on the literature on other deer species (Rosenberry et al. 2001; Bowman et al. 2002; Long et al. 2005).

Experiments

Four different initial population sizes (100, 300, 600 and 1200 individuals) and three general location patterns (aggregated, semi-aggregated and disaggregated) were tested.

The chosen initial population sizes reflect the level of uncertainty regarding the total population size for the region. Recent estimates vary from 300 to 1200 individuals (including the Argentinean side, Aldridge & Montecinos 1998; Smith-Flueck, 2000; Aldridge & Velasquez 2006; park rangers, pers. comm.). Therefore the range used includes the best and worst of these situations.

A similar situation exists regarding the spatial distribution of populations. Using available information on “stable” huemul populations in the region, 16 population areas were defined (Aldridge & Velasquez 2006; park rangers, pers. comm.; Villa et al. 2004). The aggregated population pattern randomly assigned all initial individuals in these areas. In the semi-aggregated pattern 85% of all individuals started in places of known populations and the rest were randomly located in any area of the region. In the disaggregated pattern all individuals were randomly located in the region. All individuals were located in grid cells containing suitable huemul habitat.

Scenarios

Three different scenarios of future development were simulated. The first one (“normal scenario”) maintained the present landscape configuration. The second scenario (“livestock scenario”) considered a 50% livestock increase in the region. The latter was generated by changing the present livestock map by increasing the number of AU per point by 50%. This means that, at a regional level, there is more area used by cattle but they tend to concentrate in the same general areas as in the normal scenario. This conservative approach was used because no information was available to predict the creation of new livestock ranching areas.

The third scenario (“reservoir scenario”) considered the creation of five reservoirs to produce hydro electrical power. This was simulated by changing the hydrographic map, adding lakes where the dams are planned to be built (Hidroaysen 2007). Each experiment involved 20 replicates.

Expression of results

At the end of each year, the model recorded the geographic location, age, and status (dead or alive) of each individual. The total number of living individuals was then used as the total population size. For that purpose individuals located in a landscape border of 5 km (10 cells) were not tallied.

Because of programming constraints the model could only handle a maximum of 2000 individuals. For that reason, populations greater than 2000 were truncated in that number. When the total population size was smaller than 10 individuals, the population was considered extinct and simulation was terminated.

Persistence probability (PP) was calculated as the proportion of simulation replicates in which the population did not go extinct. For each scenario the population size at any given time was the average of the population size of all 20 replicates at that time. Confidence intervals for population size were created using the standard deviation of all 20 replicates.

Sensitivity analysis

Persistence probability (PP) was used as the variable on which the sensitivity analysis was conducted. The sensitivity of the model was analyzed as the change in PP relative to change in the value of a given parameter (Parameter_x) (Jørgense 1994). An initial condition of 600 individuals and semi-aggregated location was considered as a *base condition* and the parameters values are indicated in Table 7.

We assessed sensitivity of the model to four parameters: weekly mortality probability due to age (WMPA), male maximum search distance (max-dist), weekly mortality probability due to roads (WMPR) and weekly mortality probability due to livestock

(WMPL). The range of values used for sensitivity analysis tried to cover the maximum range of biologically meaningful values (Table 8).

RESULTS

Model behavior

Population trajectories experienced a process of adjustment during the first 10 years, in which an increase of the population during two first years and a later decrease of the population size was generally observed. Most likely this was due to the adjustment of the age distribution to the curve of the age specific annual mortality rate and an effect of family formation which is the result of individuals' initial location.

Model Calibration

The best set of parameters produced by the calibration gave the value parameter presented in Table 9. With these values the individual home range varied from 125 to 550 has. The average maximum movement distance showed similar values to the adult individual observed with established home range. Because there are not radiotelemetry data for young huemules, values for the latter were estimated from the literature (Rosenberry et al. 2001; Bowman et al., 2002; Long et al. 2005).

Normal scenario and base condition

The population trajectory for the “normal” scenario and the “base” condition (600 individuals and semi-aggregated location) showed a sustained growth from year 20 until reaching a population size of 2000+ individuals by year 50. Persistence probability was 100% (Fig. 3). Emigration to Argentina occurred at an average 1 to 2% of the population each year. The main mortality cause was associated with the weekly mortality probability due to age (WMPA), with an average of 74% of the deaths during the 50 years of simulation. The second cause was fawn death due to the death of the mother. Mortality due to livestock (WMPL) was on average 2.5%, representing approximately five individuals per year. Mortality due to roads (WMPR) was of 0.7%, which represents an average of one to two individuals per year. The latter values are similar to CONAF records of no more than three individuals hit by cars in a year (park rangers, pers. comm.).

Effect of initial conditions

When initial population size was 300 or more individuals, trajectories showed a positive growth rate. These rates increased with greater initial population sizes. Persistence probability was 100% in all populations of 300 or more individuals with the only exception of the population of 300 individuals with a disaggregated location. A decline was observed for initial populations of 100 individuals with persistence probabilities ranging between 5 and 40% (Fig. 4a). The initial population location had an important

effect on the rate of population growth. For initial population sizes of 300, 600 and 1200, an aggregated initial location produced greater growth rates, followed by semi aggregated and finally a disaggregated initial location (Fig. 4b, c, d).

Future development scenarios

Populations had similar trajectories in all simulated scenarios. The livestock scenario showed a slightly smaller rate of growth than the “normal scenario”, but in most cases, this difference was not statistically significant (overlapping 95% confidence intervals, Fig. 5a, b, c). Only when initial population size was 1200 (Fig. 5d), the livestock scenario had a significantly smaller population between years 12 and 20, but after that, differences were attenuated. The reservoir scenario showed an increased growth rate in relation to the “normal scenario” but, again, this difference was insignificant (Fig. 5). The latter trends were similar for different initial population sizes, but differences were less evident when starting with 300 or fewer individuals (Fig. 5a, b).

For initial population sizes of 600 and 1200 individuals at the end of simulation period all of the trajectories converged (Fig. 5c, d), but this is an artifact of averaging 20 population trajectories that are truncated at 2000 individuals (appr. 1600 without the edge).

In all scenarios population persistence was 100% for initial populations of 300 or more individuals. For 100 individuals it was 55% for the reservoir scenario, 40% for the

normal scenario and 35% for the livestock scenario, although these values are not significantly different ($z \leq 1.27$, $p > 0.1$).

Sensitivity analysis

The model was very sensitive to weekly mortality probability rates due to age (WMPA) and to male maximum search distance (max-dist) (Table 10); this means that small changes in these parameters will have an important effect on population persistence probability. For example persistence probability was 30% when male maximum search distance was 2 km, whereas persistence rose to 100% when max-dist was 4 and 8 kilometres.

On the other hand, for WMPL and WMPR, the persistence probability was 100% in all tested values. However, in spite of the latter, there were evident differences in the population trajectories (Fig. 6a, b, c, d).

DISCUSSION

There is a great degree of uncertainty regarding the huemul population status in spite of the amount information available for the species. Ours is the first formal attempt to use such information to estimate a population trend for this rare deer.

Unfortunately there are not independent sources of information to validate the present model. We used radiotelemetry data to calibrate the model in relation to some of the parameters governing movement behavior, but these datasets were obtained inside and around a protected area, which may bias the estimation of variables such as home range size. However, there is some evidence that, at least, the model performed qualitatively well. For example, although the model showed a high sensitivity to some of the studied parameters, it is interesting that most cases and scenarios resulted in a positive population growth. This trend agrees with census data obtained by CONAF in Tamango since the year 1985. Although it is not possible to discard the fact that the trend observed in Tamango may be partly due to a re-grouping of individuals in an area with a greater level of protection than the surroundings, anecdotal evidence (e.g. increasing sighting reports by tourists and researchers) suggests that the trend is widespread in the region.

The latter pattern suggests that some limiting factor(s) might have ceased to operate in

the last decades. For example, a significant reduction in hunting, which was previously legal (Smith-Flueck 2000) could explain part of the trend. In 1933 the Chilean government started a colonization program for the Aisén region, giving an important amount of land to settlers, who, between 1933 and 1952 burned more than 35,000 km² of forests to clear land for raising livestock (Quintanilla, 2007). Although there are not direct accounts on the effects that these fires (some of which lasted for years) and the associated disturbance had on wildlife, it seems reasonable that they might have had a long lasting impact on some species.

Numerous studies emphasize the importance of some key demographic parameters in determining population viability for threatened species, particularly those related to the mortality rates and the factors that influence recruitment (Wiegand et al. 1998;1999; Kramer-Schadt et al 2004b; Wiegand 2004a). The present model was particularly sensitive to weekly mortality probabilities. We obtained an age-specific weekly mortality curve from survival data for several known individuals collected by CONAF park rangers in and around Tamango National Reserve. Besides the “informal” nature of these data, it might be argued that they probably suffer from the same bias as the movement dataset because mortality is expected to be lower in a reserve. However, being close to the town of Cochrane, human influence on huemules is important in this reserve. In fact, an important number of fawns born in the reserve have been killed by dogs that come from the surrounding ranches. Besides, in the model we explicitly incorporated additional mortality sources associated to factors more important outside

protected areas, such as livestock, roads, towns, etc., and thus we believe that the mentioned bias was substantially reduced.

In several scenarios the regional population size surpassed the maximum allowed by the simulation model (2000, approximately 1500 when discounting for edge effect). However, had the model considered some density dependent factors (e.g. competition, disease transmission, etc.), growth rates might have decreased at high population sizes.

In the present study, the initial conditions of the model (i.e. population size and location) had an important effect on population dynamics and persistence probabilities. The fact that persistence decreased significantly when the initial population was 100 individuals suggests that at a population threshold exists, under which the regional population tends to become extinct. If the latter assumption is correct, it may be predicted that the isolated populations in central Chile (approximately 40 individuals, Povilitis 2002) may be declining to extinction. Unfortunately for the species, different studies giving account of a population decrease in this region (Povilitis 1998; 2002; Aldridge & Montencino 1998) support our prediction.

Related to the mentioned threshold is the positive effect that initial population aggregation had on persistence probability. At a regional level, populations may persist only where densities are higher than a minimum viable density (Silva & Downing 1994). Therefore, when overall population sizes are small, metapopulation persistence may be

avored be local aggregation of individuals produced either by landscape configuration or conspecific attraction (Stephens & Sutherland 1999, Greene & Stamps, 2001).

The high sensitivity of the model to male maximum search distance (i.e. the distance at which males were capable of detecting females in heat) highlights the importance that conspecific attraction had in structuring spatial population configuration in this model, and reaffirms the importance of the scale at which individuals perceive the landscape in understanding huemul population dynamics (Povilitis 1998).

Both evaluated scenarios of future development had negligible impacts on the regional huemul population trajectories, and certainly their effect was much smaller than that of many parameters and initial conditions of the model.

The livestock scenario simulated a hypothetical 50% increase in the regional livestock population. However, this scenario was incomplete because the census upon which we built the livestock map did not include the geographic location of approximately 33% of the ranches. If there is a threshold in the effect of regional livestock mass on huemul populations, this missing information might have reduced the relative impact of this scenario. Additionally, we took a conservative approach and projected the increase in livestock mass in areas that already had cattle and sheep ranches. Had we spread the new livestock mass throughout the region, the effect on huemul populations might have been higher. However, we could not do that because we had no way to estimate the location of new economically and technically suitable livestock ranching areas.

Although we modelled the effect of livestock as one parameter, there are two main mechanisms by which livestock might negatively affect huemul populations. First is direct competition for space and other resources. However, experiences with other cervids suggest that main impacts occur at high cattle densities (1.7 AU/ha) whereas at low densities (less than 0.5 AU/ha) the coexistence of the species is observed and there is a low effect on habitat selection (Kie et al. 1991;1996; Loft et al. 1991;1993). Our model considered a maximum of 0.5 AU/ha based on the livestock densities used in the region (Scheu et al. 1998, Cruces et al. 1999), which suggests that this mechanism might not be very important.

The second mechanism is the impact through the effect of other organisms associated to livestock. It has been argued that disease might have played a role in the past species decline (Povilitis 1984, Simonetti 1995). Also park rangers have detected several cases of huemules (mostly young) killed by dogs associated to cattle ranches.

Overall, the effect of livestock on huemules seems to be one of the weakest parts of our model. The fact that, on average, only 2.5% mortality (approximately five individuals per year) was associated to livestock and the low sensitivity of the model to this parameter (of known biological significance), suggests that other approach is needed. Although dogs seem to be the most important of the known causes of huemul mortality, currently their direct effect is difficult to model because they are not recorded in the livestock census.

In the reservoir scenario we simulated the flooding of 5.9 km² distributed in five artificial lakes that will be used to run a hydroelectric facility. This large project has been subjected to much criticism because of the impact it may have on part of the unique Patagonian biota. However, not only did the reservoir scenario not reduce huemul population size or persistence but even showed a positive, although not significant, effect. This counterintuitive pattern might be a result of the very barrier effect of reservoirs. Populations in fragmented landscapes tend to be more aggregated (Bjornstad et al. 1998, Hoyle 2005), and the present model showed an important effect of aggregation on population size. Although huemules were allowed to swim by the model, most frequently individuals would avoid crossing water and therefore “accumulate” near reservoirs likely increasing their rate of encounter.

