

**Examining the possible effect of forest area,
abundance of snakes and snake species
richness on the abundance of short-toed eagle,
in Spain.**

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by

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Abstract

It is a well known fact that short-toed eagle preys on snakes and nests on trees. However, it is unknown how forest area, abundances of different snake species and snake species richness affect the abundance of short-toed eagle. Therefore, path analysis, a method that estimates direct and indirect effects using multiple regression equations, was used to identify and measure the presumed causal relationships that have support on the observed data. The presumed causal relationships were established based on knowledge about natural history, functional hypothesis, professional experience and expert's intuition. Data about abundance of snakes and short-toed eagles are un-existent. Therefore, relative abundances of snakes and short-toed eagles, estimated based on occurrence data, were used as indirect estimations of abundance.

The results revealed that the relative abundances of *Malpolon monspesulanus*, *Rhinechis scalaris*, *Hemorrhhis hippocrepis* and *Natrix natrix* may not have a significant direct effect on the relative abundance of short-toed eagle. Besides, snake species richness does not seem to influence directly the relative abundance of the eagle. Apparently, snake species richness may affect directly only the relative total abundance of snakes, which it seems to affect, directly, the relative abundance of the eagle. Moreover, forest area also seems to affect, directly, the relative abundance of short-toed eagle.

Path analysis does not prove or disprove causality. Thereby, a replication of the present research, using data from other countries, could increase the level of certainty that the direct and indirect effects identified and measure in the present thesis may represent causal relationships. Besides, new theories should be tested.

Key words: Short-toed eagle, *Circaetus gallicus*, snake species richness, snakes, forests, kernel density, path analysis.

Resumen

Es un hecho conocido que el águila culebrera se alimenta de culebras y anida en árboles. Sin embargo, no se conoce como el área de bosques, abundancias de diferentes especies de culebras y la riqueza de especies de culebras afecta la abundancia del águila culebrera. Por lo tanto, un método que estima efectos directos e indirectos usando ecuaciones de regresión múltiple, fue usado para identificar y medir las posibles relaciones causales que tiene soporte en los datos observados. Las posibles relaciones causales fueron establecidas en base a conocimiento de historia natural, hipótesis funcionales, experiencia profesional e intuición de expertos. No existen datos acerca de la abundancia de culebras y águilas culebreras. En consecuencia, abundancias relativas de culebras y águilas culebreras, estimadas en base a observaciones, fueron usadas como mediciones indirectas de abundancia.

Los resultados revelaron que las abundancias relativas de *Malpolon monspesulanus*, *Rhinechis scalaris*, *Hemorrhoids hippocrepis* y *Natrix natrix* posiblemente no tienen un efecto directo significativo sobre la abundancia relativa del águila culebrera. Además, la riqueza de especies de culebras no parece influenciar directamente la abundancia del águila. Aparentemente, la abundancia de especies de culebras podría afectar directamente solo la abundancia relativa total de culebras, la cual parece afectar directamente la abundancia relativa del águila. Además, el área de bosques también parece afectar directamente la abundancia relativa del águila culebrera.

Análisis de trayectoria no prueba ni niega causalidad. Por lo tanto, una replica del la presente investigación, usando datos de otros países, podría incrementar el nivel de certidumbre de que los efectos directos e indirectos identificados y medidos en la presente tesis pueden representar relaciones causales. Además, nuevas teorías deberían ser evaluadas.

Palabras clave: Águila culebrera, *Circaetus gallicus*, riqueza de especies de culebras, culebras, bosques, kernel, análisis de trayectoria.

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“Search through me, O God, and know my heart. Examine me, and know my disquieting thoughts, and see whether is in me any painful way, and lead in the way of time indefinite” (Psalms 139: 23-24). “ ... , and the appointed time ... to give reward to ... those fearing your name, the small and the great...” (Revelation 11:18). As worshiper of the creator of the heavens and the Earth, and all the wonderful things that human beings enjoy on Earth, I thank him for the merciful way he protects me and my family: “For this is what Jehovah of armies has said ... for he that is touching you is touching my eyeball” (Zechariah 2: 7).

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Glossary

Autoecology: “The part of ecology that deals with individual species and their reactions to environmental factors” (*Unesco-Unep* 1983).

Chi-square: “A measure of the discrepancy existing between the observed and expected variance-covariance matrices” (Gnanadesikan, 1997).

Coefficient of determination: “Is the percentage of variance in one variable that is accounted for by the variance in the other variable” (Salkind, 2004).

Correlation coefficient: “Reflects the amount of variability that is shared between two variables and what they have in common” (Salkind, 2004).

Covariance: “Is a measure of how much two variables change together” (Gravetter and Wallnau, 2009).

Critical ratio (CR): “Is computed dividing the regression weight by its standard error. It indicates how many standard errors above or below zero the regression weight is” (Arbuckle, 2007).

Foraging: “Is a cyclical activity in which a behavioural acts lead to the final consumption of each unit of food” (Fox et al. 2001).

Goodness of fit of a model: “A measure of the agreement between observed and expected variance-covariance matrices. The expected variance-covariance matrix is determined by a theoretical model” (Cramer and Howitt, 2004).

Home range: “Is defined as the area an individual animal uses during its normal activities, such as obtaining food, gaining access to mates, and raising young” (Martin and Handasyde, 1999).

Interspecific competition: “Is an interaction in which species inhibit each other such that increased abundance of one species leads to lower growth rates of the other species. Interspecific competition is a major force determining species abundances” (May and McLean, 2007).

Kernel density estimation: “Is a non-parametric technique for density estimation in which a known density function (the kernel) is averaged across the observed data points to create a smooth approximation” (Fotheringham et al. 2000).

Kurtosis: “The sharpness of a peak on a curve of a probability density function” (Cramer and Howitt, 2004).

Model: “A model can be defined as a representation of reality that attempts to explain the behaviour of some aspect of it” (Miller and Starr, 1969).

Multicollinearity: “is a high level of correlation within the set of explanatory variables... that affects the independence of explanatory variables, and the precision of regression coefficient estimates, as well” (Cramer and Howitt, 2004).

Natural history: “Is the science which treats of the earth and all natural objects upon its surface and within its crust” (Tenney, 1866).

Outlier: “Is an observation that deviates so much from other observations as to arouse suspicion that it was generated by a different mechanism” (Cramer and Howitt, 2004).

Path analysis: “An analysis in which three or more variables are ordered by the researcher in terms of their presumed causal relationships” (Cramer and Howitt, 2004).

Path coefficient: “Path coefficients represent the direct effects of one variable on another in the path model” (Cramer and Howitt, 2004). “Path coefficients are standardized regression coefficients” (Bryman and Cramer, 2003).

Path diagram: “Shows the presumed causal relationships between three or more variables... The causal relationships between the variables are shown on the diagrams by arrows” (Cramer and Howitt, 2004).

Path model: “Refers to a causal model in which the relationships between the variables have been represented by magnitudes of effects along paths connecting the variables in the model” (Cramer and Howitt, 2004).

Regression coefficient: “Is the coefficient of any regressor in a regression equation” (Cramer and Howitt, 2004).

Regurgitated pellet: “All indigestible materials are compacted in the stomach, of many birds of prey, into a pellet, which is regurgitated”(Peeters and Peeters, 1997).

Significance level: “The significance level α of the test of a statistical hypothesis H_0 is the probability of rejecting H_0 when it is true” (Cramer and Howitt, 2004) In path analysis the significance level (P) indicates the probability that the critical ratio is different from zero (Arbuckle, 2007).

Skewness: “A form of asymmetry in a unimodal frequency d distribution. The distribution is positively skewed more than 50% of elements lie below

the mean, and negatively skewed when more than 50% of elements lie above the mean” (Cramer and Howitt, 2004).

Spatial autocorrelation: “Describes how an attribute is distributed over space – to what extent the value of the attribute in one zone depends on the values of the attribute in neighbouring zones”(Fotheringham et al. 2000).

Species richness: “Is the diversity of species within an ecological community” (Dyke, 2008).

Squared multiple correlation: “Measures the proportion of the observed total variability in an specific response that is accounted for by its regression on the remaining responses, and hence provides a measure of common or shared variance” (Gnanadesikan, 1997).

Standard error of a parameter: “Measures how sensitive the estimate of the parameter is to changes in a few observations in the sample” (Schroeder et al. 1986).

Structural Equation Modelling: “Is a confirmatory, multivariate technique that looks at causal relationships between variables in a diagrammatic form” (Foster et al. 2006).

Variance: “Is the average squared distance from the mean” (Gravetter and Wallnau, 2009).

Variance-covariance matrix: “Is made up of variance terms on the diagonal and covariance terms on the off-diagonal” (Schumacker and Lomax, 1996).

1. Introduction:

Short-toed eagle (*Circaetus gallicus*) has a wide distribution in southern and central Europe (Martinûa and Katzirûb, 1999). However, since the 19th century its populations have been declining in several European regions. There is not a unique explanation about the possible causes of its decline (Gil and Pleguezuelos, 2001). Nowadays it is considered a rare species in many European countries (Barbaro et al. 2003, Birdlife International, 2004, Sacchia et al. 2004, Valevski, 2008, Berezovikov et al. 2009). The low reproductive rate and high diet specialization make short-toed eagle vulnerable to extinction (Morbioli, 2001).

Considering that snakes are the main preys of short-toed eagle, any change in the populations of snakes could affect the population of the eagle. In Europe, many snake species have specialized requirements of habitat and food, which make them vulnerable (Filippi and Luiselli, 1999, O'shea, 2005, Edgar and Bird, 2005, Santos et al. 2008). Several snake species are threatened by extinction (Ujvari et al. 2002, Edgar and Bird, 2005, O'shea, 2005, Santos et al. 2008), and 19 to 27 snake species require active management for their conservation, mainly as a consequence of land use change (Greene, 2000, Santos et al. 2008). Climate change could worsen that situation (O'shea, 2005, Santos et al. 2008). In Spain, snake species are not only threatened by land use change, but also by excessive use of pesticides and introduction of exotic species (Marquez and Lizana, 2007). As a consequence, in the last decade, several snake species have experienced a retreat in their distribution (Mañosa, 2003, Marquez and Lizana, 2007, Pleguezuelos et al. 2007, Santos et al. 2008).

The decrease in the population of snakes is not the only factor that could affect the abundance of short-toed eagle. Considering that short-toed eagle nests on forests, (Sanchez-Zapata and Calvo, 1999) changes in forest area could also affect its population. Europe has experienced a long and continuous process of deforestation (Goudie, 2006). During the last century many European countries have made considerable efforts to stop it (Palo and Vanhanen, 2000). However, deforestation is still one of the main environmental problems of many European countries (Schnabel, 2001), included Spain (Geeson et al. 2002, Borzel, 2003).

1.1. Autoecology of short-toed eagle in Spain:

Short-toed eagle is a temporal inhabitant of Spain, where it breeds. In winter it migrates, through the Strait of Gibraltar, to the savannah, in the south of the Sahara desert (Bildstein, 2006, Agostini and Mellone, 2008). During migration it displays a passive flight taking advantage of thermals (Agostini et al. 2002). When it comes back to Spain, since March to April, it tends to occupy the same territories (Ontiveros, 2005), mainly areas with patches of forests where it nests (Sanchez-Zapata and Calvo, 1999). Around May and June the female incubates, for 40 days, a unique egg. Sixty to eighty days later the small eagle leaves the nest. It reaches the adulthood after 4 years. It can live 17 years in freedom. (Cramp and Simmons, 1980, Darawshi, 2007).

Short-toed eagle has short toes and a pointed heel (Breuil et al. 1998), which explains its specialized diet (Breuil et al. 1998, Morbioli, 2001). At least 80% of its diet is composed by snakes, reason why it is called Snake-eagle (Bernard, 2003, Malafosse, 2009). The rest of its diet is composed by small birds, rodents, squirrels, insects and hedgehogs (Forschler, 2000, Malafosse, 2009). There is scientific evidence that short-toed eagle has some immunity to snake poison (Darawshi, 2007). On top of that, the assemblage of feathers provides it an extra protection. The eagle localizes its preys from air (Ontiveros, 2005). Small preys are eaten on flight. Big snakes are killed and eaten on the floor (Breuil et al. 1998).



Figure 1 - 1: Short-toed eagle on flight.



Figure 1 - 2: Short-toed eagle eating.

Image source: <http://short-toed-eagle.net/>

1.2. Snake species of Spain:

Spain has 13 snake species. Ten of them pertain to the family Colubridae, and three to the family Viperidae (See TABLE 1-1) (Galan, 2004, Ontiveros, 2005, Pleguezuelos, 2005, Brito, 2006, Martinez-Freira, 2009).

TABLE 1 - 1: Snake species of Spain.

Family	Scientific name
Colubridae	<i>Hemorrhois hippocrepis</i>
	<i>Hierophis viridiflavus</i>
	<i>Coronella austriaca</i>
	<i>Coronella girondica</i>
	<i>Macroprotodon brevis</i>
	<i>Zamenis longissimus</i>
	<i>Rhinechis scalaris</i>
	<i>Malpolon monspesulanus</i>
	<i>Natrix maura</i>
	<i>Natrix natrix</i>
Viperidae	<i>Vipera aspis</i>
	<i>Vipera latastei</i>
	<i>Vipera seoanei</i>

Pictures of the 13 snake species are included in Appendix 7.3.

1.3. Research problem:

The distribution of specialist feeders is expected to coincide with the distribution of their preys (Newton, 1998). However, it is not clear how snake species richness and abundances of different snake species affect the abundance of short-toed eagle (Moreno-Rueda and Pizarro, 2007). Moreno-Rueda and Pizarro (2007) found that snake species richness had a contribution predicting the probability of occurrence of short-toed eagle, in south-eastern Spain. The authors mentioned two possible explanations for this result. Firstly, it could be that each short-toed eagle specializes on different preys; thereby, more snake species would attract more individuals (See figure 1-3, arrow 1). Secondly, snake species richness could be directly related to the total abundance of snakes (Moreno-Rueda and Pizarro, 2007), which could have an

effect on the abundance of the eagle (Vlachos and Papageorgiou, 1994, Ontiveros, 2005, Moreno-Rueda and Pizarro, 2007) (See figure 1-3, arrows 2 and 3).

Gil and Plaguezuelos (2001) found that in south-eastern Spain the snake species *Malpolon monspesulanus*, *Rhinechis scalaris*, and *Hemorrhois hippocrepis* constituted the main preys of short-toed eagle (See Figure 1-3, arrows 4, 5 and 6). However, in other areas a different snake species is reported to be its main prey. It is reported that in Dardia forest (north-eastern Greece), the snake *Natrix natrix* is the favourite prey of short-toed eagle (Bakaloudis et al. 1998). In Landes de Gascogne forests (south-western France), the main prey of short-toed eagle is *N. natrix* (Barbaro et al. 2003). Also, in eastern Slovakia, *N. natrix* is reported to be one of the main preys of short-toed eagle (Danko et al. 2007). Therefore, it is possible that *N. natrix* is an important prey of short-toed eagle in Spain (See figure 1-3, arrow 7). It is also possible that the combination of the abundance of the 'main preys' together affect the abundance of the eagle.

M. monspesulanus is an ophiophagous snake, which indicates that it preys on other snakes (Pleguezuelos, 2009, Feriche, 2004, Santos et al. 2008). Pianka (2000) thinks that when a predator preys on dominant species, it reduces the competition allowing the presence of more species. Thereby, it is likely that the abundance of *M. monspesulanus* affects snake species richness (See Figure 1-3, arrow 8), which as stated before, could affect the abundance of the eagle.

The abundance of snakes is not the only factor that could affect the abundance of short-toed eagle. The eagle needs forests for nesting. In consequence, forest area could also affect the abundance of the short-toed eagle (Sanchez-Zapata and Calvo, 1999) (See Figure 1-3, arrow 12). Moreover, forests could be important for snakes as well. Many snake species depend directly on forests either as refuge or source of food (Galan, 2004, Pleguezuelos, 2005, Brito, 2006, Martinez-Freira, 2009). Thereby, forest area could have a direct effect on snake species richness and total abundance of snakes (See Figure 1-3, arrows 10 and 11), which could affect, as mentioned before, the abundance of short-toed eagle.

Data about the abundance of snake species and short-toed eagles in Spain are un-existent. Thereby, relative abundances based on occurrence data were used. The most appropriate way to represent the possible influence of forest area, relative abundance of snakes and snake species richness on the relative abundance of short-toed eagle is through an influence diagram (See Figure 1-3). This diagram is meant to understand the broad structure of a system (Pidd, 1996).

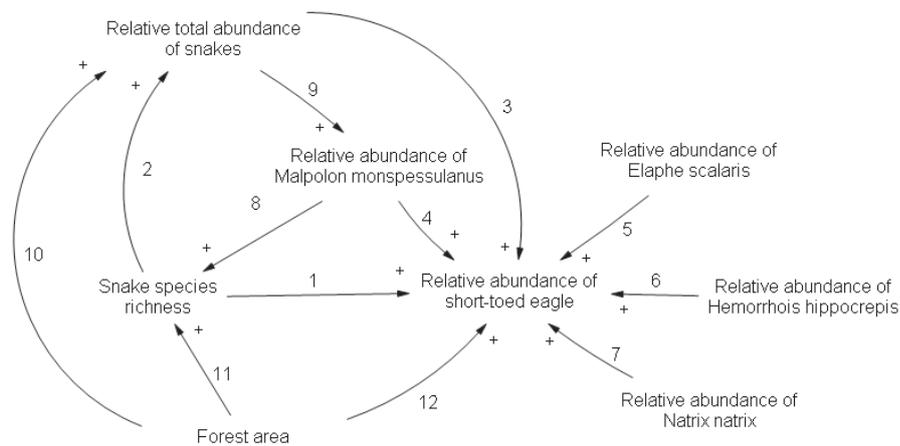


Figure 1 - 3: Influence diagram of the possible direct and indirect effects of forest area, relative abundance of snakes and snake species richness on the relative abundance of short-toed eagle.

Legend: + Positive correlation.

In order to examine how forest area, relative abundance of snakes and snake species richness affect the relative abundance of short-toed eagles it is necessary to incorporate all the possible effects into a formal and well-structured explanatory model (Pidd, 1996). Explanatory models are based on theory, and their function is to understand underlying mechanisms and processes (DeVries et al. 1998, Skitmore and Marson, 1999, Lucertini et al. 2004). The prior knowledge incorporated into explanatory models enhances their stability and the interpretability of results (Leeuw, 1986, Skitmore and Marson, 1999). Path analysis is a very useful explanatory method to model presumed causal relationships among independent and dependent variables. On top of that, it allows some variables to be dependent making it possible to identify and measure not only possible direct effects but also possible indirect effects (Keane, 1993, Raykov and Marcoulides, 2000). Therefore, path analysis can contribute to analyze the way in which forest area, relative abundance of snakes and snake species richness could affect the relative abundance of short-toed eagle. In path analysis, the influence diagram of Figure 1-3 is called path diagram.

1.4. Research objectives:

1.4.1. General objective:

Examine the possible influence of forest area, relative abundance of snakes and snake species richness on the relative abundance of short-toed eagle (See Figure 1-3).

1.4.2. Specific objectives:

- Examine the possibility that snake species richness affect, directly or indirectly, the relative abundance of short-toed eagle.
- Examine the possibility that the relative total abundance of snakes affect, directly or indirectly, the relative abundance of short-toed eagle.
- Examine the possibility that the relative abundance of the ‘main preys’ of short-toed eagle (*Malpolon monspesulanus*, *Rhinechis scalaris*, and *Hemorrhhis hippocrepis*) affect the relative abundance of short-toed eagle.
- Examine the possibility that the relative abundance of *Natrix natrix* affect, directly, the relative abundance of short-toed eagle.
- Examine the possibility that forest area affect, directly or indirectly, the relative abundance of short-toed eagle.

1.5. Research questions:

- Has snake species richness any direct or indirect effect on the relative abundance of short-toed eagle?
- Has the relative total abundance of snakes any direct or indirect effect on the relative abundance of short-toed eagle?
- Has the relative abundance of the ‘main preys’ of short-toed eagle (*Malpolon monspesulanus*, *Rhinechis scalaris*, and *Hemorrhhis hippocrepis*) any direct or indirect effect on the relative abundance of short-toed eagle?

- Has the relative abundance of *Natrix natrix* a direct effect on the relative abundance of short-toed eagle?
- Has forest area any direct or indirect effect on the relative abundance of short-toed eagle?

1.6. Research hypothesis:

1.6.1. Hypothesis 1.

H0 = Snake species richness has not any direct or indirect effect on the relative abundance of short-toed eagle.

1.6.2. Hypothesis 2.

H0 = The relative total abundance of snakes has not any direct or indirect effect on the relative abundance of short-toed eagle.

1.6.3. Hypothesis 3.

H0 = The relative abundances of the 'main preys' of short-toed eagle (*Malpolon monspesulanus*, *Rhinechis scalaris*, and *Hemorrhois hippocrepis*) have no effect on the relative abundance of short-toed eagle.

1.6.4. Hypothesis 4.

H0= The relative abundance of *Natrix natrix* has no direct effect on the relative abundance of short-toed eagle.

1.6.5. Hypothesis 5.

H0= Forest area has not any direct or indirect effect on the relative abundance of short-toed eagle.

1.7. Research outputs:

- Discussion about the conflicts or agreements between the theories used to develop the hypothesis, and the results.
- Ecological interpretation of the proposed effects that, according to the results, could affect significantly the relative abundance of short-toed eagle.
- Recommendations of specific studies that should be carried out to increase the existent knowledge about the factors that affect the abundance of short-toed eagle.

2. Materials and methods:

2.1. Study area:

The study area was Spain. The country has a total area of 499,542 km² (Dobson, 2006). Spain was selected due to the apparent stable population of short-toed eagle in that country (Gil and Pleguezuelos, 2001, Sacchia et al. 2004), and the large and recent occurrence data of short-toed eagles and snakes that the Spanish Ministry of Environment has collected (*Inventario Nacional de Biodiversidad 2007*, Perez-Mellado and Cortazar, 2007). The mentioned occurrence data and the spatial information of Spanish forests available in Corine 2000 (*Corine Land Cover 2009*) could contribute to analyze the possible influence of forest area, relative abundance of snakes and snake species richness on the relative abundance of short-toed eagle.

2.2. Data description:

In the first trimester of 2000, the Ministry of Environment of Spain (MMA) began collecting occurrence data from recent provincial inventories and biodiversity projects, in order to create the inventory of reptiles of Spain. However, for 3711 cells (10 x 10 km) of the country there was no data. By April of 2002 the MMA had finished sampling the mentioned cells (Perez-Mellado and Cortazar, 2007). Besides, with the purpose of creating an inventory of breeding birds of the country, occurrence data of short-toed eagles, for the whole country, were collected during 5 years of field work organized by MMA, from 1998 to 2002. All habitats of each cell (10 x 10 km) were sampled. Breeding season was taken into account to decide the dates when each cell had to be visited (*Inventario Nacional de biodiversidad 2007*). The occurrence data for short-toed eagle and the 13 snake species present in Spain are accessible online on the website of the Global Biodiversity Information Facility Network: <http://data.gbif.org>, with an accuracy of 7,000m.

Spatial information of Spanish forests is available, in raster format, in Corine 2000. This product was generated by the European Environment Agency using satellite data, aerial photography, topographic maps, medium-scale thematic maps and statistical information of land cover. The spatial resolution of the product is 100 x 100m. Corine Land Cover 2000 and a detailed description of the methodology used

to generate the product are accessible on the website of the European Environment Agency: <http://dataservice.eea.europa.eu> (*Corine land cover 2009*).

2.3. Software requirements:

Several software packages were used for the preparation and analysis of the data:

TABLE 2 - 1: Software used in the present thesis.

Software	Description
ArcGIS	Desktop: GIS software
SPSS	Statistical software
Amos (Student version)	Software for path analysis
Excel	Calculation sheets

2.4. Field work:

Path diagrams are constructed based on the available knowledge about natural history, functional hypothesis, professional experience and expert's intuition (Carrascal, 2001). Thereby, the main activity during fieldwork was to discuss the proposed effects of Figure 1-3 with experts in short-toed eagle and herpetologists, in order to incorporate new possible effects based on their professional experience and intuition. Besides, it was fundamental to get a rapid view of the habitats in which short-toed eagle forages and nests, before starting the modelling work.

2.5. Research workflow:

Path analysis is a powerful tool to analyze presumed causal relationships. However, as all statistical methods, its power depends on the fulfilment of assumptions. Therefore, a sequence of steps was necessary to be certain that the data fitted the conditions of the method. Firstly, the occurrence data were transformed, using kernel density estimator, into relative abundances, forest area was calculated based on Corine 2000, and snake species richness was created adding up snake species presences. Secondly, a linearity test was performed for each pair of variables involved in proposed direct effects and, when necessary, transformations were done. Thirdly, the possible presence of outliers was analyzed. Fourthly, a spatial

autocorrelation index was computed and tested for significance. Fifthly, a normality assessment was carried out to check the distribution of the data. Sixthly, a multicollinearity test was carried out. Finally, the possible direct and indirect effects were incorporated into a model, which was tested and assessed.

2.6. Occurrence density estimation:

Kernel density estimator was used to estimate the relative abundances of snakes and short-toed eagles. The relative abundances of snakes and short-toed eagles were created using occurrence data, under the assumption that as the abundance of a species increases, the amount of occurrences of that species increases as well. The relative abundance (%) of the thirteen snake species, estimated using kernel density, are presented in Appendix 7.4. The relative total abundance of snakes was created summing up the relative abundances of the thirteen snake species of Spain. A spatial resolution of 10 x 10km was used as output for all density estimations.

Occurrence data do not reveal the fact that the intensity of occurrence of any species varies gradually in the borders of its distribution (Bowman and Azzalini, 1997). In other words, they do not reflect the true distribution of a population (Cerrito, 2007). Kernel density estimator is a non-parametric method with powerful capabilities to estimate the true probable distribution, even with noisy data (Fischer et al. 2001, Elith et al. 2006). Kernel density estimator is widely used to estimate the relative abundance of a species using occurrence data (Schenone et al. 2004, Tellmann et al. 2008, Mendes et al. 2009).

Kernel density estimator fits a curved surface around each known location, to interpolate its whole neighbourhood, established by the bandwidth. Thereby, the interpolated values are lower than the center cell, and decrease with the distance. Each time a kernel is fitted, it moves until the whole study area has been interpolated (See Figure 2-1). The new value of each location is estimated summing up all the kernel surfaces that overlay it (See Figure 2-2) (Silverman, 1986, Fischer et al. 2001, Cerrito, 2007). The way in which kernel density (f) is estimated is described below:

$$f(x) = \frac{1}{nh} \sum_{i=1}^n K\left(\frac{x - x_i}{h}\right)$$

Where, h is the bandwidth and K is the kernel function (Gaussian).

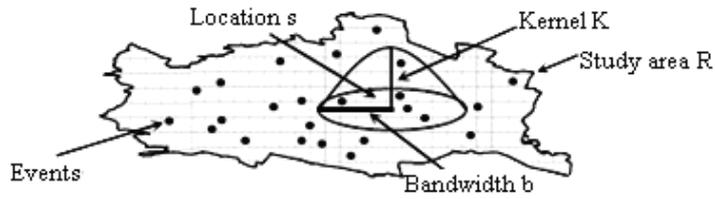


Figure 2 - 1: Kernel density interpolation (Fischer et al. 2001).

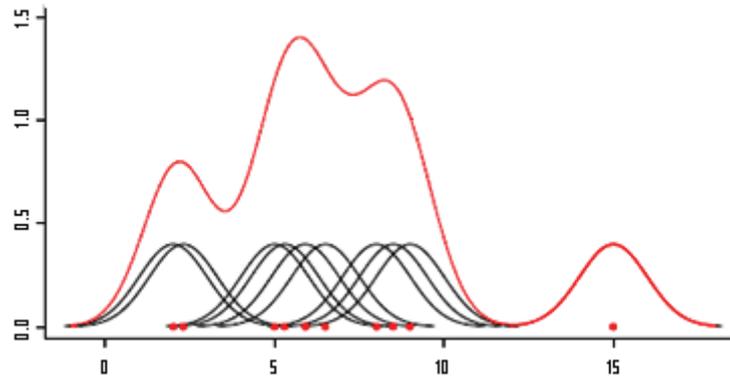


Figure 2 - 2: Kernel density estimation (Fischer et al. 2001).