It is important to highlight the fact that although the direct effect of water reservoirs on the regional huemul population trends may be minimal, our model did not include a series of factors associated to reservoir building and operation such as, roads, camps, powerlines and land change around the lake shore, that may indeed be more harmful than the existence of a few new water bodies.

Additionally, the model did not take into account population genetics, a factor that might be negatively affected by an increase in landscape fragmentation. However, we believe that the overall effect of the planned water reservoirs in changing the regional landscape connectivity for the species should be minimal. Also, theoretical and empirical studies

suggest that the effects of fragmentation only reach significant levels when the remaining habitat is less than 40% of the landscape (Fahrig 1997;1998). Huemules use an important diversity of vegetation types (Smith-Flueck 2000), concordant with their ample distribution in the past. Overall, suitable huemul habitat covers 63.7% of the regional landscape which is much higher than the mentioned threshold.

Management implications

Although limited in its ability to produce accurate quantitative predictions, the present model is helpful in identifying relevant information that should be the basis of a successful recovery program for the species.

For example, the importance that initial population size and spatial aggregation had on population trajectories underscores the urgency of conducting a study aimed at estimating total population size and distribution for the species throughout its range. Although having such an estimate might seem an obvious goal, it is interesting to note that the official Conservation Plan for the species in Chile (CONAF & CODEFF 2001) does not even mention it, likely because it is deemed as an unsurmountable task. Alternatively, the plan is based on studying and quantifying individual (presumably discrete) “populations” but there is not a formal rationale to transform those values into an estimate of total population size. Nowadays there are several techniques that allow for the estimation of total population sizes from local data (e.g. Robertson et al. 1995, Barber & Gelfand 2007, Pople et al 2007). Most likely these techniques will require a

redesign of local sampling efforts, shifting from a “census” paradigm to an estimation of point densities and to define suitable covariables to be used in the interpolation models.

Other crucial biological information includes survival data (preferably outside protected areas), juvenile dispersal patterns and spatial perception of individuals. Research efforts should be directed to fill the latter information gaps.

Indirectly, the model also highlighted the need for information on dogs, and their effect on huemul mortality and habitat selection patterns. A fortunate “by product” of this study is that, after attending a preliminary presentation of results, local officials are considering including information on dogs in the next livestock census. The importance of the latter is twofold. First, it will allow to incorporate the abundance of dogs as a separate variable from livestock in a future version of the model. But the most significant consequence is that it may become a first step to work along with the ranchers to reduce damage by dogs (e.g. eventually with the use of dog breeds adapted for the protection of both the cattle and the wild fauna, Marker et al. 2005).

Although highly disturbed by past fires and land use change, Aisén remains as a largely unpopulated region, with roughly 50% of the area under some level of legal protection. The amount of apparently suitable habitat (approximately 183,000 km² in the region) contrasts with the reduced population size of the species, again, pointing to the past effect of fire, hunting and/or disease.

The evidence provided by this model suggests that the huemul population in Aisén region has the potential to recover if limiting factors are kept under control. Unlike the situation in Argentina, where populations are apparently declining (Flueck & Smith-Flueck 2006), probably due to low densities and high level of habitat fragmentation, the species seems to be increasing in the studied area.

If our interpretation of the results of the present model is correct and huemules are, in fact, increasing in the Aisén region, by no means this implies that a “laissez faire” management approach should be adopted. On the contrary, the disproportionate effect that stochastic events have on small populations (Shaffer 1981) underscores the importance of actively facilitating recovery, until the species has reached a “safe” population level. The latter requires understanding the way in which the species naturally recovers and how it responds to management actions such as reintroductions and habitat restoration (Gardmark et al. 2003).

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TABLES

Table 1. Landscape layers.

Layer	Categories
Land use	<ul style="list-style-type: none"> - Deciduous forest - Nothofagus forest - Steppes - Scrub - Grassland - Bogs - Herbaceous vegetation - No vegetation - Urban areas - Ice camp and glaciers
Ecotones	<ul style="list-style-type: none"> - 250 meters from the forest border - More than 250 metros from the forest border
Slope (%)	<ul style="list-style-type: none"> - 0 – 15 - 15 - 50 - More than 50
Altitude (m)	<ul style="list-style-type: none"> - 0 – 800 - 800-1200 - More than 1200
Aspect	<ul style="list-style-type: none"> - Northeast to Norwest - South
Hidrography	<ul style="list-style-type: none"> - River - Lakes
Road	<ul style="list-style-type: none"> - Paved road - Unpaved roads - Prints(i.e. foot prints)
Town	<ul style="list-style-type: none"> - Cities (1000 to 5000 habitants) - Smaller towns (50 to 1000 habitants)
Livestock Animal Units (UA)	<ul style="list-style-type: none"> - 0.5 UA/há in scrub, steppes and grassland - 0.25 UA/há in forest

Table 2. Movement probability matrix.

	Deci- duous forest	Notho- -fagus forest	Ste- ppes	Scrub	Grass- land	Bogs	Herb- aceous vegeta- -tion	No vegeta- -tion	Urban areas	Ice camp and glaciers	Lake	River	Argen- -tina border
Deciduous forest	74*	3	7	10	10	10	10	6	5	1	5	5	50
Nothofagus forest	10	10	1	80	10	10	10	50	5	1	5	5	50
Steppes	16	1	64	20	50	50	50	40	5	1	5	5	50
Scrub	5	14	3	78	10	10	10	40	5	1	5	5	50
Grassland	50	50	50	50	50	50	50	10	5	1	5	5	50
Bogs	10	10	50	50	10	50	50	10	5	1	5	5	50
Herbaceous vegetation	10	10	50	10	50	50	50	10	5	1	5	5	50
No vegetation	71	50	40	40	10	10	10	29	5	1	5	5	50
Urban areas	95	95	95	95	95	95	95	95	1	1	5	5	50
Ice camp and glaciers	99	99	99	99	99	99	99	99	1	1	1	1	50
Lake	95	95	95	95	95	95	95	95	95	1	1	1	50
River	95	95	95	95	95	95	95	95	95	1	1	1	50
Argentina border	50	50	50	50	50	50	50	50	50	50	50	50	50

- This value represents the relative probability of weekly movement among grids between actual land use (row) and the next grid cells (column).
- Grey values were estimated from telemetry data and white values were estimated from the literature.

Table 3. Survival data.

Individual Age	Age-specific annual mortality rates (%)		
	Base value for model	125% from based value (sensitivity analysis)	75% from based value (sensitivity analysis)
1	40	50	30
2	10	12.5	7.5
3	5	6.25	3.75
4	5	6.25	3.75
5	5	6.25	3.75
6	5	6.25	3.75
7	5	6.25	3.75
8	5	6.25	3.75
9	5	6.25	3.75
10	5	6.25	3.75
11	10	12.5	7.5
12	35	43.75	26.25
13	50	62.5	37.5
14	100	100	75

Table 4. Movement pattern.

	Start week	Annual duration
Male hit	7 ds=3	13 ds=2
Reproductive season	9 ds=3	11 ds=5
Winter season	12 ds=3	26 ds=4
Birth season	41 ds=5	9 ds=5

Table 5. Movement probabilities modifier due to landscape attributes.

Layers	Category	Adult Male and female		Young	Pregnant female	
		Summer	Winter	All year	Rest of the year	Birth season
Huemuls density (individual/cells)	0	100	100	100	100	100
	1 - 4	50	75	75	50	25
	> 5	10	50	75	10	1
Ecotone	+ 250 m	100	50	100	50	25
	- 250 m	50	100	50	100	100
Slope	0 - 10 %	100	100	100	25	10
	10 - 50 %	50	50	75	75	75
	> 50 %	10	10	50	100	100
Altitude	0 - 800 m.	100	100	100	100	75
	800 - 1200 m.	50	75	75	75	100
	+ 1200 m.	10	50	50	50	50
Aspect	north	100	100	100	100	100
	south	75	75	75	50	50
Hidrography	no	100	100	100	100	100
	river	50	50	50	50	25
	lake	50	50	50	50	25
Roads	Unpaved road	30	30	30	15	5
	Foot print	50	50	50	25	5
Town	no	100	100	100	100	100
	Cities	10	10	10	5	1
	Smaller towns	20	20	20	5	1
Livestock	0 UA	100	100	100	100	100
	0.25 UA	20	30	30	10	5
	0.5 UA	10	15	15	5	2

Table 6. Landscape-related mortality.

Layers	Category	Mortality probability per week (%)
Hydrography	River	2
	Lake	2
Town	Cities	3
	Smaller towns (50 a 1000)	2
Road	Unpaved road	1
	Foot print	1
Livestock	0.25 AU(Animal unit)	1
	0.5 AU(Animal unit)	2

Table 7. Parameters for model based condition.

Parameters	Parameter based value
Population size	- 600
Population location	- Semi-aggregate
Weekly mortality probability (WMPR)	- See table 3
Male maximum search distance (Max-dist)	- 8 km
Weekly mortality probability due to roads (WMPR)	- 0.1 %
Weekly mortality probability due to livestock (WMPL)	- 1 % (for 0.25 UA)
	- 2 % (for 0.5 UA)

Table 8. Parameters used in sensitivity analysis.

Parameters	Base value used in the model	Parameter values	
Weekly mortality probability (WMPR)	Table 3	125 % from based value	75 % from based value
Male maximum search distance (Max-dist)	8 kilometer	2 kilometer	4 kilometer
Weekly mortality probability due to roads (WMPR)	0.1 %	0.5 %	1 %
Weekly mortality probability due to livestock (WMPL)	1 % (for 0.25 UA) 2 % (for 0.5 UA)	2 % (for 0.25 UA) 4 % (for 0.5 UA)	4 % (for 0.25 UA) 8 % (for 0.5 UA)

- Max-dist values were 2, 4 and 8 km. This range values were obtained from literature of other deer research (Abbott, 1997; Kie, 2002), and are values related to landscape perception and male movement in peak seasons. Distances further than 8 km were not tested since this value assures a 100% survival rate WMPR range values were obtained from literature.
- WMPL as the same as age-specific annual mortality rates, base values were estimated by interviewing the park ranger and researchers. The range values try to cover the best and worst estimated conditions as suggested by the research.

Table 9. Calibration result.

Parameters	Individuals fenology				
	Male with couple	Male without couple	Female	Pregnant Female	Young
Maximum weekly movement distance	500 *	Until 1000 *	500 *	Until 1000 *	Until 1000
Male attraction	0.8 *	1 *	-	-	-
Home range tendency	Memory span 0.6 *	0.6 *	0.6 *	0.6 *	0.6
	Gravity 0.8 *	0.8 *	0.8 *	0.8 *	0.5

(*) Parameters adjusted with telemetry data.

Table 10. Sensitivity analysis result.

Parameters	Change in parameter								
	25%	50%	75%	100%	125%	200%	400%	500%	1000%
Weekly mortality probability (WMPR)	-	-	0	0	-0.64	-	-	-	-
Male maximum search distance (Max-dist)	0.93	0		0	-	-	-	-	-
Weekly mortality probability due to roads (WMPR)	-	-	-	0	-	-	-	0	0
Weekly mortality probability due to livestock (WMPL)	-	-	-	0	-	0	0	-	-

$$Sx = \frac{(P.P._1 - P.P._0) / P.P._0}{(\text{Parameter}_1 - \text{Parameter}_0) / \text{Parameter}_0}$$

Sx: Sensitivity.

P.P.₀: Persistence probability for basic model situation.

P.P.₁: Persistence probability after change the parameter.

Parameter₀: Parameter value in the model base condition.

Parameter₁: Change in parameter value.