As stated above, the bandwidth is a scaling factor that determines the size of the neighbourhood that influences each site; thereby, controlling the smoothness of the density estimate (Gerard and Schucany, 1998, Fischer et al, 2001, Kostaki, 2004). Least squares cross-validation was used to estimate the optimum bandwidth. The method uses a process of cross-validation to minimize the integrated squared error, which is the difference between the estimated and true density functions (Wand and Jones, 2000). The true density function is unknown; thereby, an approximation is used (Silverman, 1986).

2.7. Estimation of snake species richness:

The occurrence data of each snake species was reclassified to represent presence or absence in each cell (10 x 10km). Snake species richness was estimated adding up the presences of all snake species.

2.8. Estimation of forest area:

Forest area was computed counting all the cells 100 x 100m of the class forests of Corine 2000, contained inside each cell 10 x 10km of the country.

2.9. Path analysis method:

Path analysis is a special case of Structural Equation Modelling designed to examine presumed causal relationships among a set of three or more variables (Asher, 1983, Goob, 2001, Oliveira et al. 2002, Cramer and Howitt, 2004). The method assumes a linear relationship between variables (Asher, 1983, Goob, 2001, Oliveira et al. 2002). Contrary to regression, which treats all explanatory variables as independent, path analysis allows some explanatory variables to be dependent, making possible to estimate direct and indirect effects (Keane, 1993). Path analysis estimates standardized direct effects, called path coefficients (standardized regression coefficients), using multiple regression equations (Byrne, 2001, Bryman and Cramer, 2003, Khsrowpour, 2002). Indirect effects are estimated based on multiplications of direct effects, according to the path of the indirect effect (Asher, 1983). Path analysis does not prove causality, but highlights the presumed causal relationships that are not contradicted by the data (Wadsworth, 1993, Grace and Pugesek, 1998, Oliveira et al. 2002).

2.9.1. Data analysis:

In path analysis, knowledge about the characteristics of the data is critical to estimate unbiased model parameters. Consequently, several steps were needed:

2.9.1.1. Linearity transformations:

Considering that path analysis assumes linear relationships between variables, linearity was tested plotting the dependent and independent variables. When the points did not seem to be distributed around a straight line it was considered as an indication of potential non-linearity in the data (Jordan, 1992, Schumacker and Lomax, 1996, Quinn and Keough, 2002). A linearization process was carried out using the method 'Ladder of transformations' proposed by Tukey (1977). This method includes 8 different transformations: y^3 , y^2 , y^1 , Sqrt y , $\log y$, y^{-1} , y^{-2} and y^{-3} . Pearson correlation coefficients were estimated to select the transformation that better linearized the data (Salkind, 2004). Transformations do not alter the relations between the variables; they only change the scale of the variables (Stamatis, 2001, Quinn and Keough, 2002).

2.9.1.2. Outlier detection:

The possible presence of outliers was analyzed inspecting normal probability plots. The main idea of looking at normal probability plots was to detect values that could not be logically explained (Kuniavsky, 2003, Meyers et al. 2006). Outliers have to be eliminated to avoid bias in the estimations (Schumacker and Lomax, 1996).

2.9.1.3. Spatial autocorrelation test:

The presence of spatial autocorrelation is one of the characteristics of the datasets that could cause bias in the estimation of model parameters (Singer and Willett, 2003). The method most commonly used to evaluate spatial autocorrelation is Moran's I (Orland, 1988, Shekhar and Xion, 2008). The method compares the values of a variable at each location with values of the same variable at other locations. In general terms, Moran's I is the ratio: similarity of pairs over total variation:

$$I = \frac{N \sum_i \sum_j W_{i,j} (X_i - \bar{X})(X_j - \bar{X})}{(\sum_i \sum_j W_{i,j}) \sum_i (X_i - \bar{X})^2}$$

Where, N is the number of cases, \bar{X} is the mean value of variable X at locations i and j , and $W_{i,j}$ is the weight applied to the comparison between the values at i and j , which is inversely proportional to the distance between the two locations (Shekhar and Xion, 2008).

In order to test the significance of the spatial autocorrelation, a Z score was estimated:

$$ZI = \frac{I - E[I]}{\sqrt{V[I]}}$$

Where, $E[I] = \frac{-1}{(n-1)}$ and $V[I] = E[I^2] - E[I]^2$

2.9.1.4. Normality Assessment:

Several approaches were taken to evaluate normality in the data. Normal probability plots were created (Morris, 1993, Mendenhall and Beaver, 1994, Thode Jr., 2002, Norman and Streiner, 2002, Marques de Sa, 2007). Shapiro-Wilks test was used to check if the residuals are normally distributed. Shapiro-Wilks test evaluates if the sample comes from a normally distributed population (Norman and Streiner, 2002). The way Shapiro-Wilks test is computed is presented below:

$$W = \frac{\left[\sum_{i=1}^N ai(x_{n-i+1} - xi) \right]^2}{\sum_{i=1}^N \left(xi - \bar{x} \right)^2}$$

Where, coefficient ai is fixed for a given sample size and is calculated based on analytical expressions. W value was tested for significance.

However, with large sample sizes, powerful tests as Shapiro-Wilks test tend to reject the assumption of normality even when the deviation from normality is minor. Therefore, skewness and kurtosis were also used to evaluate the distribution of the data, and particularly to estimate the degree of non-normality in the data sets (Hancock and Mueller, 2006). A deviation from normality is considered extreme when skewness is higher than 2 and kurtosis is higher than 7 (Pugesek et al. 2003, Hancock and Mueller, 2006). Skewness measures the symmetry of the distribution curve, and kurtosis its peakedness (Kerr et al. 2002):

$$\text{Kurtosis} = \left(\frac{\sum z^4}{n} \right) - 3$$

$$\text{Skewness} = \left(\frac{\sum z^3}{n} \right)$$

Where, z is the distance, measured in standard deviations, from each observation to the mean.

2.9.1.5. Multicollinearity assessment:

Multicollinearity tests prevent the user from including in the model variables that are interdependent. Multicollinearity could cause errors in the estimation of the model parameters, and increase the standard errors of the estimates (Huan et al. 2002, Grewal et al. 2004). Variance inflation factor (VIF) was used to test multicollinearity. VIF estimates the strength of the linear relationship between two explanatory variables:

$$\text{VIF} = \frac{1}{1 - R^2}$$

Where, R^2 is the coefficient of determination for the regression of one of the independent variables on all the other independent variables (Grewal et al. 2004).

By rule of thumb, VIF values higher than 10 are considered unacceptable levels of collinearity (Forthofer et al. 2006). The problem of multicollinearity may be

compensated through a large sample size (Grewal et al. 2004). However, considering that the problems with multicollinearity are difficult to mitigate, unacceptable levels of collinearity were excluded from the analysis using the following procedure: The variable with highest collinearity was eliminated and VIF was computed again. Then, that variable was restored and the variable with second highest collinearity was eliminated and VIF computed again. Finally, that variable was restored and the variable with third highest collinearity was eliminated and VIF estimated again. The main purpose of this cyclic process was to know what sets of variables could be included in a model in order to avoid unacceptable levels of collinearity.

2.9.2. Selection of the method to estimate model parameters:

There are several methods to estimate model parameters. The selection of the method is critical to compute unbiased estimates. Maximum Likelihood (ML) and Generalized Least-Squares (GLS) are the most common methods. Asymptotically Distribution-free (ADF) is rarely used (Singer and Willett, 2003). ADF gets more accurate estimates than ML or GLS only when the sample sizes are larger than 5000, the models are very simple and the distribution of the data is extremely deviated from normality. ML give accurate estimates only when the data are normally and independently distributed (Hoyle, 1995, Marcoulides, 2000). GLS yields unbiased estimates when autocorrelation is present in the data (Berry and Feldman, 1985, Barreto and Howman, 2006).

GLS estimates a variance-covariance matrix based on observations that are not meant to be spatially independent (Dormann et al. 2007, Rahbek, 2007). This method minimizes a weighted function of the squared residuals giving low weight to the residuals associated to observations with large disturbances as a consequence of autocorrelation (Kennedy, 1992). In other words, when autocorrelated residuals are present in the datasets, the minimization of the weighted sum of squared residuals carried out by GLS allows computing unbiased estimates (Kennedy, 1992, El-Shaarawi and Piegorsch, 2002, Singer and Willett, 2003, Ismail, 2005). The weighted sum of squared residuals is:

$$\sum_{i=1}^N \frac{(y_i^f - y_i)^2}{\sigma_i^2}$$

Where, \hat{y}_i is the regression estimate, y_i is the actual observation, and σ^2 is the uncertainty of each observation (y_i).

As stated above GLS aims to find a regression line with the lowest weighted sum of squared residuals. Then,

$$\sum_{i=1}^N \frac{(a_1 + a_2 x_i - y_i)^2}{\sigma^2 i}$$

Where, a_1 is the intercept, and a_2 is the slope.

However, the weighted sum of squared residuals is created assigning to each residual a weight inversely proportional to its size (Kennedy, 1992).

Although GLS assumes that the data is normally distributed, when the distribution of the data is not extremely deviated from normality GLS still gives accurate estimates. Extreme kurtosis is more probable to pose problems to GLS than extreme skewness (Cutance and Ecob, 1987, Raycov and Marcoulides, 2000, Byrne, 2001, Pugesek et al. 2003, Hardy and Bryman, 2004). Consequently, considering that the data was significantly autocorrelated and kurtosis was not extreme, GLS method was selected to estimate model parameters (Hoyle, 1995, Pugesek et al. 2003, Rao et al. 2008).

2.9.3. Construction of models to be tested:

As a consequence of multicollinearity, it was not possible to evaluate the proposed effects included in the influence diagram of Figure 1-3 using a unique model. Instead four different models, called A, B, C, and “Additional model” were constructed:

The high correlation between relative total abundance of snakes and relative abundance of *Malpolon monspesulanus* ($r = 0.787$), and between relative abundance of *Rhinechis scalaris* and the relative abundance of *M. monspesulanus* ($r = 0.938$) caused unacceptable levels of collinearity. The high correlation between relative abundance of *R. scalaris* and relative abundance of *M. monspesulanus* was also detected by Gil and Pleguezuelos (2001) in South-eastern Spain. They think that the correlation is caused by preference for similar habitats.

As a consequence of the collinearity problems explained above, it was not possible to include the proposed effect of the relative abundance of *M. monspesulanus* on the relative abundance of short-toed eagle (See Figure 1-3, arrow 4) and the proposed effect of the relative total abundance of snakes on the relative abundance of short-toed eagle (See Figure 1-3, arrow 3) together in the same model. In order to evaluate both proposed effects, models A and B were needed. Model A excludes the proposed effect of the relative abundance of *M. monspesulanus* on the relative abundance of short-toed eagle (See Figure 2-3), and model B excludes the proposed effect of the relative total abundance of snakes on the relative abundance of short-toed eagle (See Figure 2-4). In other words, models A and B include the same variables. Models A and B just differ in the proposed effect that was dropped to avoid unacceptable levels of collinearity.

The specification of models A and B copes with unacceptable levels of collinearity avoiding the presence of proposed effects 3 and 4 together in the same model. However, it is possible that the best fitting model is actually a combination of final models A and B. Therefore, it is necessary to construct a model that includes proposed effects 3 and 4 together. This model, called “additional model” copes with unacceptable levels of collinearity excluding from the analysis the proposed effect 5, which is the effect of the relative abundance of *R. scalaris* on the relative abundance of short-toed eagle (See Figure 2-6).

The only purpose of Model C is to evaluate if the sum of the relative abundances of the ‘main preys’ of short-toed eagle has a significant effect on the relative abundance of short-toed eagle (See Figure 2-5).

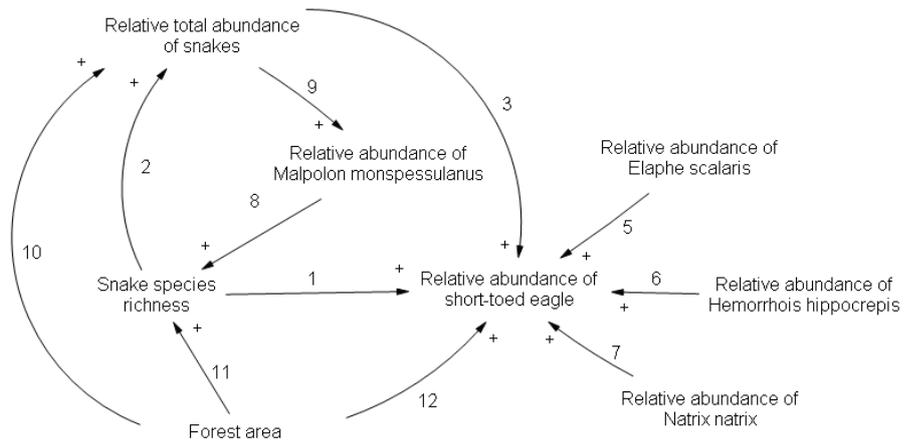


Figure 2 - 3: Path diagram of model A

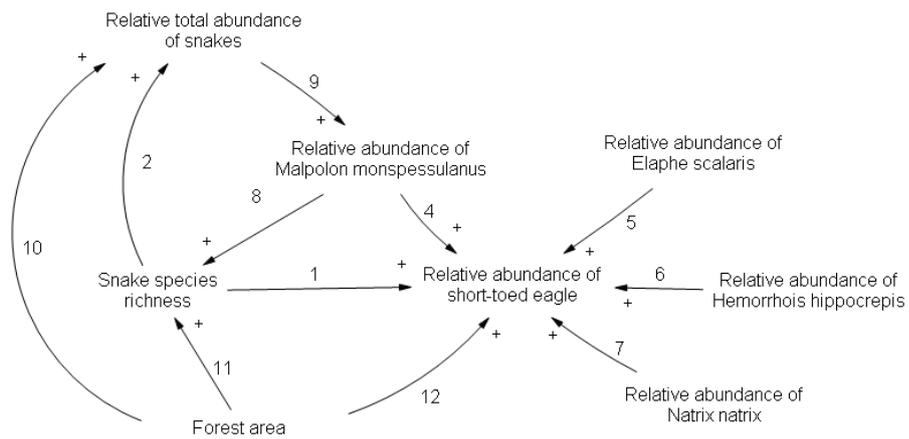


Figure 2 - 4: Path diagram of model B

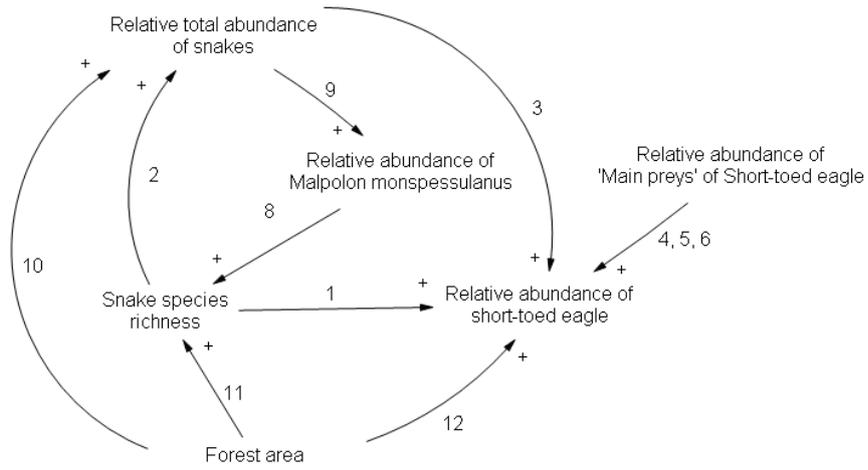


Figure 2 - 5: Path diagram of model C.

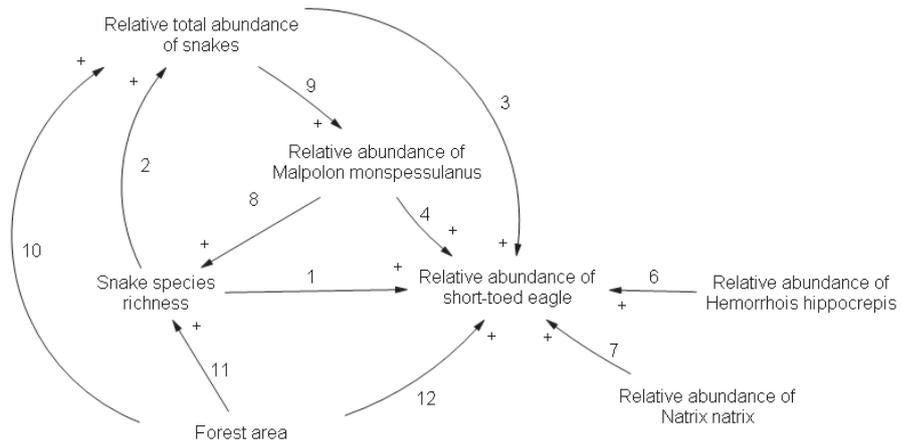


Figure 2 - 6: Path diagram of "Additional model".

2.9.4. Estimation of model parameters:

Before running path analysis, to remove the effect of using different units, dependent and independent variables were standardized to a mean of zero and standard deviation of 1 (Wadsworth, 1993, Oliveira et al. 2002). Then, path coefficients for all proposed effects were estimated using Generalized Least-Squares (GLS). In order to estimate confidence intervals of path coefficients, a bootstrap method was used with 2000 bootstrap samples. Bootstrapping is a statistical method to derive robust standard errors and confidence intervals of path coefficients. The method performs a successive analysis of random samples with replacement from the full sample (Byrne, 2001, Arbuckle, 2007). Other parameters estimated by path analysis were: squared multiple correlations and Chi-square.

The squared multiple correlation (R^2) measures the variability of the dependent variable that is accounted for by its explanatory variables (Oliveira et al. 2002).

$$R^2 = R_{yx1x2} = \sqrt{\frac{r_{yx1}^2 + r_{yx2}^2 - 2r_{yx1}r_{yx}r_{x1x2}}{1 - r_{x1x2}^2}}$$

Chi-square (χ^2) measures how much the implied (reproduced) and sample (observed) variance-covariance matrices of the path model differ. The difference between both matrices is stored as residual matrix. As the residual values of the residual matrix increase decreases the goodness of fit of the model (Schumacker and Lomax, 1996, Raycov and Marcoulides, 2000, Goob, 2001).

$$\chi^2 = I - S$$

Where, I is the implied or estimated variance-covariance matrix, and S is the sample or observed variance-covariance matrix.

2.9.5. Model-trimming approach:

After running path analysis not all the proposed effects were significant. Therefore, it was necessary to eliminate insignificant effects using a model-trimming approach: The model was re-specified eliminating the proposed effect with lowest path

coefficient; then, the model was run to estimate again the path coefficients. This procedure was repeated until all the remaining effects had a significant contribution in the model (See Figure 2-7). In other words, the mentioned cyclic procedure was stopped only when Chi-square and the four indices of fit indicated that having eliminated a proposed effect worsened the fit of the model. Besides, a decline of the squared multiple correlation after having eliminated a proposed effect was also an indication that the proposed effect could have a contribution in the model. Eliminating insignificant effects, one by one, using a systematic approach, balances type I and II errors (Byrne, 2001, Khsrowpour, 2002).

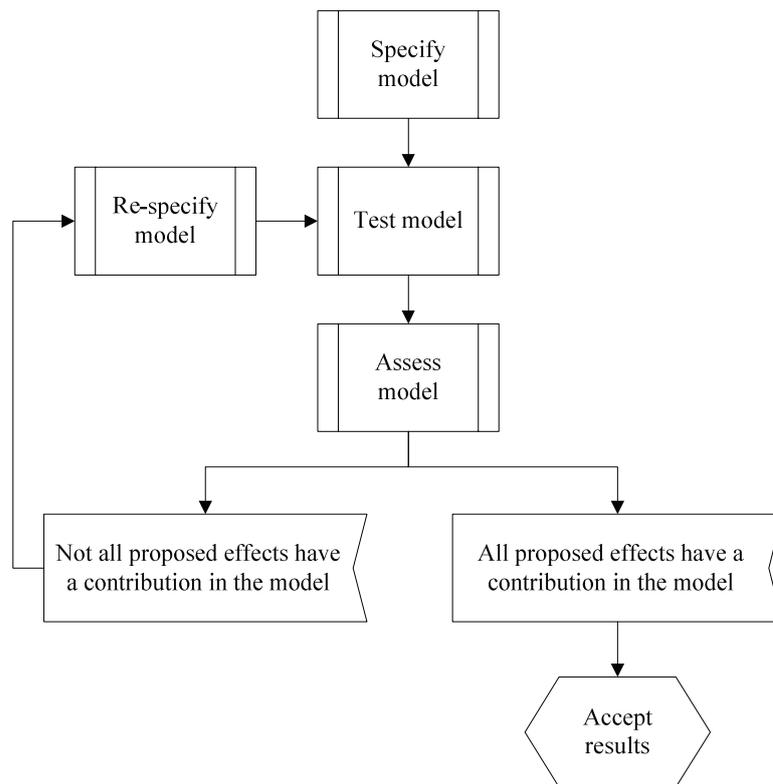


Figure 2 - 7: Model-trimming approach (adapted from Derek and Rao, 2000).

2.9.6. Model comparison:

The comparison between the models A and B with best fit was carried out subtracting the Chi-square of the first model from the Chi-square of the second model, and this value was tested for significance (Albright and Park, 2008). Besides, four indices of fit were used to contribute in the evaluation of the models: Incremental fit index (NCP), Expected cross validation index (ECVI), Incremental fit index (IFI) and Akaike's information criterion (AIC) (Schumacker and Lomax, 1996, Byrne, 2001). The purpose of using several indices of fit was to increase the level of certainty when selecting the best model. The mentioned indices of fit are described below:

2.9.6.1. Incremental fit index:

Incremental fit index (IFI) measures how much better the model fits the data compared to the baseline model. The baseline model is called independence model or null model. In the baseline model all path coefficients are zero. The index ranges from 0 to 1. Zero means that the fit of the proposed model equals the baseline model, and 1 indicates a perfect fit (Bollen, 1986, Schumacker and Lomax, 1996, Byrne, 2001, Loehlin, 2004).

$$IFI = \frac{(x^2_{null} - x^2_{model})}{(x^2_{null} - df_{model})}$$

Where, x^2 is Chi-square.

2.9.6.2. Noncentrality parameter:

Noncentrality parameter (NCP) measures the discrepancy between the hypothesized model and the true model (Byrne, 2001). In other words, it estimates the extent to which the proposed model fails to fit the observed data. The lower the NCP index the better the fit of the model (Schumacker and Lomax, 1996, Raycov and Marcoulides, 2000, Byrne, 2001).

$$NCP = \max(0, x^2 - df)$$

Where, χ^2 is Chi-square and df are degrees of freedom, which are calculated subtracting the number of parameters to be estimated from the total number of sample moments (sample variances and covariances).

2.9.6.3. Expected cross validation index:

Expected cross validation index (ECVI) calculates the discrepancy between the fitted and expected covariance matrices (Browne and Cudeck, 1993, Byrne, 2001). ECVI evaluates if a model is likely to cross-validate across sub-samples of the same size. Simple models with good fit are more likely to cross-validate than more complex models. The lower the ECVI index the better the fit of the model (Schumacker and Lomax, 1996, Raycov and Marcoulides, 2000, Loehlin, 2004).

$$ECVI = \frac{\chi^2_{model}}{(n-1)} + 2 \frac{q}{(n-1)}$$

Where, χ^2 is Chi-square and q is the number of parameters to be estimated.

2.9.6.4. Akaike's information criterion:

Akaike's information criterion (AIC) compares the fit of the proposed model with the fit of the original covariance matrix. It addresses the issue of parsimony in the model fit taking into account the goodness of fit and the number of estimated parameters. The lower the AIC index the better the fit of the model (Schumacker and Lomax, 1996, Raycov and Marcoulides, 2000, Byrne, 2001, Loehlin, 2004).

$$AIC = \chi^2_{model} + 2q$$

Where, χ^2 is Chi-square and q is the number of parameters to be estimated.

2.9.7. Validation procedure:

The replication approach is the most reliable method to validate a path model. The models were run with half of the data, randomly selected, and the other half was used for validation (Schumacker and Lomax, 1996, Pidd, 1996). Each stage of the

path analysis procedure was validated (including the different tests used to analyze the data). During the model trimming process, the validation procedure aimed to prevent eliminating proposed effects that did have a contribution in the model. Besides, the estimation of confidence intervals of path coefficients and four indices of fit contributed in the validation process. Even when bootstrapping works as validation procedure, the software “Amos”, used in the present thesis, estimates confidence intervals only for path coefficients and standard errors. However, it was also important to validate other path parameters such as squared multiple correlations, Chi-square and indices of fit, which justifies to have split the data to create running and validation procedures as indicated above.

3. Results:

3.1. Data analysis:

The analysis revealed the characteristics of the data. Firstly, the inspection of the normal probability plots (See Appendix 7.1.3.) indicates that there are not extreme values that could not be logically explained. Secondly, most of the proposed effects included in the influence diagram of Figure 1-3 were not linear. The transformation that was used for each proposed effect is reported, in bold letters, in Appendix 7.1.1. All selected transformations had a significant correlation at a confidence level of 99% (2-tailed). Thirdly, the spatial autocorrelation test that was carried out revealed that all the evaluated variables of the path diagram are significantly spatial autocorrelated. Appendix 7.1.2 shows the Moran's I index and significance levels. Fourthly, the normal probability plots and normality test show that the explanatory variables are not normally distributed. However, the low values of skewness and kurtosis revealed that the non-normality is not severe. Skewness, kurtosis, normality test and normal probability plots are reported in Appendix 7.1.3. Finally, the collinearity test shows that the relative total abundance of snakes, relative abundance of *Rhinechis scalaris* and the relative abundance of *Malpolon monspesulanus* have high VIF caused by high correlations between the relative abundance of *M. monspesulanus* and the relative abundance of *R. scalaris* ($r = 0.938$), and between the relative abundance of *M. monspesulanus* and the relative total abundance of snakes ($r = 0.787$). Appendix 7.1.4 shows the VIF for all the variables, and the way in which acceptable levels of collinearity were achieved.

3.2. Path analysis:

The process of eliminating insignificant effects mentioned on the model trimming section, heading 2.9.5, was performed using the path coefficients displayed in Appendix 7.2. However, in order to clarify and emphasize that a proposed effect was eliminated only if both, running and validation procedures, indicated that the proposed effect had the lowest contribution in the model (lowest path coefficient). Each path coefficient of the running procedure was compared with the corresponding path coefficient of the validation procedure. The highest value of each proposed effect was displayed in the path diagrams, inside parenthesis. The proposed effect with lowest path coefficient is displayed with red numbers (See

below figures). Besides, the confidence interval of the lowest path coefficient, estimated using bootstrapping, is included below each figure. The path diagrams label each possible effect with a number from 1 to 12. Standardized direct effects, standard errors, critical ratios (computed dividing the regression coefficient by its standard error) and significance levels of critical ratios are included in Appendix 7.2.

3.2.1. Models A:

As stated in heading 2.8.3., model A was constructed dropping the possible effect of the relative abundance of *Malpolon monspessulanus* on the relative abundance of short-toed eagle, in order to avoid unacceptable levels of collinearity. The initial A model was called 1A.

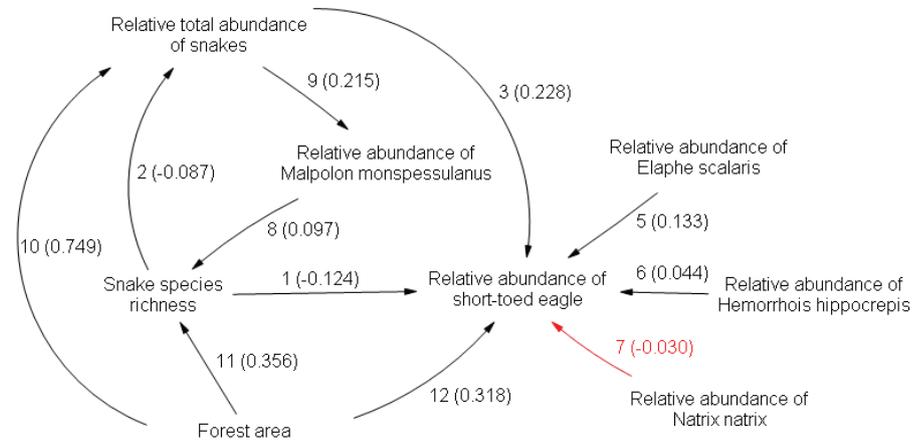


Figure 3 - 1: Model 1A

The path coefficient of the proposed effect 7 had a confidence interval of -0.053 to 0.030 in the running procedure, and -0.075 to 0.009 in the validation procedure, with a confidence level of 99%. A new model was re-specified deleting the proposed effect 7.