FIGURES

Figure 1: Study area

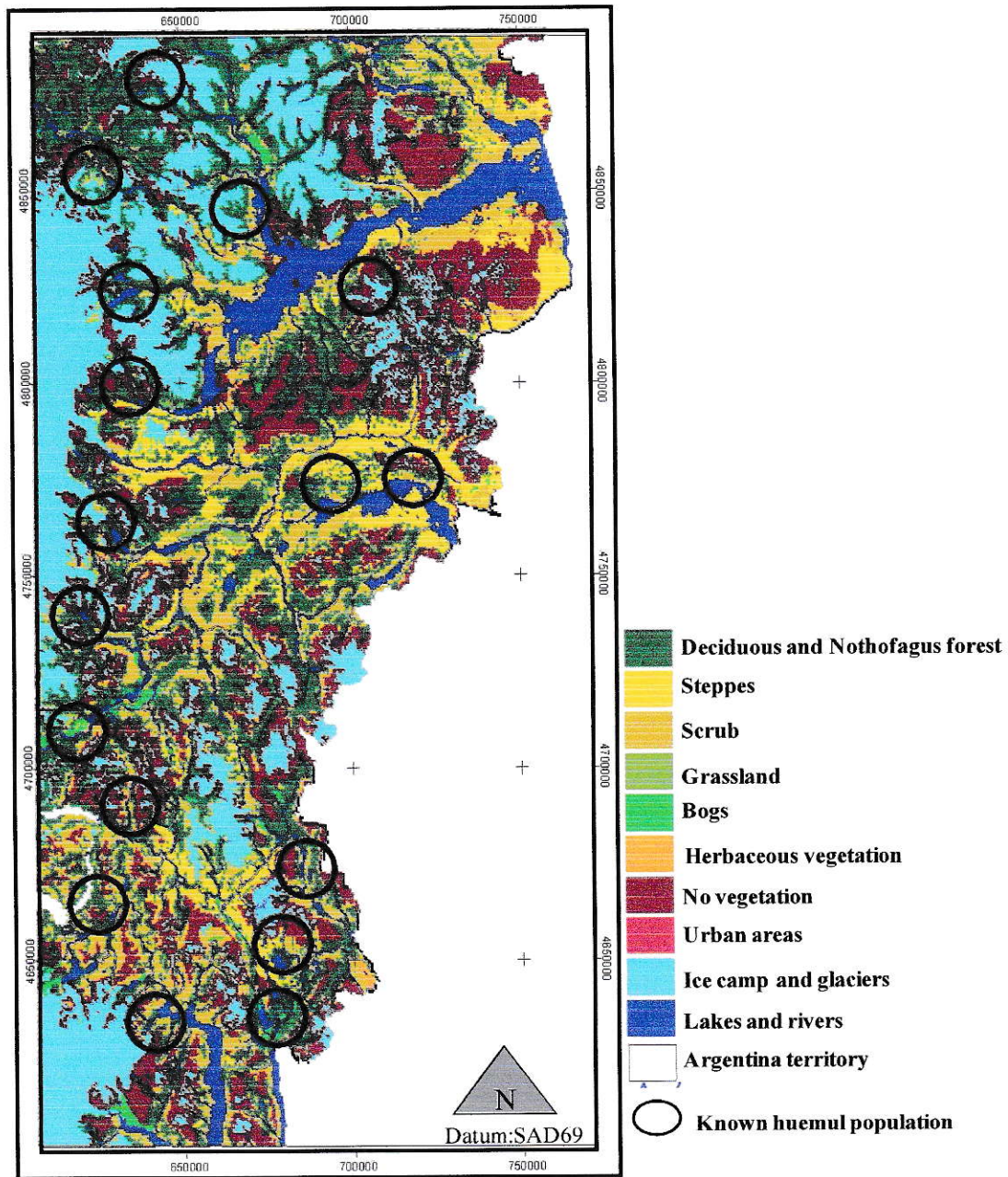


Figure 2: Model diagram

This flow chart shows the different model components. The entry variables are size and initial population location. The exit variable is the population size. This takes into account weekly and monthly cycles.

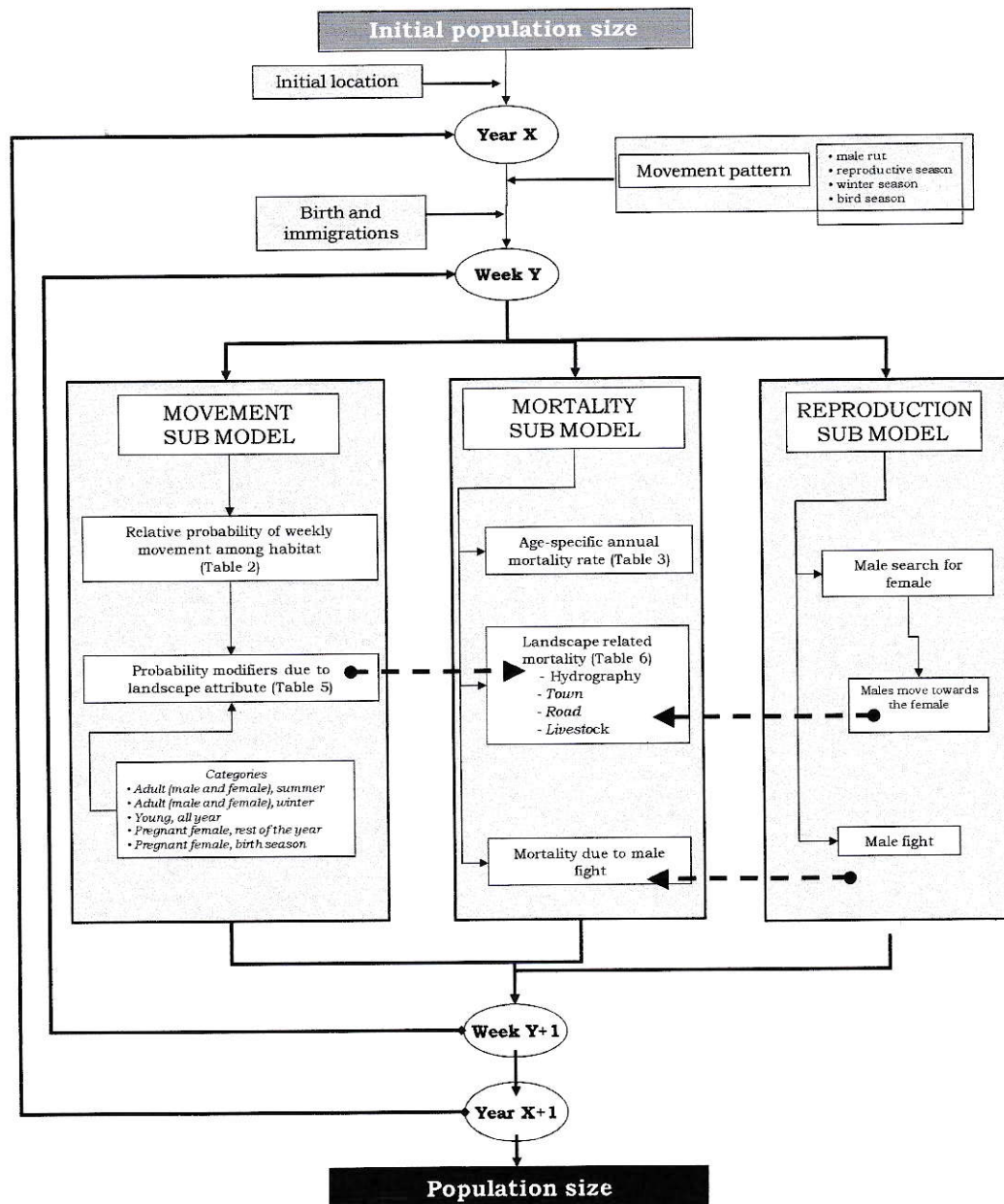


Figure 3: Normal scenario

Population trajectory for present landscape scenario. The Initial population size was composed of 600 individuals and the initial location was semi-aggregated. The population trajectories curve showed a process of adjustment during the first 10 years, in which there was a population increase during two first years followed by a decrease in the population size (grey zone). This situation was attributed to model adjustment. After this adjustment trajectory showed a stable population growth. The Persistence probability was 100%.

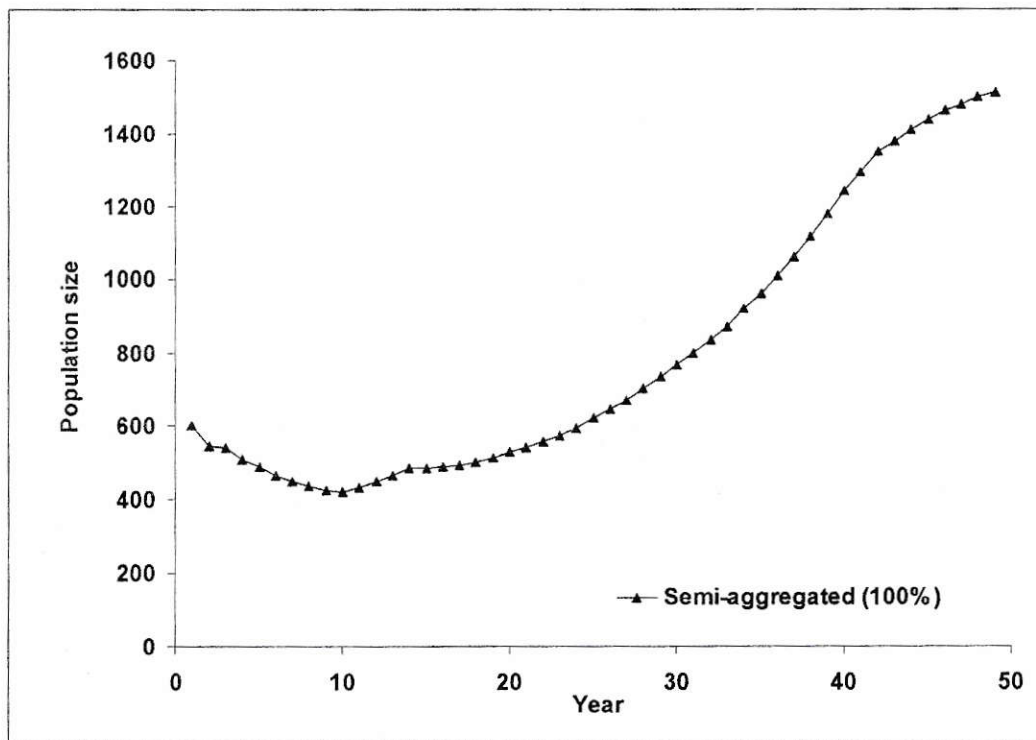


Figure 4: Model sensitivity to the initial conditions

Population trajectories of different sizes and initial population location. Population sizes = 5a: 100 individuals; 5b: 300 individuals; 5c: 600 individuals; 5d: 1200 individuals. Initial locations = aggregated; semi-aggregated and disaggregated
 Persistence probability P.P. = $\frac{\text{number of repetitions that did not eradicate}}{\text{number of repetitions}}$

Populations that weren't eradicated are considered when the population size at 50 years of simulation is greater than 30 individuals.

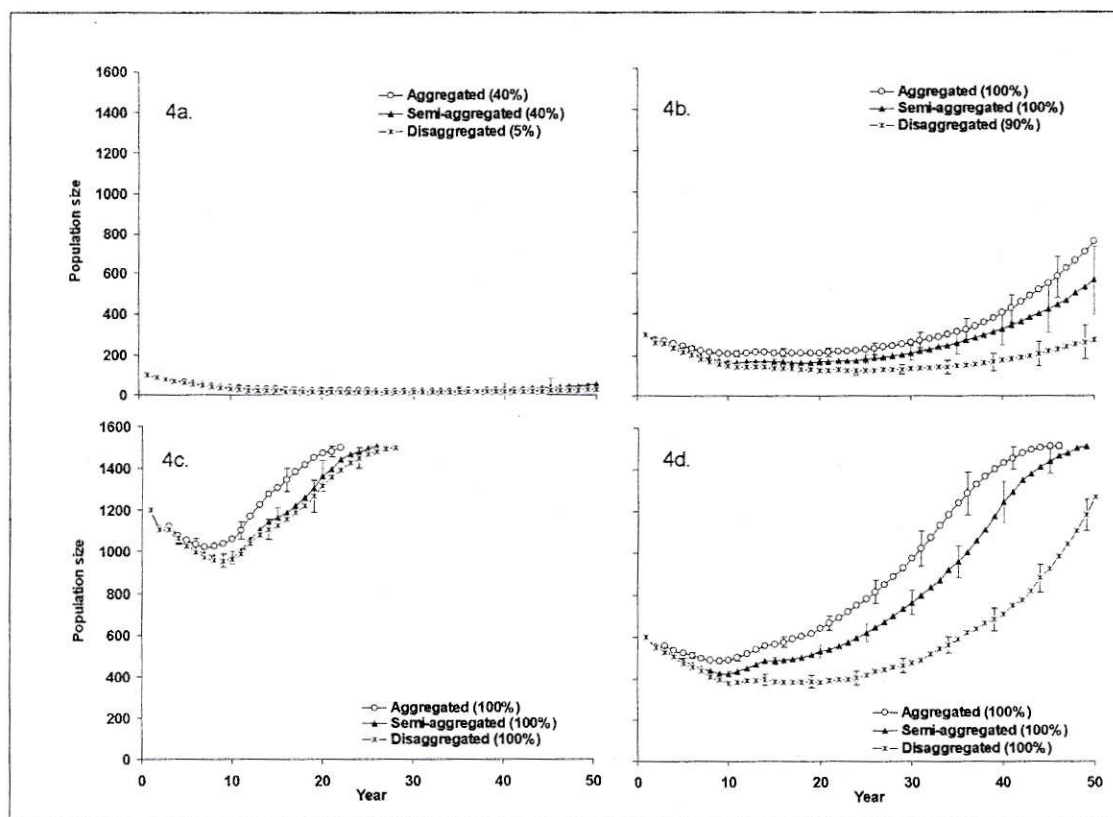


Figure 5: Effects of the landscape changes on the population dynamic

Population trajectories for the distinct simulated landscape scenarios.