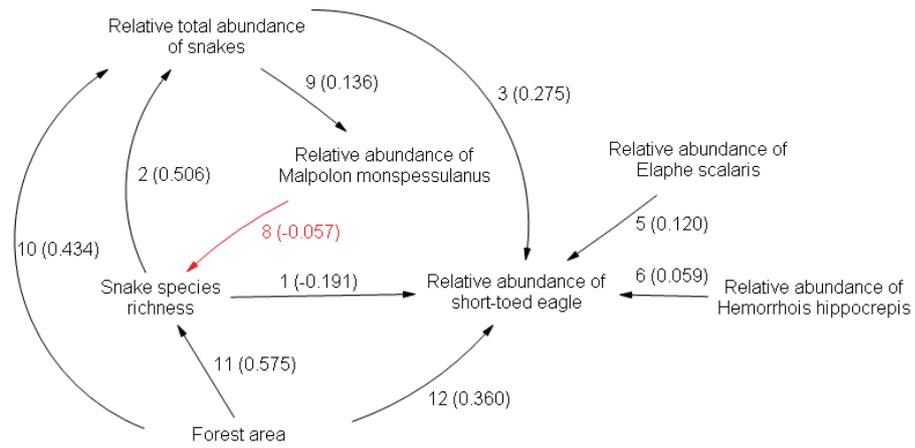


Figure 3 - 2: Model 2A

The path coefficient of the proposed effect 8 had a confidence interval of -0.121 to 0.050 in the running procedure, and -0.151 to 0.031 in the validation procedure, using a confidence level of 99%. A new model was re-specified deleting the proposed effect 8.

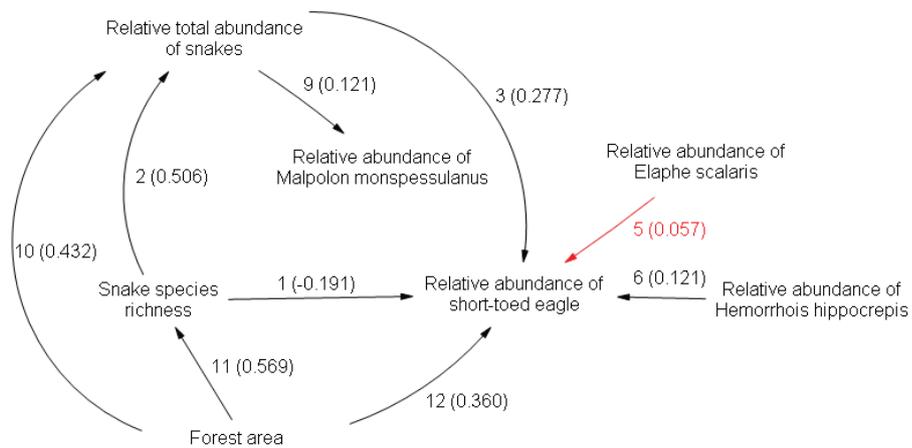


Figure 3 - 3: Model 3A

The path coefficient of the proposed effect 5 had a confidence interval of -0.017 to 0.127 in the running procedure, and -0.012 to 0.119 in the validation procedure, with a confidence level of 99%. A new model was re-specified deleting the proposed effect 5.

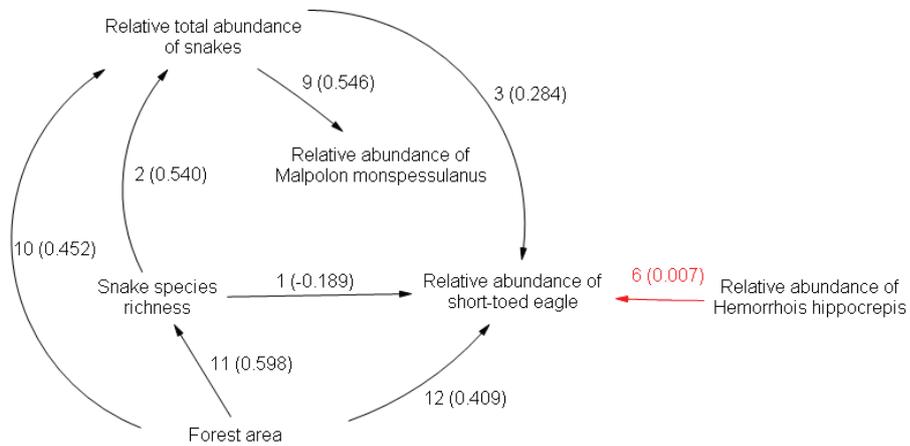


Figure 3 - 4: Model 4A

The path coefficient of the proposed effect 6 had a confidence interval of -0.056 to 0.062 in the running procedure, and -0.053 to 0.065 in the validation procedure, using a confidence level of 99%. A new model was re-specified deleting the proposed effect 6.

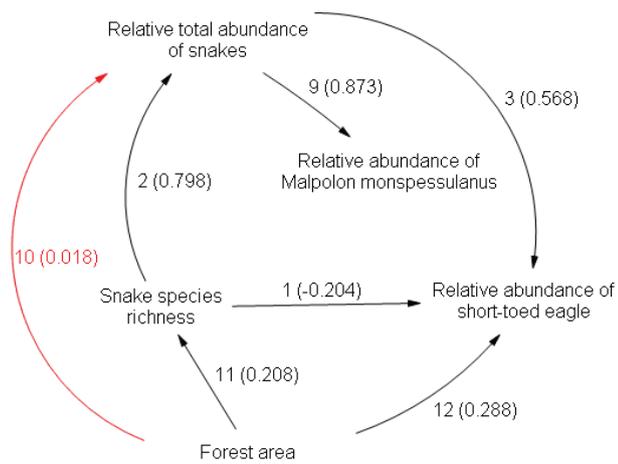


Figure 3 - 5: Model 5A

The path coefficient of the proposed effect 10 had a confidence interval of -0.029 to 0.064 in the running procedure, and -0.055 to 0.041 in the validation procedure, using a confidence level of 99%. A new model was re-specified deleting the proposed effect 10.

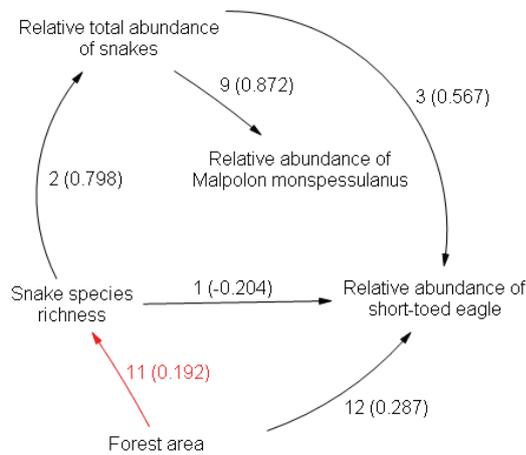


Figure 3 - 6: Model 6A

The path coefficient of the proposed effect 11 had a confidence interval of 0.118 to 0.269 in the running procedure, and 0.106 to 0.269 in the validation procedure, with a confidence level of 99%. A new model was re-specified deleting the proposed effect 11.

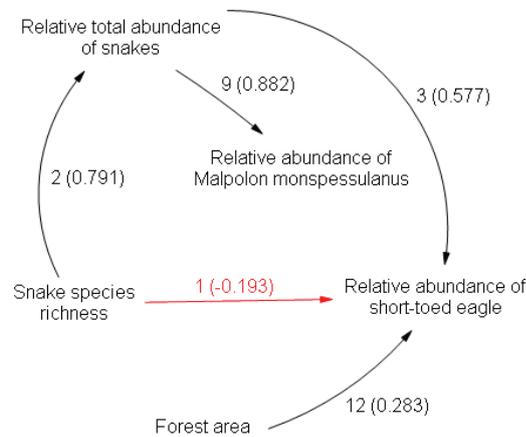


Figure 3 - 7: Model 7A

The squared multiple correlation of snake species richness in model 6A is 0.036 in the running procedure and 0.037 in the validation procedure, which indicates that around 3% of the variability of snake species richness was accounted for by forest area. In other words, forest area had no significant effect on snake species richness. Path analysis shows that the proposed effect 1 had the least contribution in model 7A. The path coefficient of the proposed effect 1 had a confidence interval of -0.282 to -0.090 in the running procedure, and -0.298 to -0.097 in the validation procedure, using a confidence level of 99%. A new model was re-specified deleting the proposed effect 1.

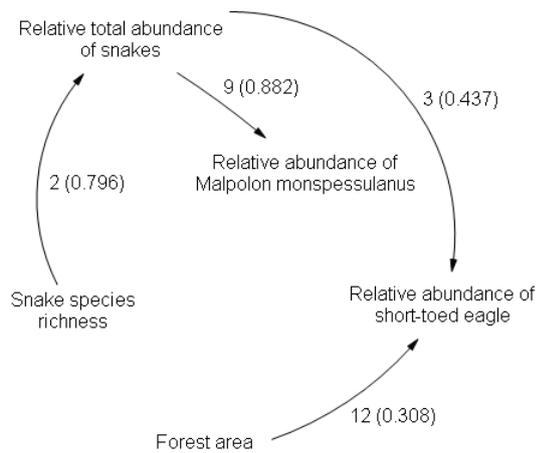


Figure 3 - 8: Model 8A

Observing the squared multiple correlation of the relative abundance of short-toed eagle, in model 8A, can be observed that having eliminated the proposed effect 1 increased around 2% the squared multiple correlation of the relative abundance of short-toed eagle from 0.278 to 0.285 in the running procedure, and from 0.270 to 0.277 in the validation procedure. In other words, snake species richness had no effect on the relative abundance of short-toed eagle. Path coefficients of model 8A revealed that the proposed effects 2, 3, 9 and 12 could have a contribution in the model (See Appendix 7.2.1.8.). The proposed effect 12 has the lowest path coefficient. However it contributes explaining some of the variability of the relative abundance of short-toed eagle. If this proposed effect were eliminated, the squared multiple correlation of the relative abundance of short-toed eagle, Chi-square and the four indices of fit would worsen (See TABLE 3-1):

TABLE 3 - 1: Evaluation of model 8A compared to a new model that excludes the proposed effect 12.

	Running procedure		Validation procedure	
	Model 8A	Without effect 12	Model 8A	Without effect 12
Chi-square	500.889	657.811	541.943	686.858
R ² of short-toed eagle	0.285	0.201	0.277	0.202
IFI	0.682	0.666	0.582	0.576
NCP	494.889	535.943	650.811	679.858
ECVI	0.268	0.286	0.348	0.359
AIC	518.889	559.943	673.811	702.858

Higher values of the index of fit IFI indicate better fit than lower values. Lower values of the indices of fit NCP, ECVI and AIC indicate better fit than higher values. Therefore, the four indices of fit reveal a better fit of model 8A compared to a new model that excludes the proposed effect 12. Besides, the Chi-square differences between model 8A and a model without effect 12 were 156.9 in the running procedure and 144.9 in the validation procedure, which are much higher than the 24.32 Chi-square predicted by the Chi-square probability table, with 7 degrees of freedom, which indicates that all the proposed effects of model 8A may have a contribution in the model.

3.2.2. Models B:

As stated in heading 2.8.3., a model B was constructed dropping the proposed effect of the relative total abundance of snakes on the relative abundance of short-toed eagle, in order to avoid unacceptable levels of collinearity. The initial B model was called 1B.

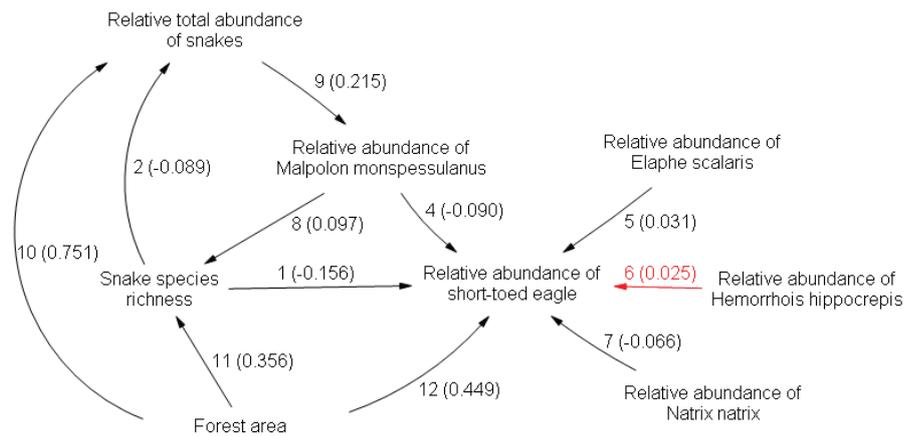


Figure 3 - 9: Model 1B

The path coefficient of the proposed effect 6 had a confidence interval of -0.021 to 0.074 in the running procedure, and -0.060 to 0.033 in the validation procedure, with a confidence level of 99%. A new model was re-specified deleting the proposed effect 6.

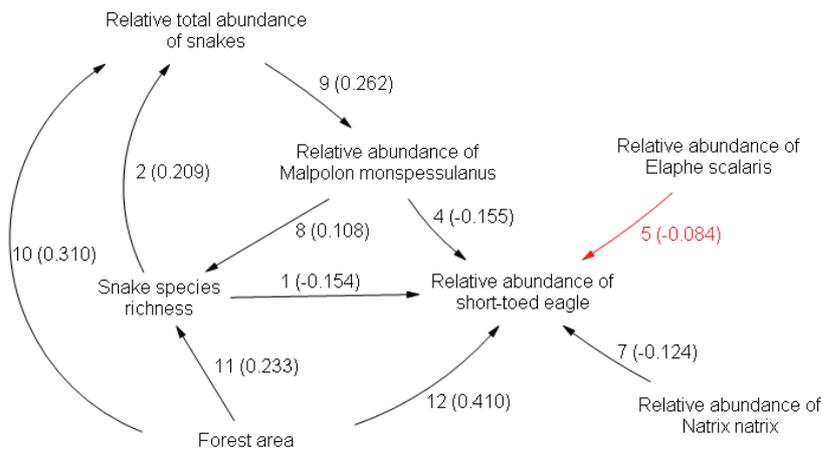


Figure 3 - 10: Model 2B

The path coefficient of the proposed effect 5 had a confidence interval of -0.184 to 0.010 in the running procedure, and -0.175 to 0.02 in the validation procedure, with

a confidence level of 99%. A new model was re-specified deleting the proposed effect 5.

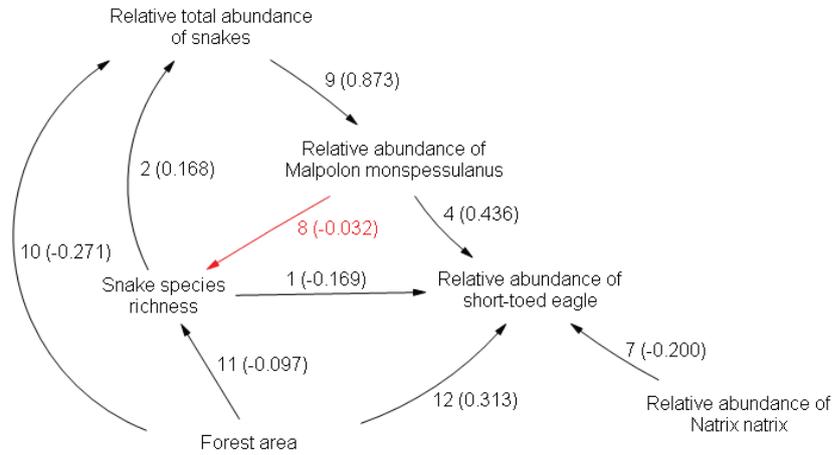


Figure 3 - 11: Model 3B

The path coefficient of the proposed effect 8 had a confidence interval of -0.071 to 0.041 in the running procedure, and -0.093 to 0.019 in the validation procedure, with a confidence level of 99%. A new model was re-specified deleting the proposed effect 8.

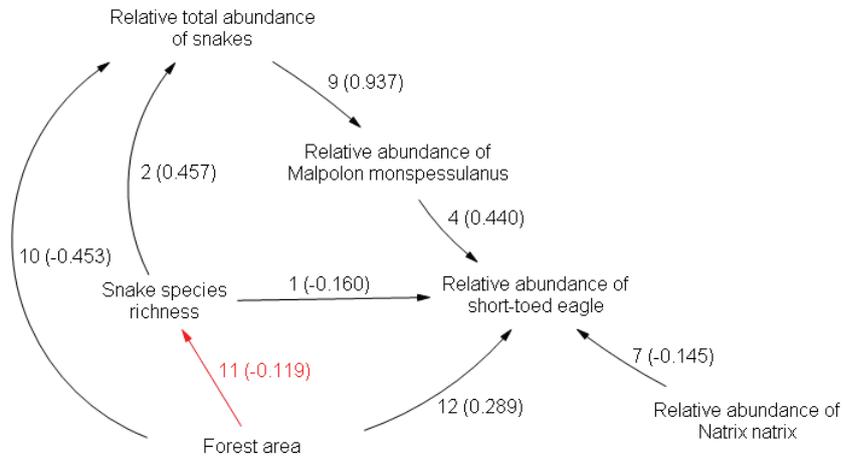


Figure 3 - 12: Model 4B

The path coefficient of the proposed effect 11 had a confidence interval of -0.131 to -0.001 in the running procedure, and -0.190 to -0.044 in the validation procedure, with a confidence level of 99%. A new model was re-specified deleting the proposed effect 11.

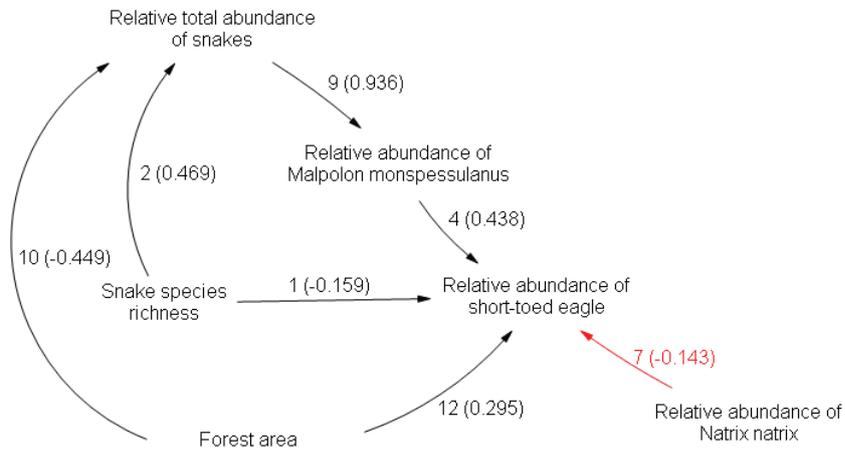


Figure 3 - 13: Model 5B

The path coefficient of the proposed effect 7 had a confidence interval of -0.186 to -0.057 in the running procedure, and -0.209 to -0.084 in the validation procedure, with a confidence level of 99%. A new model was re-specified deleting the proposed effect 7.

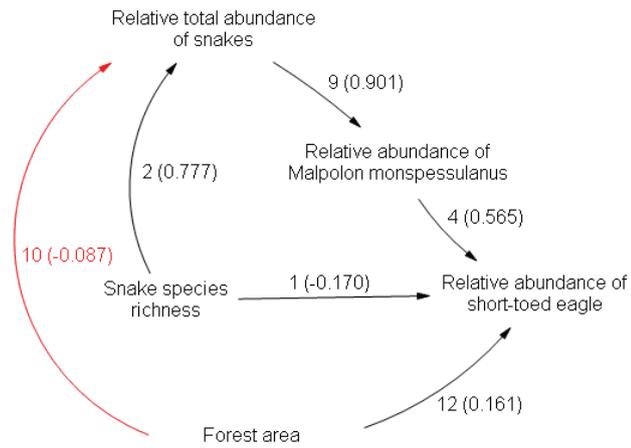


Figure 3 - 14: Model 6B

The path coefficient of the proposed effect 10 had a confidence interval of -0.107 to -0.020 in the running procedure, and -0.135 to -0.043 in the validation procedure, with a confidence level of 99%. A new model was re-specified deleting the proposed effect 10.

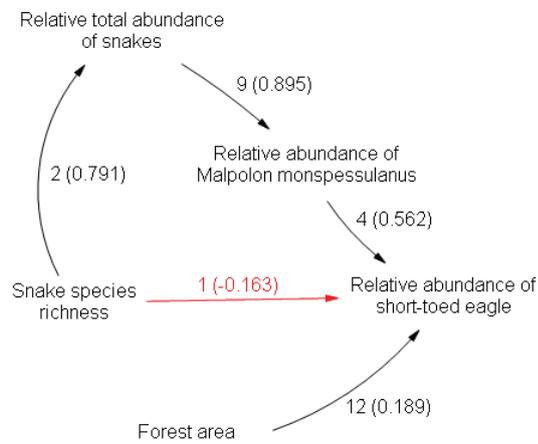


Figure 3 - 15: Model 7B

The path coefficient of the proposed effect 1 had a confidence interval of -0.256 to -0.087 in the running procedure, and from -0.252 to -0.077 in the validation procedure, with a confidence level of 99%. A new model was re-specified deleting the proposed effect 1.

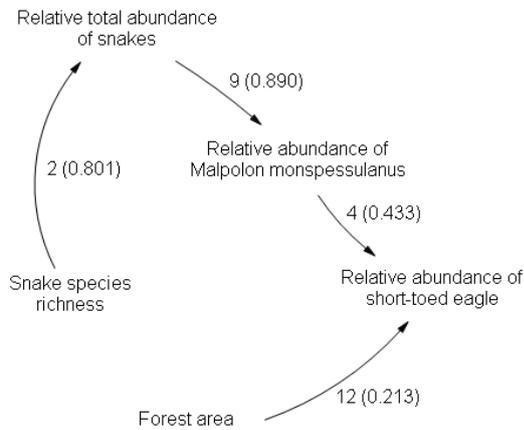


Figure 3 - 16: Model 8B

After having eliminated the proposed effect 1, the squared multiple correlation of the relative abundance of short-toed eagle dropped from 0.245 to 0.233 in the running procedure and from 0.242 to 0.229 in the validation procedure, which indicates that less than 2% of the variability of the relative abundance of short-toed eagle was accounted for by snake species richness. In other words, snake species richness had no significant effect on the relative abundance of short-toed eagle. Path coefficients of model 8B reveal that the proposed effects 2, 4, 9 and 12 could have a contribution in the model (See Appendix 7.2.2.8.). The proposed effect 12 has the lowest path coefficient. However it contributes explaining some of the variations of the relative abundance of short-toed eagle. If this proposed effect were eliminated, the squared multiple correlation of the relative abundance of short-toed eagle, Chi-square and indices of fit would worsen (See TABLE 3-2):

TABLE 3 - 2: Evaluation of model 8B compared to a new model that excludes the proposed effect 12.

	Running procedure		Validation procedure	
	Model 8B	Without effect 12	Model 8B	Without effect 12
Chi-square	545.451	657.811	595.598	686.858
R ² of short-toed eagle	0.233	0.201	0.229	0.202
IFI	0.654	0.582	0.633	0.576
NCP	539.451	650.811	589.598	679.858
ECVI	0.291	0.348	0.314	0.359
AIC	563.451	673.811	613.598	702.858

Higher values of the index of fit IFI indicate better fit than lower values. Lower values of the indices of fit NCP, ECVI and AIC indicate better fit than higher values. Therefore, the four indices of fit reveal a better fit of model 8B compared to a new model that excludes the proposed effect 12. Besides, the Chi-square differences between model 8B and a model without effect 12 were 112.36 in the running procedure and 91.26 in the validation procedure, which are much higher than the 24.32 Chi-square predicted by the Chi-square probability table, with 7 degrees of freedom, which indicates that all the proposed effects of model 8B may have a contribution in the model.

3.2.3. Model C:

As stated in heading 2.8.3., model C was constructed exclusively to test if the relative abundance of the ‘main preys’ of short-toed eagle had a significant effect on the relative abundance of short-toed eagle. The initial model was called 1C.

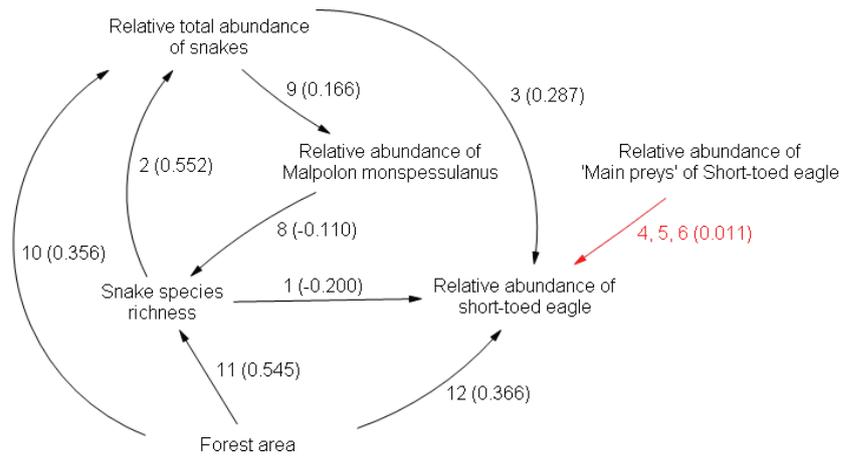


Figure 3 - 17: Model 1C

The path coefficient of the proposed effect 4,5,6 had a confidence interval of -0.072 to 0.083 in the running procedure, and -0.069 to 0.086 in the validation procedure, with a confidence level of 99%. Thereby, the relative abundance of “main preys” of short-toed eagle had not a significant direct effect on the relative abundance of short-toed eagle; therefore, no contribution in the model.

3.2.4. Comparison between models 8A and 8B:

Chi-square and four indices of fit were used to compare models 8A and 8B, in order to know which one fits the data better.

TABLE 3 - 3: Goodness of fit of models 8A and 8B

	Model 8A		Model 8B	
	Running procedure	Validation procedure	Running procedure	Validation procedure
Chi-square	500.889	541.943	545.451	595.598
Degrees of freedom	6	6	6	6
IFI	0.682	0.666	0.654	0.633
NCP	494.889	535.943	539.451	589.598
ECVI	0.268	0.286	0.291	0.314
AIC	518.889	559.943	563.451	613.598

Higher values of the index of fit IFI indicate better fit than lower values. Lower values of the indices of fit NCP, ECVI and AIC indicate better fit than higher values. Therefore, the four indices of fit reveal a better fit of model 8A compared to model 8B. Besides, Chi-square of model 8B is significantly worse than Chi-square of model 8A, with a probability of 99%. The Chi-square difference between both models is 45.00 in the running procedure and 53.66 in the validation procedure. Which are higher than the 24.32 Chi-square predicted by the Chi-square probability table, with 6 degrees of freedom, which indicates that model 8A fits the data significantly better than model 8B.

3.2.5. Evaluation of “Additional model”:

As stated in heading 2.9.3. in order to analyze if the best fitting model is model 8A or a combination of model 8A and 8B, a model called “Additional model” was constructed. Figure 3-18 shows the initial “Additional model”, and Figure 3-19 shows the final “Additional model”, after the process of model trimming. The final “Additional model” is the same than model 8A. Thereby, the best fitting model is model 8A, and not a combination of models 8A and 8B. The detailed model-trimming process is included in Appendix 7.2.4.

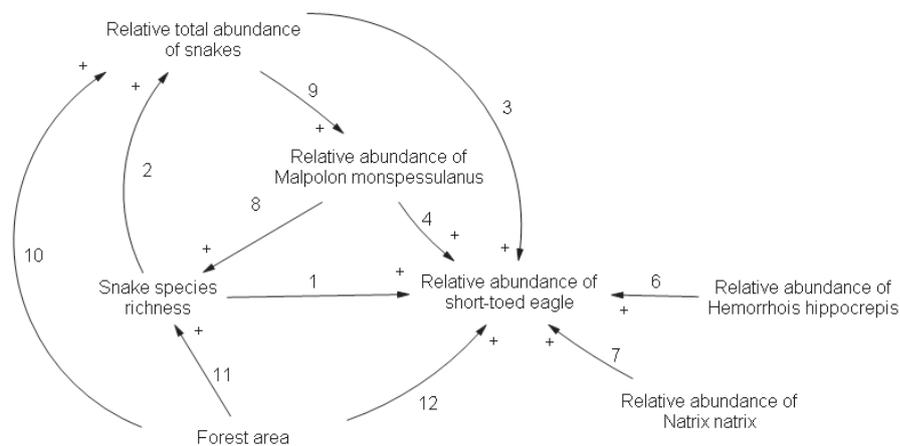


Figure 3 - 18: Initial “Additional model”

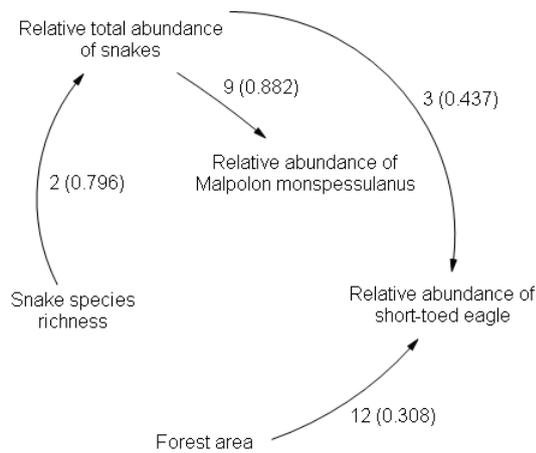


Figure 3 - 19: Final “Additional model”

3.2.6. Direct and indirect effects of model 8A:

Standardized direct effects of model 8A are presented in TABLE 3-4, and its confidence intervals are included in TABLE 3-5. Standardized indirect effects of model 8A and its confidence intervals are presented in TABLES 3-6 and 3-7. Squared multiple correlations of the dependent variables of model 8A are presented in TABLE 3-8. The final 8A model is presented in Figure 3-20 as schematic diagram, and includes squared multiple correlations (R^2) for running and validation procedures.