Population sizes = 5a: 100 individuals; 5b: 300 individuals; 5c: 600 individuals; 5d: 1200 individuals.

Initial location is semi-aggregated.

In parenthesis is the survival probability of the PP population.

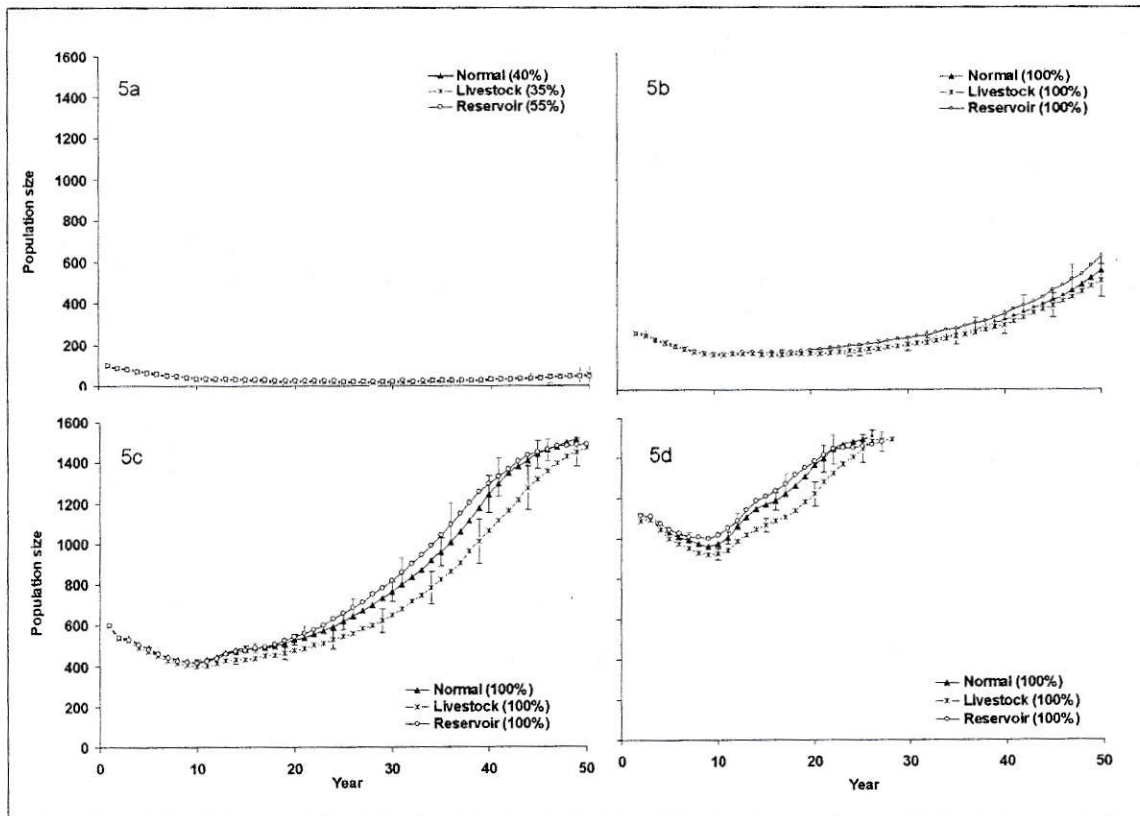
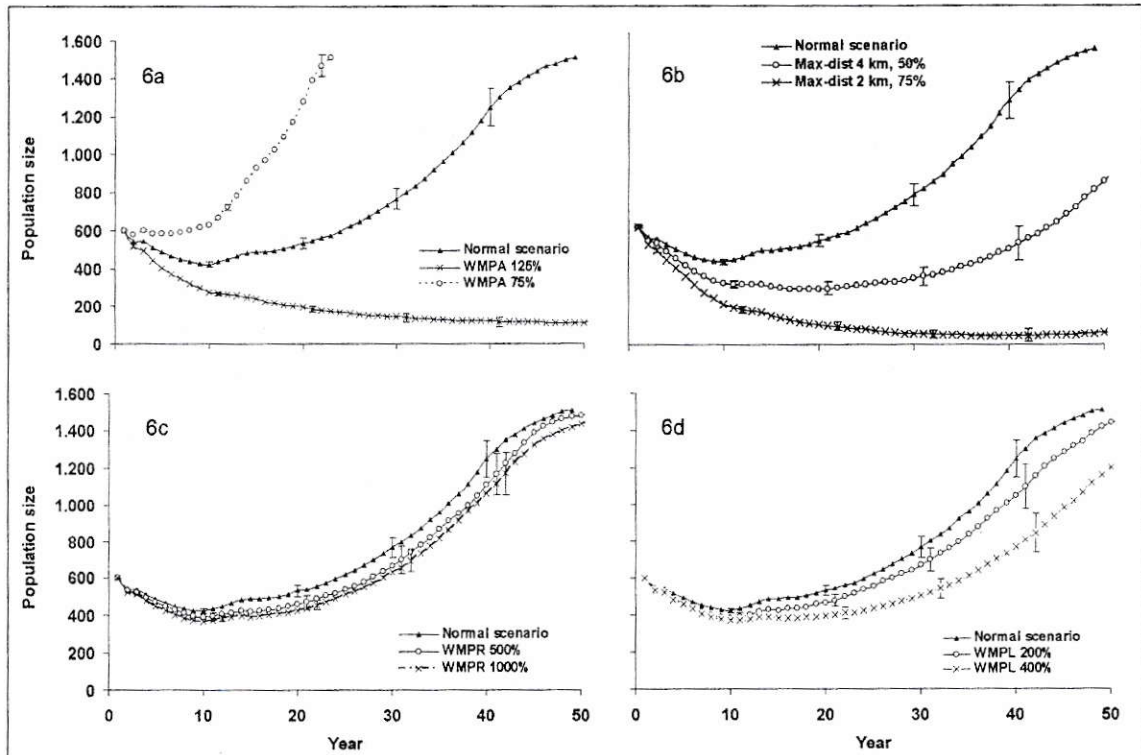


Figure 6: Effects of sensitivity analysis over population trajectories

Population trajectories for the distinct parameters evaluated (see table 7). 6a: Weekly mortality probability (WMPR); 6b: Male maximum search distance (Max-dist). 6c: Weekly mortality probability due to roads (WMPR); 6d: Weekly mortality probability due to livestock (WMPL).



APPENDIX 1. EXTENDED MODEL DESCRIPTION

The main purpose of this model is to describe the dynamics and, particularly, the viability of huemul populations under different development scenarios in the Aisen region. The model simulated the movements, reproduction and deaths of individuals during a 50-year period through three sub models; movement, mortality and reproduction (Fig. 2).

The model used two basic matrices: the first is a collection of individuals (the population) and their attributes and the second, a raster representation of the landscape.

All individual are characterized by the following state variables: identity number, sex, age, and spatial location. A unique identity number and sex label (male or female, 1/1 proportion) is given to each individual at the beginning of the simulation or when they are born. Age is assigned randomly (3-14 years, uniform distribution) to all individuals at the beginning of the simulation. Newborns are 0 years old. Age is increased by one at the end of the year. Spatial location of individuals is determined by the movement sub model (see Sub models), or during the initialization process (see Initialization).

Females are characterized by two additional codes: “offspring code” which is equal to the identity number of their offspring (twins are not allowed by the model) and “family code”, a unique identifier for the mother and their present couple. Males are also characterized by this “family code” identifying the females impregnated by them during the present season and a “couple code” identifying mates, with a maximum of two.

Family groups formed each year with a maximum number of three, one male and two female. Formation is in mating period, if the male “Couple code” is less than 3, then the female will have the same “family code”.

Individuals less than one year old are considered fawns. Males one to two years old are considered juveniles, and males more than two years old and females more than one year old are referred to as adults. Fawns have the same family code as their mothers.

Randomness in the model operates at two hierarchical levels, seasonality and individual behavior. Seasonality includes the simulation of processes and events related to change in a seasonal fashion, such as reproductive behavior and general movement and habitat selection patterns. The processes are male rut, reproductive season, winter movement and birth season. Movement patterns are represented by a normally distributed function composed by biological information from the literature (Aldridge y Montecinos, 1998; Smith-Flueck, 2000), and are calculated every year with a random variation of initial week and length of period to include some differences, in climate condition that exist between years (Table 4). Individual behavior includes movement and mating decisions.

Initialization

Initial population size and general location pattern of individuals are parameters that are defined before the beginning of the simulation. At initialization individual state variables are assigned values. Following the general location pattern (see Experiments) individuals are located randomly in grid cells containing appropriate habitat conditions (excluding lakes, river, ice camp, roads, towns, and cattle presence). Family groups are formed by grouping individuals at 8 kilometers distances or less a maximum of one male and two females per family.

Submodels

Movement sub model: This sub model defines individuals' location through time based on a "movement probability matrix (MPM)" containing the relative probabilities of weekly movements among grid cells with different land uses (see "movement data") plus a series of modifiers derived from seasonality, sedentariness and landscape features.

1. - *Seasonality:* individuals change their general movement during the year according to seasonal changes in the species' phenology and weather (e.g. snow). At the beginning of the year the model built the normal distribution function for "movement pattern". Each week, individuals randomly choose a number, which is uniformly distributed between 0 and 1, and if it is smaller than the movement pattern number for that week, they assume this movement pattern changing its habitat selection (Table 4).

2. - *Sedentariness:* This element is composed of three factors: maximum distance of weekly movements, male attraction to mates, and home range tendency. Maximum distance of weekly movement defines the maximum number of cells that an individual can move in one week. Male attraction defines the male tendency of movement close to his present mate(s). Home range tendency is defined by the tendency of an individual to move towards a "gravity center" and it is governed by two parameters: "memory span" referring to the number of previous spatial locations that are saved in memory to calculate the gravity center, and "gravity" that defines the influence of the gravity center on the future position.

3. *Landscape attributes.* Movement probabilities are eventually modified by information regarding landscape features such as ecotones, hidrography, slope, altitude, aspect, roads, towns and livestock and co specific density (Table 5). The effects of most of these variables on huemul movement were estimated from biological information on the species (Povilitis 1983; Aldridge & Montecinos 1998; Povilitis 1989; Frid 1994; Frid 1999; Frid 2000; Smith-Flueck, 2000). The effects of livestock and co specific density were estimated from literature on other deer species (Kie et al. 1991; Loft et al. 1991; Kie et al. 1996; Abbott et al. 1997; Kie et al. 2002).

The movement algorithm starts when an individual randomly chooses an arrival cell. It then assesses the probability of moving to such cell by multiplying the probability in the MPM times the probabilities of the modifiers. The algorithm then compares such

probability with a random number that is the result of multiplying n uniformly distributed random numbers between 0 and 1, with n being the number of modifiers used in the algorithm. If this latter number is smaller, it executes the movement. Otherwise the individual chooses another cell. This procedure is repeated a maximum of five times, after which the individual stays in the origin cell. The algorithm is applied to all individuals, with the exception of fawns, that move along with their mothers.

Because huemules are known to swim, the model allowed individuals to pass through cells containing lakes or rivers. However individuals were not allowed to “stay” in such cells. For that purpose, each time an individual entered a cell covered by water, it increased its movement speed, performing up to five movements in a normal 1-week time step. After that, if the individual still remained in a water cell, it drowned. Besides, each time an individual was present in a water cell an additional death probability was applied (see “mortality sub model”).

Mortality sub model: each week, deaths can happen due to three factors. First, age-specific annual mortality rates (see survival data) are transformed into weekly mortality probabilities (WMRA). Second, there is a landscape-related mortality rate that takes values greater than 0 when individuals are in a cell with a river, lake, livestock, road or town (Table 6). Third, males face an additional source of mortality when they fight for females (0.1 %). We used a low value of probability due to studies that indicate that fights leading to death or serious injury are rare. Clutton Brock (et al. 1979) found two cases of injury in a total sample of 107 observed fights of *Cervus elaphus*. For the huemul the observed fights present a low level of injury with those individuals that did not have death as the direct cause.

In all of the cases these probabilities are contrasted with random numbers uniformly distributed between 0 and 1, and if greater, individuals are “killed” and taken out of the simulation.

Reproduction sub model: this sub model is invoked when males test their individual probability of entering into rut. As a first phase males search for a female in estrous present within a maximum search distance of 8 km (max-dist). Secondly, males move towards the female in a straight line within one time step. During this phase males face the landscape-related mortality in all grid cells present in their route. If males survive to reach the female's grid cell, they look for other adult males present in the cell, and, if other adult males are present they engage in a fight (that neither may or may nor result in the death of one of the opponents). If there are not other males in the female's cell or if the individual wins the fight, mating occurs.