A description of the table headings is shown below:

SDE = Standardized direct effects.

SIE = Standardized indirect effects.

SE = Standard errors of the regression coefficients.

CR = Critical ratios (Regression coefficient/standard error).

P = Significance level of the critical ratios.

Arrow = Proposed direct effect.

Snake species richness → **Relative abundance of *M. monspesulanus*** = Indirect effect of snake species richness on the relative abundance of *Malpolon monspesulanus*.

Snake species richness → **Relative abundance of *C. gallicus*** = Indirect effect of snake species richness on the relative abundance of *Circaetus gallicus* (short-toed eagle).

TABLE 3 - 4: Standardized direct effects of model 8A.

Arrow	Running procedure				Validation procedure			
	SDE	SE	CR	P	SDE	SE	CR	P
2	0.784	0.129	53.621	<0.001	0.796	0.122	56.377	<0.001
3	0.437	0.286	20.924	<0.001	0.430	0.266	21.030	<0.001
9	0.872	0.007	67.946	<0.001	0.882	0.007	72.067	<0.001
12	0.308	1.505	13.574	<0.001	0.304	1.548	13.277	<0.001

TABLE 3 - 5: Confidence intervals of standardized direct effects (confidence level = 99%) of model 8A, estimated using bootstrap method.

Arrow	Running procedure				Validation procedure			
	Lower bound	Upper bound	SE	P	Lower bound	Upper bound	SE	P
2	0.756	0.809	0.009	<0.001	0.772	0.819	0.010	<0.001
3	0.372	0.503	0.024	<0.001	0.359	0.487	0.025	<0.001
9	0.848	0.890	0.007	<0.001	0.861	0.899	0.008	<0.001
12	0.249	0.376	0.023	<0.001	0.244	0.363	0.023	<0.001

TABLE 3 - 6: Confidence intervals of standardized indirect effects (confidence level = 99%) of model 8A, estimated using bootstrap method, in running procedure.

Indirect effect	Running procedure				
	SIE	Lower bound	Upper bound	SE	P
Snake species richness → Relative abundance of <i>M. monspesulanus</i>	0.683	0.659	0.705	0.008	<0.001
Snake species richness → Relative abundance of <i>C. gallicus</i>	0.342	0.289	0.398	0.025	<0.001

TABLE 3 - 7: Confidence intervals of standardized indirect effects (confidence level = 99%) of model 8A, estimated using bootstrap method, in validation procedure.

Indirect effect	Validation procedure				
	SIE	Lower bound	Upper bound	SE	P
Snake species richness → Relative abundance of <i>M. monspesulanus</i>	0.702	0.681	0.723	0.009	<0.001
Snake species richness → Relative abundance of <i>C. gallicus</i>	0.342	0.287	0.390	0.021	<0.001

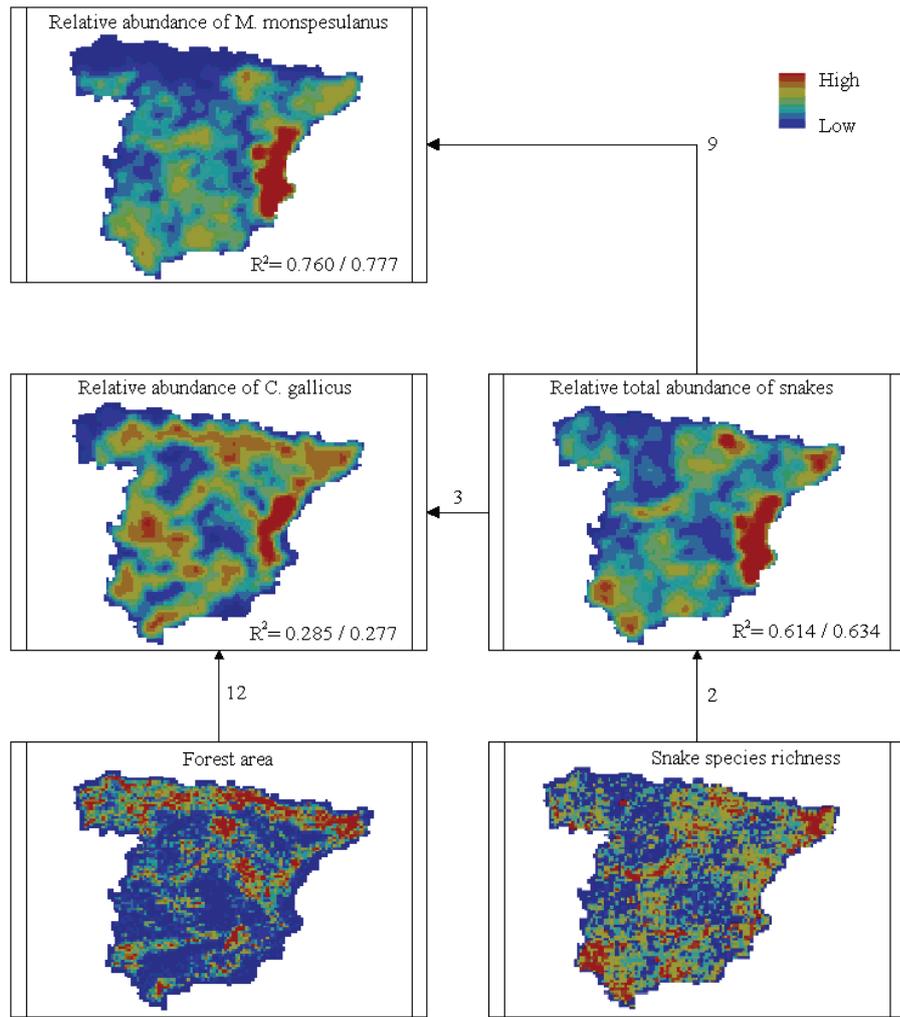


Figure 3 - 20: Schematic diagram of model 8A

4. Discussion:

4.1. Effect of snake species richness on the relative abundance of short-toed eagle:

Path analysis revealed that, apparently, snake species richness has not a direct effect on the relative abundance of short-toed eagle, which could mean that each short-toed eagle does not specialize on different preys, as Moreno-Rueda and Pizarro (2007) thought. It also revealed that it is possible that snake species richness affect the relative total abundance of snakes. In fact, Moreno-Rueda and Pizarro (2007) noticed that in their study area, in south-eastern Spain, zones where snake species richness was higher, ophidian abundance was higher as well. The possible effect of snake species richness on the relative total abundance of snakes could indicate that competition among snake species is low. Spanish snake species prey on a wide range of preys (Regalado, 2004, Santos, 2004, Santos and Pleguezuelos, 2004), which could keep a low interspecific competition. On top of that, it is possible that snakes reduce competition for food with other snake species becoming active at a different time of the day (Moreno-Rueda and Pizarro, 2007).

Besides, path analysis revealed that the relative total abundance of snakes could affect directly the relative abundance of short-toed eagle. In fact, Bakaloudis et al (1998) mention that Dardia forest, north-eastern Greece, supports the highest density of reptiles in Europe, and a very high density of short-toed eagles. The effect of the relative total abundance of snakes on the relative abundance of short-toed eagle could indicate that short-toed eagle is a generalist that feeds on many snake species according to their local abundance. Indeed, when Gil and Pleguezuelos (2001) analyzed the diet of short-toed eagle they found a correlation between the presence of *Malpolon monspesulanus*, *Rhinechis scalaris* and *Hemorrhois hippocrepis* in short-toed eagle's pellets, and the abundance of those species in the study area.

However, the effect of the relative total abundance of snakes on the relative abundance of short-toed eagle was not strong as expected, considering the relevance of food availability for predators (Newton, 1998). The strength of the relationship could have several possible explanations: Firstly, it is liable that not all snake species have the same probability to be captured by short-toed eagle. For example: *Natrix maura* spends most of the time in water bodies (Bakaloudis et al. 1998), *Malpolon monspesulanus* could get more exposed due to specific thermoregulation needs (Pleguezuelos, 2009), snakes could become less accessible in areas with dense

vegetation (Bakaloudis, 2009). Secondly, even though short-toed eagle has physiological adaptations as short-toes and a pointed heel to capture snakes (Breuil et al. 1998) it seems that when lizards, rodents and other small animals are abundant, the eagle does not miss the opportunity to get extra fat (Darawshi, 2007). Fat is the fuel that makes the long migration possible (Agostini et al. 2002, Faaborg, 2002). For example, Darawshi (2007) mentions that it is common to see, in Israel, groups of short-toed eagles hunting rodents, in agricultural fields, during plowing and harvesting activities. Under those specific agricultural events rodents constitute the main preys of short-toed eagle.

The relative total abundance of snakes could not only affect the relative abundance of short-toed eagle, but also the relative abundance of *Malpolon monspesulanus*, which could indicate that *M. monspesulanus* is also a generalist that preys on many snake species according to their local abundance. However, apparently, the inclusion of *M. monspesulanus* in the estimation of the relative total abundance of snakes over-estimated the possible effect as shown in the additional analysis of Appendix 7.5. *M. monspesulanus*, as short-toed eagle, does not prey exclusively on snakes. It is reported that *M. monspesulanus* preys also on small mammals and birds (Pleguezuelos, 2009). Therefore, the stronger effect of the relative total abundance of snakes on the relative abundance of *M. monspesulanus*, compared to the effect of the relative total abundance of snakes on the relative abundance of short-toed eagle, could be an indication that accessibility to preys is not an important factor for *M. monspesulanus* as it could be for short-toed eagle. However, it could also indicate that the relative total abundance of snakes is a more relevant factor for *M. monspesulanus* than for short-toed eagle. Short-toed eagle requires not only preys but also forests for nesting, while *M. monspesulanus* nests on many kinds of habitats (Pleguezuelos, 2009).

However, considering that path analysis does not prove causality, the effect of the relative total abundance of snakes on the relative abundances of short-toed eagle and *M. monspesulanus* could indicate not only that short-toed eagle and *M. monspesulanus* may feed on many snake species according to their local abundance, as stated before. The relative total abundance of snakes could be correlated to the total abundance of snakes and their common preys (small rodents for example) together, which could suggest that the total abundance of snakes and their common preys together could be the variable affecting the relative abundances of short-toed eagle and *M. monspesulanus*.

4.2. Effect of the relative abundances of *M. monspesulanus*, *R. scalaris*, *H. hippocrepis* and *N. natrix* on the relative abundance of short-toed eagle:

Path analysis revealed that it is not so viable that any of the snake species, that were considered as possible main preys of short-toed eagle, have a significant effect on the relative abundance of the eagle. This finding could be the reason why Niamir (2009) could not increase the predictive power of a short-toed eagle distribution model, using the availability of the three 'main preys' of short-toed eagle. *Malpolon monspesulanus*, *Rhinechis scalaris* and *Hemorrhois hippocrepis* are the biggest and most abundant snakes of south-eastern Spain (Gil and Pleguezuelos, 2001). The method to evaluate the diet of short-toed eagle, used by Gil and Pleguezuelos (2001), in south-eastern Spain, consists in analyzing regurgitated pellets. This method makes possible to identify the parts of the preys that have not been digested (Mersmann et al. 1992, Vlachos and Papageorgiou, 1994, Redpath et al. 2001). However, there is evidence that diurnal raptors can digest even bones (Houston and Copsey, 1994, Bochenski et al. 1997, Katzner et al. 2006), which, apparently, adds bias to the method. Mersmann et al. (1992) tested the method using captive bald eagles. They conclude that the method over-represents medium sized and big sized preys, and under-represents small preys. Scientific research carried out by Redpath et al. (2001) and Jordan (2003) confirms that the analysis of regurgitated pellets under-represents small preys. Besides, according to Peeters and Peeters (1997) even preys of the same size may not be equally digestible. In consequence, the method "analysis of regurgitated pellets", used by Gil and Pleguezuelos (2001), could have identified the snake species that are difficult to digest by the digestive juices of short-toed eagle, instead of the preys that the eagle preys on.

Path analysis revealed that the relative abundance of *M. monspesulanus*, apparently, has no effect on snake species richness, consequently, no indirect effect on the relative abundance of short-toed eagle. Pianka (2000) mentions that predators as the ophiophagous snake *M. monspesulanus* could reduce competition among preys allowing the presence of more species. However, generalizations, in ecology, do not mention the set of circumstances that need to be present for the generalization to become true (Cotgreave and Forseth, 2002, Jorgensen and Fath, 2007, Pickett et al. 2007). It is likely that the mentioned generalization is valid only under high interespecific competition. Interespecific competition takes place when different species require the same limiting resource (Cronk and Fennessy, 2001). In Spain, snake species feed on a wide range of preys (Regalado, 2004, Santos, 2004, Santos and Pleguezuelos, 2004), which could keep a low interespecific competition. On top

of that, apparently, snakes reduce competition for food with other snake species becoming active at a different time of the day (Moreno-Rueda and Pizarro, 2007).