Calibration

Parameters used in the movement sub model (maximum distance of weekly movements, male attraction to mates, home range tendency, memory span and gravity) were subjected to calibration using telemetry data from 12 individuals from the Tamango

National Reserve. The procedure compared the position of the virtual deer over the simulation period with those from the telemetry database. The proportion of matching locations was used as an index parameter performance. The extent of home ranges was used as a control given that home ranges should fall between the size ranges reported in the literature (25 - 444 ha, Povilitis 1983, 1984; Gill et al. 2008). For all parameters except maximum distance of weekly movement, values ranging between 0.1 and 0.9 were tested. For every parameter combination a total of 50 simulations were run. For maximum distance of weekly movement, the model assumed that juvenile or single males and pregnant females can move up to 1000 m (2 cells) per week, this was based on the literature on other deer species (Rosenberry et al. 2001; Bowman et al. 2002; Long et al. 2005)

Parameters used in the movement sub model (i.e. “male attraction to mates” and “home range tendency”) were subject to calibration using telemetry data from 12 individuals from the Tamango National Reserve. For that purpose the model simulated a population of 50 individuals over a 5 year period. From these, the model chose 12 individuals featuring similar attributes to those of the radio tracked animals (e.g. initial spatial location, sex, age, family groups, etc). The model recorded the position of the virtual deer over the simulation period and compared these locations with those from the telemetry database. The proportion of matching locations was used as an index parameter performance. Additionally, the model recorded the extent of the resulting home ranges. The latter was used as a control given that home ranges should fall between the size ranges reported in the literature (25 - 444 ha, Povilitis 1983, 1984; Gill et al. 2008).

For all three parameter values between 0.1 and 0.9 were tested, and for every parameter combination a total of 50 simulations were run.

Parameter “Maximum distance of weekly movements” was not included in the calibration, because telemetry data showed almost no movement beyond one grid cell (500 m) for a week, probably due to the fact that most individuals had well established home ranges. Based on the literature on other deer species (Rosenberry et al. 2001; Bowman, and col, 2002; Long et al. 2005) the model assumed that juvenile or single males and pregnant females can move up to 1000 m (2 cells) per week.

Experiments

Four different initial population sizes (100, 300, 600 and 1200 individuals) and three general location patterns (aggregated, semi-aggregated and disaggregated) were tested.

The chosen initial population sizes reflect the level of uncertainty regarding the total population size for the region. Recent estimates vary from 300 to 1200 individuals (including the Argentinean side, Aldridge & Montecinos 1998; Smith-Flueck, 2000; Aldridge & Velasquez 2006; park rangers, pers. comm.). Therefore the range used includes the best and worst of these situations.

A similar situation exists regarding the spatial distribution of populations. Using available information on “stable” huemul populations in the region, 16 population areas were defined (Aldridge & Velasquez 2006; park rangers, pers. comm.; Villa et al. 2004). The aggregated population pattern randomly assigned all initial individuals in these areas. In the semi-aggregated pattern 85% of all individuals started in places of known populations and the rest were randomly located in any area of the region. In the disaggregated pattern all individuals were randomly located in the region. All individuals were located in grid cells containing suitable huemul habitat.

For sensitivity analysis a “basic model situation” with 600 individuals as an initial population size and semi-aggregated spatial distribution was considered (Table 7).

Scenarios

Three different scenarios of future development were simulated. The first one (“normal scenario”) maintained the present landscape configuration. The second scenario (“livestock scenario”) considered a 50% livestock increase in the region. The latter was generated by changing the present livestock map by increasing the number of AU per point by 50%. This means that, at a regional level, there is more area used by cattle but they tend to concentrate in the same general areas as in the normal scenario. This conservative approach was used because no information was available to predict the creation of new livestock ranching areas.

The third scenario (“reservoir scenario”) considered the creation of five reservoirs to produce hydro electrical power. This was simulated by changing the hydrographic map, adding lakes where the dams are planned to be built (Hidroaysen 2007).

Each experiment involved 20 replicates.

Expression of results

At the end of each year, the model recorded the geographic location, age, and status (dead or alive) of each individual. The total number of living individuals was then used as the total population size. For that purpose individuals located in a landscape border of 5 km (10 cells) were not tallied.

Because of programming constraints the model could only handle a maximum of 2000 individuals. For that reason, populations greater than 2000 were truncated in that number. When the total population size was smaller than 10 huemules, the population was considered extinct and simulation was terminated.

Persistence probability (PP) was calculated as the proportion of simulation replicates in which the population did not go extinct.

For each scenario the population size at any given time was the average of the population size of all 20 replicates at that time. Confidence intervals for population size were created using the standard deviation of all 20 replicates.

Sensitivity analysis

Persistence probability (P.P.) was used as the variable on which the sensitivity analysis was conducted. The sensitivity of the model was analyzed as the change in P.P. relative to change in the value of a given parameter (Parameter_x) (Jørgense 1994). An initial condition of 600 individuals and semi-aggregated location was considered as a *base condition* and the parameters values are indicated in Table 7.

Sensitivity (S_x) was calculated as follows:

$$S_x = \frac{(P.P._1 - P.P._0) / PP_0}{(\text{Parameter}_1 - \text{Parameter}_0) / \text{Parameter}_0}$$

Where PP₁ is the value of persistence probability after a change the Parameter₀; PP₀ is the value for basic model situation. Parameter₁ is the test value of parameter *P*, (all other parameters kept at standard value during test), and Parameter₀ is the parameter value for basic model situation (Jørgense 1994).

We assessed sensitivity of the model to four parameters: weekly mortality probability due to age (WMPA), male maximum search distance (max-dist), weekly mortality probability due to roads (WMPR) and weekly mortality probability due to livestock (WMPL). The range of values used for sensitivity analysis tried to cover the maximum range of biologically meaningful values (Table 8).

APPENDIX 2. MODEL CODE

```

Screen 12
Randomize timer
'stop
      'Par metros
Pbmpelea=1
Pbmrio=200
Pbmlago=200
Pbmpueb=300
Pbmald=200
Pbmpav=100
Pbmnopav=100
Pbmual=100
Pbmua2=200
mindist=16
open "aisenrnd.dat" as #2 len=16
field#2, 2 as uso$,2 as eco$, 2 as pend$, 2 as alti$, 2 as expo$, 2 as hidro$, 2 as urb$,
2 as ua$
for cy= 1 to 576
for cx= 1 to 286
registro = (cy-1)*286+cx
get#2, registro
uso=cvi(uso$)
eco=cvi(eco$)
pend=cvi(pend$)
alti=cvi(alti$)
expo=cvi(expo$)
hidro=cvi(hidro$)
urb=cvi(urb$)
ua=cvi(ua$)
pset (cy+20,300-cx),uso
pset (cy+20,300-cx),ua
next cx
next cy
      STOP
' IBM HUEMUL V1
open "Pbuso01.csv" for input as #1
'#2 es el uso de suelo en .dat
open "PBml0.csv" for input as #3
open "chetotal.csv" for input as #4

'DIMENSIONA MATRIZ TEMPORAL DE HUEMULES
dim htempo%(2000,15)

'DIMENSION MATRIZ DE PROB DE CAMBIO DE GRD POR USO DE SUELO
dim pbcuso%(16,16)
for b=1 to 15
input#1, pbcuso%(b,1), pbcuso%(b,2), pbcuso%(b,3), pbcuso%(b,4), pbcuso%(b,5),
pbcuso%(b,6), pbcuso%(b,7), pbcuso%(b,8),
pbcuso%(b,9), pbcuso%(b,10), pbcuso%(b,11), pbcuso%(b,12), pbcuso%(b,13),
pbcuso%(b,14), pbcuso%(b,15), pbcuso%(b,16)
next b
close#1

'DIMENSION MATRIZ DE PROB DE MUERTE ALEATORIA
dim pbmedad%(14)
for f=1 to 14
input#3, pbmedad%(f)
next f
close#3

```

```

'DIMENSION MATRIZ DE INMIGRACION
  dim pbinmi%(282,2)
  for f=1 to 282
    input#4, pbinmi%(f,1), pbinmi%(f,2)
  next f
close#4
open "rdm.csv" for append as #6
open "muertes.csv" for append as #7
open "censos.csv" for append as #8
open "loca.csv" for append as #9
'write#6, "repeti", "ano", "huemules", "nacimientos", "muertes", "mbebe", "edad", "rio",
"lago", "ciudad", "pueblo", "aldea", "pav", "nopav", "ganado", "peleas", "madre",
"argentina", "nado"
'write#7, "repeti", "ano", "sem", "(h,6)", "(h,1)", "(h,2)", "(h,4)", "(h,5)"
'write#8, "repeti", "ano", "total huemules", "totaljuvenil", "total adultos", "total
crias", "machojuv", "hembrajuv", "macho adulto", "hembra adulta"
'write#9, "repeti", "ano", "sem", "(h,6)", "(h,1)", "(h,2)", "(h,3)", "(h,4)", "(h,8)",
"(h,9)", "(h,10)", "(h,11)", "(h,12)"

for repeti = 1 to 20   'RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
'DIMENSIONA MATRIZ INDIVIDUOS INICIAL DEL MODELO
'1 : x
'2 : y
'3 : sexo / macho=0 / hembra=1 / hembra pre=ada=2 / muerto=-1
'4 : edad
'5 : causa de muerte/1=variesgo/2=aleatorea/3=pelea/
'6 : codhuemul
'7 : para el macho si visito una hembra
'8 : codigo madre
'9 : codigo hijo/a
'10: codigo padre/familia
'11: Ambito de hogar en x
'12: Ambito de hogar en y
'13: Nfmero de familiares
'14: Nfmero de hijo/a de las madres"

huemules = 100          'HUEMULES
dim huemul%(huemules,15)
'input ";"pp
'beep
codigo=100
codmadre=500
codfamilia=700
' CONDICIONES INICIALES EN EL MODELO
for h=1 to huemules
  ccastillo=int(1/100*huemules)
  gralcarrera=int(1/100*huemules)
  leon=int(2/100*huemules)
  baker=int(2/100*huemules)
  chnorte=int(4/100*huemules)
  jeinemeni=int(5/100*huemules)
  baguala=int(5/100*huemules)
  tamango=int(7/100*huemules)
  chacabuco=int(5/100*huemules)
  surcochr=int(2/100*huemules)
  canales1=int(5/100*huemules)
  canales2=int(5/100*huemules)
  pascua=int(10/100*huemules)
  laramona=int(5/100*huemules)
  ohiggins=int(10/100*huemules)
  ohigginsnorte=int(10/100*huemules)
  asignaxy:
    huemul%(h,1) = int(rnd*250)+15
    huemul%(h,2) = int(rnd*550)+15
if h>=1 and h<ccastillo then
  if huemul%(h,1)<75 or huemul%(h,1)>168 or huemul%(h,2)<1 or huemul%(h,2)>23 then goto
  asignaxy
end if

```

```

if h>=ccastillo and h<=(ccastillo+gralcarrera) then
  if huemul%(h,1)<106 or huemul%(h,1)>123 or huemul%(h,2)<99 or huemul%(h,2)>115 then goto
  asignaxy
end if
if h>(ccastillo+gralcarrera) and h<=(ccastillo+gralcarrera+leon) then
  if huemul%(h,1)<38 or huemul%(h,1)>72 or huemul%(h,2)<115 or huemul%(h,2)>142 then goto
  asignaxy
end if
if h>(ccastillo+gralcarrera+leon) and h<=(ccastillo+gralcarrera+leon+baker) then
  if huemul%(h,1)<89 or huemul%(h,1)>107 or huemul%(h,2)<211 or huemul%(h,2)>229 then goto
  asignaxy
end if
if h>(ccastillo+gralcarrera+leon+baker) and h<=(ccastillo+gralcarrera+leon+baker+chnorte)
then
  if huemul%(h,1)<26 or huemul%(h,1)>46 or huemul%(h,2)<188 or huemul%(h,2)>343 then goto
  asignaxy
end if
if
  h>(ccastillo+gralcarrera+leon+baker+chnorte) and
  h<=(ccastillo+gralcarrera+leon+baker+jeinemeni) then
  if huemul%(h,1)<190 or huemul%(h,1)>219 or huemul%(h,2)<224 or huemul%(h,2)>252 then
  goto asignaxy
end if
if
  h>(ccastillo+gralcarrera+leon+baker+chnorte+jeinemeni) and
  h<=(ccastillo+gralcarrera+leon+baker+chnorte+jeinemeni+baguala) then
  if huemul%(h,1)<190 or huemul%(h,1)>219 or huemul%(h,2)<224 or huemul%(h,2)>252 then
  goto asignaxy
end if
if
  h>(ccastillo+gralcarrera+leon+baker+chnorte+jeinemeni+baguala) and
  h<=(ccastillo+gralcarrera+leon+baker+chnorte+jeinemeni+baguala+tamango) then
  if huemul%(h,1)<139 or huemul%(h,1)>169 or huemul%(h,2)<234 or huemul%(h,2)>250 then
  goto asignaxy
end if
if
  h>(ccastillo+gralcarrera+leon+baker+chnorte+jeinemeni+baguala+tamango) and
  h<=(ccastillo+gralcarrera+leon+baker+chnorte+jeinemeni+baguala+tamango+chacabuco) then
  if huemul%(h,1)<165 or huemul%(h,1)>208 or huemul%(h,2)<205 or huemul%(h,2)>224 then
  goto asignaxy
end if
if h>(ccastillo+gralcarrera+leon+baker+chnorte+jeinemeni+baguala+tamango+chacabuco) and
h<=(ccastillo+gralcarrera+leon+baker+chnorte+jeinemeni+baguala+tamango+chacabuco+surcochr
) then
  if huemul%(h,1)<59 or huemul%(h,1)>76 or huemul%(h,2)<340 or huemul%(h,2)>357 then goto
  asignaxy
end if
if
h>(ccastillo+gralcarrera+leon+baker+chnorte+jeinemeni+baguala+tamango+chacabuco+surcochr)
and
h<=(ccastillo+gralcarrera+leon+baker+chnorte+jeinemeni+baguala+tamango+chacabuco+surcochr
+canalesn) then
  if huemul%(h,1)<2 or huemul%(h,1)>35 or huemul%(h,2)<361 or huemul%(h,2)>398 then goto
  asignaxy
end if
if
h>(ccastillo+gralcarrera+leon+baker+chnorte+jeinemeni+baguala+tamango+chacabuco+surcochr+
canalesn) and
h<=(ccastillo+gralcarrera+leon+baker+chnorte+jeinemeni+baguala+tamango+chacabuco+surcochr
+canalesn+canaless) then
  if huemul%(h,1)<2 or huemul%(h,1)>30 or huemul%(h,2)<460 or huemul%(h,2)>505 then goto
  asignaxy
end if
if
h>(ccastillo+gralcarrera+leon+baker+chnorte+jeinemeni+baguala+tamango+chacabuco+surcochr+
canalesn+canaless) and
h<=(ccastillo+gralcarrera+leon+baker+chnorte+jeinemeni+baguala+tamango+chacabuco+surcochr
+canalesn+canaless+pascua) then
  if huemul%(h,1)<50 or huemul%(h,1)>85 or huemul%(h,2)<487 or huemul%(h,2)>518 then goto
  asignaxy
end if

```

```

if
h>(ccastillo+gralcarrera+leon+baker+chnorte+jeinemeni+baguala+tamango+chacabuco+surcochr+
canalesn+canaless+pascua) and
h<=(ccastillo+gralcarrera+leon+baker+chnorte+jeinemeni+baguala+tamango+chacabuco+surcochr
+_canalesn+canaless+pascua+laramona) then
if huemul%(h,1)<23 or huemul%(h,1)>84 or huemul%(h,2)<549 or huemul%(h,2)>576 then goto
asignaxy
end if
if
h>(ccastillo+gralcarrera+leon+baker+chnorte+jeinemeni+baguala+tamango+chacabuco+surcochr+
canalesn+canaless+pascua+laramona) and
h<=(ccastillo+gralcarrera+leon+baker+chnorte+jeinemeni+baguala+tamango+chacabuco+surcochr
+_canalesn+canaless+pascua+laramona+ohiggins) then
if huemul%(h,1)<112 or huemul%(h,1)>153 or huemul%(h,2)<476 or huemul%(h,2)>532 then
goto asignaxy
end if
if
h>(ccastillo+gralcarrera+leon+baker+chnorte+jeinemeni+baguala+tamango+chacabuco+surcochr+
canalesn+canaless+pascua+laramona+ohiggins) and
h<=(ccastillo+gralcarrera+leon+baker+chnorte+jeinemeni+baguala+tamango+chacabuco+surcochr
+_canalesn+canaless+pascua+laramona+ohiggins+ohigginsnorte) then
if huemul%(h,1)<117 or huemul%(h,1)>149 or huemul%(h,2)<149 or huemul%(h,2)>437 then
goto asignaxy
end if
cx=huemul%(h,1)
cy=huemul%(h,2)
gosub regist
if uso > 6 then goto asignaxy
if pend= 3 then goto asignaxy 'pend
if alti=3 then goto asignaxy 'alt
if hidro> 0 then goto asignaxy 'hidro
if urb > 0 then goto asignaxy 'urb
if ua> 0 then goto asignaxy 'ganado
huemul%(h,3) = int(rnd*2)
huemul%(h,4) = int(rnd*9)+3
huemul%(h,5) = 0
huemul%(h,6) = codigo
codigo=codigo+1
huemul%(h,11) = huemul%(h,1)*10
huemul%(h,12) = huemul%(h,2)*10
pset(20+huemul%(h,2), 300-huemul%(h,1)), 15
' circle(20+huemul%(h,2), 300-huemul%(h,1)),3,15
next h
'stop

'LIMITES ZONAS INCIALES
'stop
' Asigna familias a poblacion inicial
for h=1 to huemules
machosfam=0
hembrasfam=0
if huemul%(h,8)>=700 then goto yatienefamilia
huemul%(h,8)=codfamilia
for hh=1 to huemules
if huemul%(hh,8)=0 then
eucli=sqr(((huemul%(h,1)-huemul%(hh,1))^2+((huemul%(h,2)-huemul%(hh,2))^2)))
if eucli < 16 and hh><h then
if huemul%(hh,3)=1 then hembrasfam=hembrasfam+1
if huemul%(h,3)=0 then machosfam=machosfam+1
if huemul%(hh,3)=0 then machosfam=machosfam+1
if hembrasfam<3 and machosfam<=1 then huemul%(hh,8)=huemul%(h,8)
end if
end if
next hh
codfamilia=codfamilia+1
yatienefamilia:
next h

```

```

'stop
' MOVIMIENTO HUEMULES
' POR AYO
' AYO
AYO
for ano = 1 to 55
color 10
'CALCULO LAS CURVAS DE PROBABILIDADES ANUALES, EL COMO VA A SER ESE AYO
' 1. PELEAS MACHOS (machos)
' Datos: semanas 7 - 20, duracion = 13 semanas, ds=2
semipelea = int(rnd*3)+6
durapelea = int(rnd*3)+12
prompelea = (semipelea*2+durpelea)/2
dsapelea = int(rnd*2)+2
cdsapelea = 2*(dsapelea*dsapelea)
' 2. APAREAMIENTO (machos y hembras)
' Datos: semanas 9 - 22, duracion = 11 semanas, ds=5
semiapa = int(rnd*3)+8
durapa = int(rnd*3)+10
promapa = (semiapa*2+durapa)/2
dsapa = int(rnd*2)+4
cdsapa = 2*(dsapa*dsapa)
' 4. MOVIMIENTO INVIERNO
' Datos: semanas 12 - 38, duracion = 26 semanas, ds=4
semiinv = int(rnd*3)+11
durainv = int(rnd*3)+25
prominv = (semiinv*2+durainv)/2
dsinv = int(rnd*3)+3
cdsinv = 2*(dsinv*dsinv)
' 3. PARICIONES (hembras)
' Datos: semanas 41 - 52, duracion = 9 semanas, ds=5
semipari = int(rnd*5)+40
durapari = int(rnd*5)+8
prompari = (semipari*2+durapari)/2
dsapari = int(rnd*2)+4
cdsapari = 2*(dsapari*dsapari)
for sem = 1 to 52
' SEMANAS
' Calcula las probabilidades semanales
PBpelea = int(2.7183^(((sem-prompelea)^2)/cdsapelea)*100)
PBapa = int(2.7183^(((sem-promapa)^2)/cdsapa)*100)
PBinv = int(2.7183^(((sem-prominv)^2)/cdsinv)*100)
PBpari = int(2.7183^(((sem-prompari)^2)/cdsapari)*100)
locate 24, 1:print "repetición: "; repeti
locate 25, 1:print "año: "; ano
locate 25, 13:print "semana:", sem
locate 26, 1:print "huemules:", huemules
locate 27, 1:print "nacimientos:", nacimientos
locate 27, 20:print "muertes:", muertes
'PROBABILIDAD DE MUERTE aleatoria 1/10.000 por semana
for h=1 to huemules
if huemul%(h,3)=-1 or huemul%(h,3)=-2 then goto dead
if huemul%(h,3)>=0 then
mdamedad=int(rnd*10000)+1
moriredad=pbmedad%(huemul%(h,4))
if mdamedad<moriredad or huemul%(h,4)>=14 then
huemul%(h,5)=2
huemul%(h,3)=-1
write#7, repeti, ano, sem, huemul%(h,6), huemul%(h,1), huemul%(h,2), huemul%(h,4),
huemul%(h,5)
end if
end if
dead:
'if huemul%(h,3)=-2 then circle(huemul%(h,1)+300, huemul%(h,2)+25), 5, 14
next h
' CUENTA HIJAS Y HEMBRAS FAMILIA
for h=1 to huemules
if huemul%(h,3)=-1 or huemul%(h,3)=-2 then goto otrohh
nhijos=0

```

```

    nfam=0
    if huemul%(h,8)=0 then
        huemul%(h,8)=codfamilia
        codfamilia=codfamilia+1
    end if
    if huemul%(h,3)>=0 then
        for n=1 to huemules
            if huemul%(h,8)=huemul%(n,8) and h><n and huemul%(n,3)><-1 then nfam=nfam+1
            huemul%(h,13)=nfam
        next n
    end if
    if huemul%(h,3)>=1 then
        for n=1 to huemules
            if huemul%(h,9)=huemul%(n,10) and huemul%(n,3)>=1 and h><n then nhijos=nhijos+1
            if huemul%(h,9)=huemul%(n,10) and huemul%(n,3)=0 and h><n and huemul%(n,4)<=2
then nhijos=nhijos+1
            huemul%(h,14)=nhijos
        next n
    end if
    otrohh:
    next h
    'CENSO TAMANGO
    if sem=16 then
        machjuv=0
        hemjuv=0
        hemadult=0
        machadult=0
        bambi=0
    if huemul%(h,3)=-1 or huemul%(h,3)=-2 then goto nocenso
    for h=1 to huemules
        if huemul%(h,1)>=139 and huemul%(h,1)<=169 and huemul%(h,2)>=234 and
huemul%(h,2)<=250 then
            if huemul%(h,3)=0 and huemul%(h,4)=2 then machjuv=machjuv+1
            if huemul%(h,3)>=1 and huemul%(h,4)=2 then hemjuv=hemjuv+1
            if huemul%(h,3)=0 and huemul%(h,4)>=3 then machadult=machadult+1
            if huemul%(h,3)>=1 and huemul%(h,4)>=3 then hemadult=hemadult+1
            if huemul%(h,4)=1 then bambi=bambi+1
        end if
    nocenso:
    next h
    juveniles=machjuv+hemjuv
    adultos=machadult+hemadult
    tothuemules=juveniles+adultos+bambi
    write#8, repeti, ano, tothuemules, juveniles, adultos, bambi, machjuv, hemjuv, machadult,
hemadult
    juveniles=0
    adultos=0
    tothuemules=0
    bambi=0
end if
'CELO MACHO
'ver si macho se apareo y no se mueve normal
for h = 1 to huemules
    if huemul%(h,3)>=1 or huemul%(h,3)=-1 or huemul%(h,3)=-2 or huemul%(h,4)<=1 then goto
nocelo
    if huemul%(h,3)=0 and huemul%(h,4)>2 and huemul%(h,7)<3 then
        mdapelea=int(rnd*100)+1
        if mdapelea<=PBpelea then
            huemul%(h,7)=1
            gosub celomacho
        end if
    end if
end if
movnormal:
nocelo:
next h
'MOVIMIENTO
for h=1 to huemules
    if huemul%(h,3)=-1 or huemul%(h,3)=-2 then goto hmuerto

```



```

    cy=huemul%(h,2)
    cx=huemul%(h,1)
    gosub regist
if huemul%(h,3)>=0 then pset(20+huemul%(h,2),300-huemul%(h,1)), 15
circle(20+huemul%(h,2), 300-huemul%(h,1)),1,15
'if huemul%(h,3)<-1 then circle(20+huemul%(h,2),300-huemul%(h,1)), 4, 12
if huemul%(h,4)<=2 and huemul%(h,3)>=1 then goto crial 'es cria hembra
if huemul%(h,4)<=2 and huemul%(h,3)=0 then goto cria2 'es cria macho

if huemul%(h,11)=0 or huemul%(h,12)=0 then
    huemul%(h,11) = huemul%(h,1)*10
    huemul%(h,12) = huemul%(h,2)*10
end if
tira=0
rep=0
tiraotravez:
    tira=tira+1
repitexy:
rep=rep+1
lar=3
largo=1
if huemul%(h,3)=2 then lar=5: largo=2
if huemul%(h,3)=0 and huemul%(h,4)<8 and huemul%(h,7)><2 then lar=5: largo=2
    mx=int(rnd*lar)-largo
    my=int(rnd*lar)-largo
    azarx=huemul%(h,1)+mx
    azary=huemul%(h,2)+my
    if azarx<=10 or azary<=10 and rep<10 then goto repitexy
    if azarx<=10 or azary<=10 and rep>=10 then
        futx=huemul%(h,1)
        futy=huemul%(h,2)
        goto mov
    end if
    promx=huemul%(h,11)/10
    promy=huemul%(h,12)/10
    phr=0.8
    if huemul%(h,4)<=5 then phr=0.1
    if huemul%(h,3)=2 then phr=0.5
'busca familia
    pesop=0.8
    pesof=0.2
    if huemul%(h,13)=0 then pesop=1: pesof=0: goto listo
    if huemul%(h,3)>=1 then pesop=1: pesof=0: goto listo
    if huemul%(h,8)=0 then pesop=1: pesof=0: goto listo
    if huemul%(h,3)=0 and huemul%(h,13)>0 then 'si es macho busca hembra
    if PBapa>1 then pesop=1: pesof=0: goto listo
    for f=1 to huemules
        if h>f and huemul%(h,8)=huemul%(f,8) and huemul%(f,3)>=1 then
            ppx=huemul%(f,1)
            ppy=huemul%(f,2)
        end if
    next f
    end if
listo:
if ppx=0 or ppy=0 then pesop=1: pesof=0
futxx=((azarx*(1-phr)+promx*phr)*pesop+(ppx*pesof))*100
futy=((azary*(1-phr)+promy*phr)*pesop+(ppy*pesof))*100
futx=(azarx*(1-phr)+promx*phr)*pesop+(ppx*pesof)
futy=(azary*(1-phr)+promy*phr)*pesop+(ppy*pesof)
if futx<3 or futx>280 or futy<3 or futy>570 then
if tira < 10 then goto tiraotravez
if tira>=10 then
    futx=huemul%(h,1)
    futy=huemul%(h,2)
    goto mov
end if
end if
    cy=huemul%(h,2)

```

```

cx=huemul%(h,1)
gosub regist
aa=uso
ah=hidro
cy=int(futy)
cx=int(futx)
gosub regist
bb=uso
bh=hidro
pbmovuso=pbcurso%(aa,bb)
mdausos=int(rnd*100)+1
if mdausos>pbmovuso and tira<5 then goto tiraotravez

if uso=10 then
  futx=huemul%(h,1)
  futy=huemul%(h,2)
  goto muv
end if
'REGULA MOVIMIENTO
' Densidad de huemules
for c=1 to huemules
  denh=0
  denslocal=0
  if c<>h and huemul%(c,1)=huemul%(h,futx) and huemul%(c,2)=huemul%(h,futy) then
    denh=denh+1
  end if
  if c<>h and huemul%(c,1)=huemul%(h,1) and huemul%(c,2)=huemul%(h,2) then
    denslocal=denslocal+1
  end if
next c
denh=denh-denslocal
gosub regulamov
'MOV POR MULTIPLICACION
multi=dh*ecot*pendi*alt*ep*hid*urba*gand ' ecot pendi alt ep hid urba gand
if dh=0 or ecot=0 or pendi=0 or alt=0 or ep=0 or hid=0 or urba=0 or gand=0 then
  pbtop=100:goto ya
pbtop=multi/1000000000000000
ya:
  pbtopcali=(pbtop/pbajust)
  mdatop=int(rnd*100)+1
  if mdatop>pbtopcali and tira<6 then goto tiraotravez
  cy=int(futy)
  cx=int(futx)
  gosub regist
  if hidro=2 then gosub natacion
  if hidro>0 or urb>1 or ua>0 then gosub riesgos
  if uso>=15 then
    mdamext=int(rnd*100)+1
    if mdamext<50 then
      huemul%(h,3)=-2
      huemul%(h,5)=13
      write#7, repeti, ano, sem, huemul%(h,6), huemul%(h,1), huemul%(h,2), huemul%(h,4),
      huemul%(h,5)
      goto hmuerto:
    end if
    if mdamext>=50 then futx=huemul%(h,1):futy=huemul%(h,2):goto muv
  end if
  if lar=5 then
    if mx=2 or mx=-2 or my=2 or my=-2 then
      cx=int((azarx+huemul%(h,1))/2)
      cy=int((azary+huemul%(h,2))/2)
    if cx<=1 or cy<=1 then goto seguir:
      gosub regist
      if hidro>0 or urb>1 or ua>0 then gosub riesgos
    end if
  end if
end if
seguir:

```

```

cx=huemul%(h,1)
cy=huemul%(h,2)
gosub regist
pset(20+huemul%(h,2),300-huemul%(h,1)),uso
muv:
  whr=0.6
  huemul%(h,11)=10*((promx*whr)+futx*(1-whr))
  huemul%(h,12)=10*((promy*whr)+futy*(1-whr))
  huemul%(h,1)=futx
  huemul%(h,2)=futy
huemulmuerto:
cria1:
cria2:
hmuerto:
next h
'MOVIMIENTO CRIAS SEPARADO POR SEXO
for h=1 to huemules
  'if huemul%(h,4)<=2 and huemul%(h,3)>=1 and huemul%(h,3)>=0 then 'es cria hembra
  if huemul%(h,4)<=2 and huemul%(h,3)>=1 then 'es cria hembra
    for n=1 to huemules
      if huemul%(h,10)=huemul%(n,9) and n><h then 'busca su madre
        huemul%(h,1)=huemul%(n,1)
        huemul%(h,2)=huemul%(n,2)
        goto criamov
      end if
    next n
  criamov:
  end if
  'if huemul%(h,4)<=2 and huemul%(h,3)=0 and huemul%(h,3)>=0 then 'es cria macho
  if huemul%(h,4)<=2 and huemul%(h,3)=0 then 'es cria macho
    for n=1 to huemules
      if huemul%(h,10)=huemul%(n,9) and n><h then
        huemul%(h,1)=huemul%(n,1)
        huemul%(h,2)=huemul%(n,2)
        goto criamovm
      end if
    next n
  criamovm:
  end if
next h
for h = 1 to huemules
cx=huemul%(h,1)
cy=huemul%(h,2)
gosub regist
next h
'MUERTE DE CRIAS POR MUERTE DE MADRE-MADRES VIUDAS
for h=1 to huemules
  if huemul%(h,3)=-1 or huemul%(h,3)=-2 then
    for c=1 to huemules
      if huemul%(c,4)=1 and huemul%(h,9)=huemul%(c,10) and h><c then
        huemul%(c,3)=-1
        huemul%(c,5)=12
        write#7, repeti, ano, sem, huemul%(c,6), huemul%(c,1), huemul%(c,2),
huemul%(c,4), huemul%(c,5)
      end if
    next c
  end if
next h
for h = 1 to huemules
if sem=9 or sem= 28 or sem=50 then
write#9, repeti, ano, sem, huemul%(h,6), huemul%(h,1), huemul%(h,2), huemul%(h,3),
huemul%(h,4), huemul%(h,8), huemul%(h,9), huemul%(h,10)
end if
next h
if sem=52 then gosub redimensiona
next sem
next ano

```

```

'close#1
erase huemul%
otrarep:
next repeti
close#6
close#7
close#8
close#9
close#10
end
'SUBROUTINAS
      'REGISTROS
regist:
registro=(cy-1)*286+cx
get#2, registro
  uso=cvi(uso$)
  eco=cvi(eco$)
  pend=cvi(pend$)
  alti=cvi(alti$)
  expo=cvi(expo$)
  hidro=cvi(hidro$)
  urb=cvi(urb$)
  ua=cvi(ua$)
return
celomacho:
      'COMIENZA EL CELO DE LOS MACHOS
      'Reconocen hemnbras y van donde ellas
      'Luego se ve si hay peleas entre machos
'Reconocen hembras
hmasercana=0
dsthmasercana=mindist
for x=1 to huemules
  if huemul%(x,3)=1 and huemul%(x,4)>1 then
    mdaapa=int(rnd*100)+1
    if mdaapa<=PBapa then
      huemul%(w,7)=1
      dx= huemul%(h,1)-huemul%(x,1)
      dy= huemul%(h,2)-huemul%(x,2)
      dist=sqr(((huemul%(h,1)-huemul%(x,1))^2+((huemul%(h,2)-huemul%(x,2))^2)))
      if dist<dsthmasercana then
        hmasercana=x
        w=x
        dsthmasercana=dist
      end if
    end if
  end if
next x
if dsthmasercana<mindist then gosub visitahembra
return
'SUBROUTINA DE VISITA HEMBRAS
  'a: visita hembra
  'b: pelea con otros machos
  'c: aparemineto
visitahembra:
difx=huemul%(w,1)-huemul%(h,1)
dify=huemul%(w,2)-huemul%(h,2)
numpuntos=int(dsthmasercana)
nptos=numpuntos+1
for k=1 to nptos
  ncix=int((huemul%(h,1)+(difx/nptos)*k))
  nciy=int((huemul%(h,2)+(dify/nptos)*k))
  if ncix<=1 or nciy<=1 then goto otrak
cx=ncix
cy=nciy
gosub regist
if hidro>0 or urb>1 or ua>0 then huemul%(h,5)=1: gosub riesgos
otrak:
next k

```

```

        huemul%(h,1)=huemul%(w,1)
        huemul%(h,2)=huemul%(w,2)
'b. Machos pelean
  for t=1 to huemules
    if huemul%(t,3)=0 and huemul%(t,4)>2 and h><t and huemul%(h,1)=huemul%(t,1) and
huemul%(h,2)=huemul%(t,2) then
      mdapelea=int(rnd*10000)+1
      if mdapelea<=Pbmpelea then
        huemul%(h,3)=-1
        huemul%(h,5)=11
        write#7, repeti, ano, sem, huemul%(h,6), huemul%(h,1), huemul%(h,2),
huemul%(h,4), huemul%(h,5)
        goto muriopelea
      end if
    end if
  next t
  muriopelea:
'3 Apareamiento
if huemul%(h,3)=-1 or huemul%(h,3)=-2 then goto machomuerto
if huemul%(h,1)=huemul%(w,1) and huemul%(h,2)=huemul%(w,2) and huemul%(w,7)=1 then
  if huemul%(h,7)=1 then huemul%(h,7)=2
    if huemul%(h,7)=2 then huemul%(h,7)=3: huemul%(w,3)=2
  if huemul%(h,13)<4 then huemul%(w,8)=huemul%(h,8)
  if huemul%(w,9)=0 then
    huemul%(w,9)=codmadre
    codmadre=codmadre+1
  end if
end if
machomuerto:
return
'SUBROUTINA DE RIESGOS
riesgos:
if huemul%(h,5)=1 then
  huemul%(h,1)=ncix
  huemul%(h,2)=nciy
end if
if hidro=1 then 'rio
  mdario=int(rnd*10000)+1
  if mdario<=Pbmrio then
    huemul%(h,3)=-1
    huemul%(h,5)=3
  write#7, repeti, ano, sem, huemul%(h,6), huemul%(h,1), huemul%(h,2), huemul%(h,4),
huemul%(h,5)
  end if
end if
if hidro=2 then 'lago
  mdalago=int(rnd*10000)+1
  if mdalago<=Pbmlago then
    huemul%(h,3)=-1
    huemul%(h,5)=4
  write#7, repeti, ano, sem, huemul%(h,6), huemul%(h,1), huemul%(h,2), huemul%(h,4),
huemul%(h,5)
  end if
end if
if urb= 2 then 'pueblo
  mdapueblo=int(rnd*10000)+1
  if mdapueblo<=Pbmpueb then
    huemul%(h,3)=-1
    huemul%(h,5)=6
  write#7, repeti, ano, sem, huemul%(h,6), huemul%(h,1), huemul%(h,2), huemul%(h,4),
huemul%(h,5)
  end if
end if
if urb= 3 then 'aldea
  mdaalde=int(rnd*10000)+1
  if mdaalde<=Pbmalde then
    huemul%(h,3)=-1

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    huemul%(h,5)=7
write#7, repeti, ano, sem, huemul%(h,6), huemul%(h,1), huemul%(h,2), huemul%(h,4),
huemul%(h,5)
end if
end if
if urb=4 then 'pavimentado
mdapav=int(rnd*10000)+1
if mdapav<=Pbmpav then
    huemul%(h,3)=-1
    huemul%(h,5)=8
write#7, repeti, ano, sem, huemul%(h,6), huemul%(h,1), huemul%(h,2), huemul%(h,4),
huemul%(h,5)
end if
end if
if urb = 5 then 'nopavimentado
mdanopav=int(rnd*10000)+1
if mdanopav<=Pbmnopav then
    huemul%(h,3)=-1
    huemul%(h,5)=9
write#7, repeti, ano, sem, huemul%(h,6), huemul%(h,1), huemul%(h,2), huemul%(h,4),
huemul%(h,5)
end if
end if
if ua = 1 then 'ganado en pradera-matorral
mdaganado=int(rnd*10000)+1
if mdaganado<=Pbmua1 then
    huemul%(h,3)=-1
    huemul%(h,5)=10
write#7, repeti, ano, sem, huemul%(h,6), huemul%(h,1), huemul%(h,2), huemul%(h,4),
huemul%(h,5)
end if
end if
if ua = 2 then 'ganado en bosque
mdaganado=int(rnd*10000)+1
if mdaganado<=Pbmua2 then
    huemul%(h,3)=-1
    huemul%(h,5)=10
write#7, repeti, ano, sem, huemul%(h,6), huemul%(h,1), huemul%(h,2), huemul%(h,4),
huemul%(h,5)
end if
end if
return
'REGULADORES DE MOVIMIENTO
regulamov:
'Separa por
' adultos verano - adultos inviernos - juveniles - hembras preñadas - parición
'Adultos verano e invierno
if huemul%(h,3)=0 or huemul%(h,3)=1 and huemul%(h,4)>3 then
    mdainv=int(rnd*100)+1
    if mdainv>PBinv then gosub movverano
    if mdainv<=PBinv then gosub movinvierno
end if
'Juveniles
if huemul%(h,4)<=3 and huemul%(h,3)<=1 then gosub movjuvenil
'Hembra preñada y pariciones
if huemul%(h,3)=2 then
    mdapari=int(rnd*100)+1
    if mdapari>PBpatri then gosub movprenada
    if mdainv<=PBinv then gosub movparicion
end if
'MACHOS Y HEMBRAS ADULTOS VERANO
movverano:
if denh<=0 then dh=100
if denh>= 1 and denh <=4 then dh=50
if denh>5 then dh=10
gosub regist
if eco=0 then ecot=100
if eco=1 then ecot=50

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if pend=1 then pendi=100
if pend=2 then pendi=50
if pend=3 then pendi=10
if alti=1 then alt=100
if alti=2 then alt=50
if alti=3 then alt=10
if expo<=1 then ep=100
if expo=2 then ep=75
if hidro=0 then hid=100
if hidro=1 then hid=50
if hidro=2 then hid=50
if urb=0 then urba=100
if urb=2 then urba=10
if urb=3 then urba=20
if urb=4 then urba=15
if urb=5 then urba=30
if urb=6 then urba=50
if ua=0 then gand=100
if ua=1 then gand=20
if ua=2 then gand=10
pbajust=0.52
return
'MACHOS Y HEMBRAS ADULTOS INVIERNO
movinvierno:
  if denh=0 then dh=100
  if denh>= 1 and denh <=4 then dh=75
  if denh>5 then dh=50
gosub regist
  if eco=0 then ecot=50
  if eco=1 then ecot=100
  if pend=1 then pendi=100
  if pend=2 then pendi=50
  if pend=3 then pendi=10
  if alti=1 then alt=100
  if alti=2 then alt=50
  if alti=3 then alt=10
  if expo<=1 then ep=100
  if expo=2 then ep=25
  if hidro=0 then hid=100
  if hidro=1 then hid=50
  if hidro=2 then hid=50
  if urb=0 then urba=100
  if urb=2 then urba=10
  if urb=3 then urba=20
  if urb=4 then urba=15
  if urb=5 then urba=30
  if urb=6 then urba=50
  if ua=0 then gand=100
  if ua=1 then gand=30
  if ua=2 then gand=15
  pbajust=0.58
return
'JUVENILES
movjuvenil:
  if denh=0 then dh=100
  if denh>= 1 and denh <=4 then dh=75
  if denh>5 then dh=75
gosub regist
  if eco=0 then ecot=100
  if eco=1 then ecot=50
  if pend=1 then pendi=100
  if pend=2 then pendi=75
  if pend=3 then pendi=50
  if alti=1 then alt=100
  if alti=2 then alt=75
  if alti=3 then alt=50
  if expo<=1 then ep=100
  if expo=2 then ep=75

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if hidro=0 then hid=100
if hidro=1 then hid=50
if hidro=2 then hid=50
if urb=0 then urba=100
if urb=2 then urba=10
if urb=3 then urba=20
if urb=4 then urba=15
if urb=5 then urba=30
if urb=6 then urba=50
if ua=0 then gand=100
if ua=1 then gand=30
if ua=2 then gand=15
pbajust=0.61
return
'HEMBRA PREYADA
movprenada:
  if denh=0 then dh=100
  if denh>= 1 and denh <=4 then dh=50
  if denh>3 then dh=10
gosub regist
  if eco=0 then ecot=50
  if eco=1 then ecot=100
  if pend=1 then pendi=25
  if pend=2 then pendi=75
  if pend=3 then pendi=100
  if alti=1 then alt=100
  if alti=2 then alt=75
  if alti=3 then alt=50
  if expo<=1 then ep=100
  if expo=2 then ep=50
  if hidro=0 then hid=100
  if hidro=1 then hid=50
  if hidro=2 then hid=50
  if urb=0 then urba=100
  if urb=2 then urba=5
  if urb=3 then urba=5
  if urb=4 then urba=10
  if urb=5 then urba=15
  if urb=6 then urba=25
  if ua=0 then gand=100
  if ua=1 then gand=10
  if ua=2 then gand=5
  pbajust=0.53
return
'PARICION
movparicion:
  if denh=0 then dh=100
  if denh>= 1 and denh <=4 then dh=25
  if denh>4 then dh=1
gosub regist
  if eco=0 then ecot=25
  if eco=1 then ecot=100
  if pend=1 then pendi=10
  if pend=2 then pendi=75
  if pend=3 then pendi=100
  if alti=1 then alt=75
  if alti=2 then alt=100
  if alti=3 then alt=50
  if expo<=1 then ep=100
  if expo=2 then ep=50
  if hidro=0 then hid=100
  if hidro=1 then hid=25
  if hidro=2 then hid=25
  if urb=0 then urba=100
  if urb=2 then urba=1
  if urb=3 then urba=1
  if urb=4 then urba=1
  if urb=5 then urba=5

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    if urb=6 then urba=5
    if ua=0 then gand=100
    if ua=1 then gand=5
    if ua=2 then gand=2
    pbajust=0.47
return
'          NATAACION
natacion:
  nada=0
  otronado:
  nada=nada+1
    nadamovx=int(rnd*5)+1
    nadamovy=int(rnd*5)+1
    aguax=futx+nadamovx
    aguay=futy+nadamovy
  cx=int(aguax)
  cy=int(aguay)
  if cx<=1 or cy<=1 then goto pasarnado:
  gosub regist
  if hidro>0 and nada<10 then
    futx=int(aguax)
    futy=int(aguay)
    goto otronado
  end if
  if hidro>0 and nada>=10 then
    huemul%(h,3)=-1
    huemul%(h,5)=14
write#7, repeti, ano, sem, huemul%(h,6), huemul%(h,1), huemul%(h,2), huemul%(h,4),
huemul%(h,5)
  end if
  futx=int(aguax)
  futy=int(aguay)
pasarnado:
return
'REDIMENSIONA MATRIZ DE HUEMULES
redimensiona:
nacimientos=0
muertes=0
mbebe=0
emig=0
inmi=0
'causas de muerte
edad=0
rio=0
lago=0
ciudad=0
pueblo=0
aldea=0
pav=0
nopav=0
ganado=0
peleas=0
mmadre=0
emi=0
mnado=0
for mm=1 to huemules
  if huemul%(mm,5)= 2 then edad=edad+1
  if huemul%(mm,5)= 3 then rio=rio+1
  if huemul%(mm,5)= 4 then lago=lago+1
  if huemul%(mm,5)= 5 then ciudad=ciudad+1
  if huemul%(mm,5)= 6 then pueblo=pueblo+1
  if huemul%(mm,5)= 7 then aldea=aldea+1
  if huemul%(mm,5)= 8 then pav=pav+1
  if huemul%(mm,5)= 9 then nopav=nopav+1
  if huemul%(mm,5)= 10 then ganado=ganado+1
  if huemul%(mm,5)= 11 then peleas=peleas+1
  if huemul%(mm,5)= 12 then mmadre=mmadre+1
  if huemul%(mm,5)= 13 then margen=margen+1

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    if huemul%(mm,5)= 14 then mnado=mnado+1
next mm
for uu=1 to huemules
if huemul%(uu,3)= 2 then nacimientos = nacimientos + 1
if huemul%(uu,3)=-1 then muertes = muertes + 1
if huemul%(uu,3)=-1 and huemul%(uu,4)=1 then mbebe = mbebe + 1
if huemul%(uu,3)=-2 then emi=emi+1
inmi=emi
next uu
'DEMOGRAFIA
manjv=0
womjv=0
manad=0
womad=0
baby=0
jv=0
ad=0
tothuem=0
for h=1 to huemules
    if huemul%(h,3)=-1 or huemul%(h,3)=-2 then goto nodemo
        if huemul%(h,3)=0 and huemul%(h,4)=2 then manjv=manjv+1
        if huemul%(h,3)>=1 and huemul%(h,4)=2 then womjv=womjv+1
        if huemul%(h,3)=0 and huemul%(h,4)>=3 then manad=manad+1
        if huemul%(h,3)>=1 and huemul%(h,4)>=3 then womad=womad+1
        if huemul%(h,4)=1 then baby=baby+1
    nodemo:
next h
jv=manjv+womjv
ad=manad+womad
tothuem=baby+jv+ad
write#6, repeti, ano, huemules, tothuem, jv, ad, baby, manjv, womjv, manad, womad,
nacimientos, muertes, emi, inmi, mbebe, edad, rio, lago, ciudad, pueblo, aldea, pav,
nopav, ganado, peleas, mnadre, mnado
canthuemules=huemules+nacimientos-muertes-emi+inmi
if canthuemules>1950 goto hacerozrarep
cuentahuem=0
for gg=1 to huemules
    if huemul%(gg,3)=-1 then goto siguegg
    if huemul%(gg,3)=-2 then goto inmigracion
    cuentahuem=cuentahuem+1
    for atr=1 to 15
        htempo%(cuentahuem,atr)=huemul%(gg,atr)
        if atr=4 then htempo%(cuentahuem,atr)=htempo%(cuentahuem,atr)+1
        if atr=7 then htempo%(cuentahuem,atr)=0
        if atr=15 then htempo%(cuentahuem,atr)=0
    next atr
    if huemul%(gg,3)=2 then
        htempo%(cuentahuem,3)=1
        cuentahuem=cuentahuem+1
        htempo%(cuentahuem,1)=huemul%(gg,1)
        htempo%(cuentahuem,2)=huemul%(gg,2)
        htempo%(cuentahuem,3)=int(rnd*2)
        htempo%(cuentahuem,4)=1
        htempo%(cuentahuem,6)=codigo
        codigo=codigo+1
    if htempo%(cuentahuem,3)=1 then htempo%(cuentahuem,8)=huemul%(gg,8) 'cod hijo de la
madre
        htempo%(cuentahuem,10)=huemul%(gg,9) 'cod hijo de la madre
    end if
inmigracion:
if huemul%(gg,3)=-2 then
    cuentahuem=cuentahuem+1
    mdapos=int(rnd*279)+1
    htempo%(cuentahuem,1)=pbinmi%(mdapos,1)-2
    htempo%(cuentahuem,2)=pbinmi%(mdapos,2)
    circle(20+htempo%(cuentahuem,2), 300-htempo%(cuentahuem,1)),5,7
    htempo%(cuentahuem,3)=int(rnd*3)
    htempo%(cuentahuem,4)=int(rnd*8)+2

```

```

        htempo%(cuentahuem,6)=codigo+2000
        codigo=codigo+1
        htempo%(cuentahuem,11)=htempo%(cuentahuem,1)*10
        htempo%(cuentahuem,12)=htempo%(cuentahuem,2)*10
    end if
    siguegg:
next gg
'canthuemules=huemules+nacimientos-muertes-emi+inmi
hacerotrarep:
if canthuemules<=1 then
    erase huemul%
    faltanan=(55-ano)
    for escribir=1 to faltanan
        sigano=ano+escribir
        write#6, repeti, sigano, 1, tothuem, jv, ad, baby, manjv, womjv, manad, womad,
nacimientos, muertes, emi, inmi, mbebe, edad, rio, lago, ciudad, pueblo, aldea, pav,
nopav, ganado, peleas, mmadre, mnado
    next escribir
    goto otrarep
end if
if canthuemules>=1950 then
    erase huemul%
    faltanan=(55-ano)
    for escribir=1 to faltanan
        sigano=ano+escribir
        write#6, repeti, sigano, 2000, tothuem, jv, ad, baby, manjv, womjv, manad, womad,
nacimientos, muertes, emi, inmi, mbebe, edad, rio, lago, ciudad, pueblo, aldea, pav,
nopav, ganado, peleas, mmadre, mnado
    next escribir
    goto otrarep
end if
erase huemul%
huemules=canthuemules
dim huemul%(huemules,15)
for gg=1 to huemules
    for atr=1 to 15
        huemul%(gg,atr)=htempo%(gg,atr)
    next atr
next gg
for vh=1 to 2000
for art=1 to 15
htempo%(vh,art)=0
next art
next vh
return

```