4.3. Effect of forest area on the relative abundance of short-toed eagle:

In Spain, forests are important habitats for several snake species. However, they are not the only habitat for those species (Galan, 2004, Pleguezuelos, 2005, Brito, 2006, Martinez-Freira, 2009), which could explain why path analysis did not detect a significant direct effect of forest area neither on the relative total abundance of snakes nor on snake species richness. Sanchez-Zapata and Calvo (1999) consider the possibility that the abundance of short-toed eagle could be affected by forest area, which is supported by the results of this thesis. The effect of forest area on the relative abundance of short-toed eagle could indicate that forest area is related to the abundance of suitable nesting sites.

However, the relationship was not strong as expected, considering that short-toed eagle needs forests for nesting. The strength of the relationship could have several possible explanations: Firstly, only adult short-toed eagles and juveniles of less than three months old require forests for nesting (Cramp and Simmons, 1980, Darawshi, 2007), but the relative abundance of short-toed eagle was estimated using occurrence data that do not differentiate the eagle's age. Secondly, considering that, apparently, short-toed eagle avoids forests for foraging, (Bakaloudis et al. 1998, Bakaloudis, 2009), it is reasonable to think that the occurrence data of the eagle could include some observations near forests and others far from them. Finally, forest area was computed using cells of forests of 100 x 100 m; however, it is possible that patches of forests of less than 100 x 100 m are also important nesting sites for short-toed eagle.

Path analysis does not prove causality, as stated before. Therefore, it is also possible that forest area is related to a variable with stronger effect on the relative abundance of short-toed eagle. In 1980, logging was permitted for the first time in several areas of Dadia forest (north-eastern Greece), which caused the fragmentation of the forest. According to Bakaloudis et al (1998), forest fragmentation originated an increase in the population of several species of raptors included short-toed eagle. Therefore, forest area could be related to the abundance of forest fragments. Forest fragmentation could allow short-toed eagle to nest near foraging habitats, which could be important to reduce the energy costs of foraging (Fox et al. 2001).

4.4. Data limitations:

The present research had several limitations: Firstly, Kernel density allowed coping with the absence of abundance data. However, kernel density could have estimated better approximations of abundance for habitat generalists than for habitat specialists. Besides, the low accuracy of the occurrence data could have also affected the quality of the abundance estimations. Secondly, as mentioned in heading 4.3, not having considered patches of forests smaller than 100 by 100 m, which is the finest spatial resolution of Corine 2000, could have affected the results. Finally, relative abundances were estimated based on occurrence data collected in an organized way, as described in heading 2.2. However, the abundance of occurrences may reflect not only how abundant a species is, but also how detectable it is. Therefore, it is possible that the use of occurrence data overestimated the actual abundances of some species and underestimated the abundances of others.

5. Conclusions and recommendations:

Path analysis could not detect that the relative abundance of the snakes that are thought to be the main preys of short-toed eagle in Spain (*Malpolon monspesulanus*, *Rhinechis scalaris* and *Hemorrhois hippocrepis*) and in other countries (*Natrix natrix*) have a significant direct effect on the relative abundance of short-toed eagle. Besides, path analysis could not reveal the existence of direct relationships between the relative abundance of *M. monspesulanus* and snake species richness, forest area and snake species richness, forest area and the relative total abundance of snakes, and snake species richness and the relative abundance of short-toed eagle. However, the results show that snake species richness could affect the relative total abundance of snakes, which, apparently, affects directly the relative abundances of the short-toed eagle and *M. monspesulanus*. In consequence, snake species richness could affect indirectly the relative abundances of both species. Moreover, forest area could also affect the relative abundance of short-toed eagle.

Path analysis does not prove causality (Grace and Pugsek, 1998). Therefore, in order to increase the level of certainty that the results of this thesis may represent actual causal relationships, occurrence data from other countries should be analyzed. Besides, new theories should be tested.

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7. Appendices:

7.1. Data analysis appendices:

Legend: R. A = Relative abundance. Arrow = Proposed direct effect.

Appendix 7.1.1.: Correlations of the linearization process.

Arrow	Transformations	R. A. of <i>Circaetus</i> <i>Gallicus</i>	R. A. of <i>Circaetus</i> <i>Gallicus</i> (Validation)
1	Snake species richness Power3	0.274	0.254
	Snake species richness Power2	0.306	0.286
	Snake species richness Power1	0.316	0.302
	Snake species richness Sqrt	0.291	0.285
	Snake species richness 10log	0.290	0.286
	Snake species richness Power-1	-0.192	-0.200
	Snake species richness Power-2	-0.158	-0.176
	Snake species richness Power-3	-0.132	-0.155
3	Relative total abundance of snakes Power3	0.241	0.208
	Relative total abundance of snakes Power2	0.350	0.330
	Relative total abundance of snakes Power1	0.438	0.436
	Relative total abundance of snakes Sqrt	0.442	0.449
	Relative total abundance of snakes Log10	0.406	0.420
	Relative total abundance of snakes Power-1	-0.176	-0.244
	Relative total abundance of snakes Power-2	-0.049	-0.095
	Relative total abundance of snakes Power-3	-0.037	-0.056
4	R. A. of <i>Malpolon monspesulanus</i> Power3	0.180	0.176
	R. A. of <i>Malpolon monspesulanus</i> Power2	0.262	0.273
	R. A. of <i>Malpolon monspesulanus</i> Power1	0.328	0.356
	R. A. of <i>Malpolon monspesulanus</i> Sqrt	0.285	0.331
	R. A. of <i>Malpolon monspesulanus</i> Log10	0.154	0.216
	R. A. of <i>Malpolon monspesulanus</i> Power-1	-0.020	-0.052
	R. A. of <i>Malpolon monspesulanus</i> Power-2	-0.007	-0.035
	R. A. of <i>Malpolon monspesulanus</i> Power-3	-0.007	-0.030

Arrow	Transformations	R. A. of <i>Circaetus</i> <i>Gallicus</i>	R. A. of <i>Circaetus</i> <i>Gallicus</i> (Validation)
5	R. A. of <i>Rhinechis scalaris</i> Power3	0.195	0.169
	R. A. of <i>Rhinechis scalaris</i> Power2	0.276	0.259
	R. A. of <i>Rhinechis scalaris</i> Power1	0.340	0.346
	R. A. of <i>Rhinechis scalaris</i> Sqrt	0.301	0.333
	R. A. of <i>Rhinechis scalaris</i> Log10	0.175	0.229
	R. A. of <i>Rhinechis scalaris</i> Power-1	-0.065	-0.065
	R. A. of <i>Rhinechis scalaris</i> Power-2	-0.051	-0.028
	R. A. of <i>Rhinechis scalaris</i> Power-3	-0.048	-0.020
6	R. A. of <i>Hemorrhhois hippocrepis</i> Power3	0.031	-0.004
	R. A. of <i>Hemorrhhois hippocrepis</i> Power2	0.085	0.053
	R. A. of <i>Hemorrhhois hippocrepis</i> Power1	0.167	0.167
	R. A. of <i>Hemorrhhois hippocrepis</i> Sqrt	0.175	0.205
	R. A. of <i>Hemorrhhois hippocrepis</i> Log10	0.135	0.184
	R. A. of <i>Hemorrhhois hippocrepis</i> Power-1	-0.049	-0.046
	R. A. of <i>Hemorrhhois hippocrepis</i> Power-2	-0.024	-0.040
	R. A. of <i>Hemorrhhois hippocrepis</i> Power-3	-0.016	-0.038
7	R. A. of <i>Natrix Natrix</i> Power3	0.160	0.156
	R. A. of <i>Natrix Natrix</i> Power2	0.228	0.207
	R. A. of <i>Natrix Natrix</i> Power1	0.298	0.264
	R. A. of <i>Natrix Natrix</i> Sqrt	0.315	0.285
	R. A. of <i>Natrix Natrix</i> Log10	0.281	0.271
	R. A. of <i>Natrix Natrix</i> Power-1	-0.061	-0.091
	R. A. of <i>Natrix Natrix</i> Power-2	-0.019	-0.063
	R. A. of <i>Natrix Natrix</i> Power-3	-0.010	-0.060
4,5,6	R. A. of main preys Power3	0.129	0.100
	R. A. of main preys Power2	0.214	0.198
	R. A. of main preys Power1	0.302	0.317
	R. A. of main preys Sqrt	0.307	0.321
	R. A. of main preys Log10	0.149	0.212
	R. A. of main preys Power-1	-0.037	-0.053
	R. A. of main preys Power-2	-0.034	-0.029
	R. A. of main preys Power-3	-0.037	-0.020

Arrow	Transformations	R. A. of <i>Circaetus gallicus</i>	R. A. of <i>Circaetus gallicus</i> (Validation)
12	Forest area Power3	0.198	0.187
	Forest area Power2	0.245	0.226
	Forest area Power1	0.300	0.272
	Forest area Sqrt	0.327	0.296
	Forest area Log10	0.325	0.295
	Forest area Power-1	-0.242	-0.228
	Forest area Power-2	-0.132	-0.141
	Forest area Power-3	-0.084	-0.096

Arrow	Transformations	R. A. of <i>Malpolon monspesulanus</i>	R. A. of <i>Malpolon monspesulanus</i> (Validation)
8	Snake species richness Power3	0.355	0.356
	Snake species richness Power2	0.444	0.433
	Snake species richness Power1	0.527	0.511
	Snake species richness Sqrt	0.547	0.532
	Snake species richness 10log	0.550	0.531
	Snake species richness Power-1	-0.365	-0.359
	Snake species richness Power-2	-0.368	-0.359
	Snake species richness Power-3	-0.346	-0.337
9	Rel. tot. abundance of snakes Power3	0.597	0.588
	Rel. tot. abundance of snakes Power2	0.696	0.689
	Rel. tot. abundance of snakes Power1	0.780	0.774
	Rel. total abundance of snakes Sqrt	0.787	0.780
	Rel. total abundance of snakes Log10	0.753	0.743
	Rel. total abund. of snakes Power-1	-0.351	-0.487
	Rel. total abund. of snakes Power-2	-0.210	-0.199
	Rel. total abund. of snakes Power-3	-0.048	-0.104

Arrow	Transformations	Total R. A. of snakes Sqrt	Total R. A. of snakes Sqrt (Validation)
2	Snake species richness Power3	0.603	0.597
	Snake species richness Power2	0.700	0.696
	Snake species richness Power1	0.784	0.778
	Snake species richness Sqrt	0.783	0.777
	Snake species richness 10log	0.781	0.774
	Snake species richness Power-1	-0.521	-0.524
	Snake species richness Power-2	-0.504	-0.502
	Snake species richness Power-3	-0.466	-0.463
10	Forest area Power3	0.103	0.139
	Forest area Power2	0.112	0.142
	Forest area Power1	0.126	0.146
	Forest area Sqrt	0.137	0.152
	Forest area 10log	0.089	0.133
	Forest area Power-1	-0.037	-0.094
	Forest area Power-2	0.002	-0.052
	Forest area Power-3	0.012	-0.032

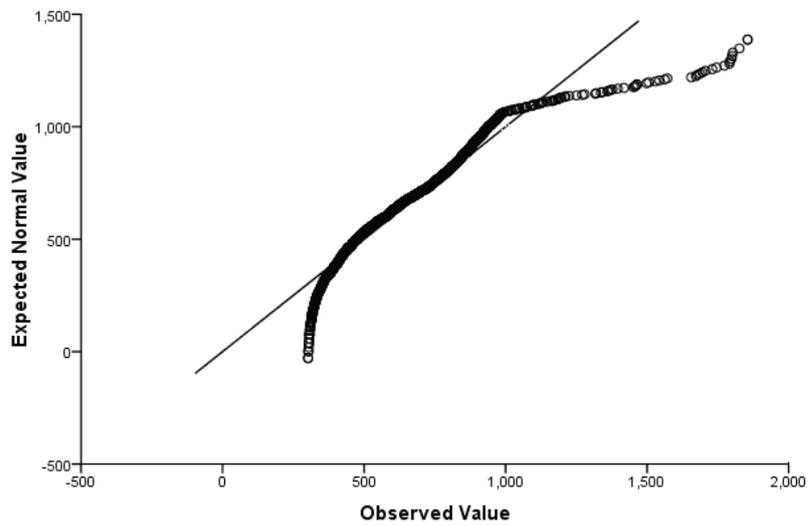
Arrow	Transformations	Snake species richness	Snake species richness
11	Forest area Power3	0.246	0.257
	Forest area Power2	0.253	0.272
	Forest area Power1	0.260	0.280
	Forest area Sqrt	0.256	0.279
	Forest area 10log	0.245	0.270
	Forest area Power-1	0.245	-0.199
	Forest area Power-2	-0.167	-0.112
	Forest area Power-3	-0.041	-0.071

Appendix 7.1.2: Moran's I Spatial autocorrelation test:

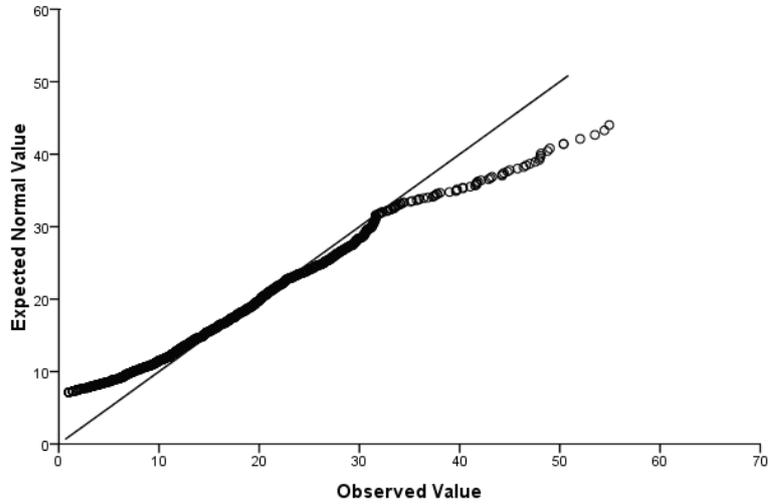
Explanatory variables	Moran's I index	P
R. A. of short-toed eagle	0.10	< 0.01
R. A. of <i>Hemorrhois hippocrepis</i>	0.21	< 0.01
R. A. of <i>Malpolon monspesulanus</i>	0.19	< 0.01
R. A. of <i>Rhinechis scalaris</i>	0.18	< 0.01
R. A. of <i>Natrix natrix</i>	0.13	< 0.01
R. A. of 'main preys' of <i>C. gallicus</i>	0.19	< 0.01
Relative total abundance of snakes	0.15	< 0.01
Snake species richness	0.11	< 0.01
Forest area	0.14	< 0.01

Appendix 7.1.3: Normal probability plots and normality tests for the variables included in models A, B and C.

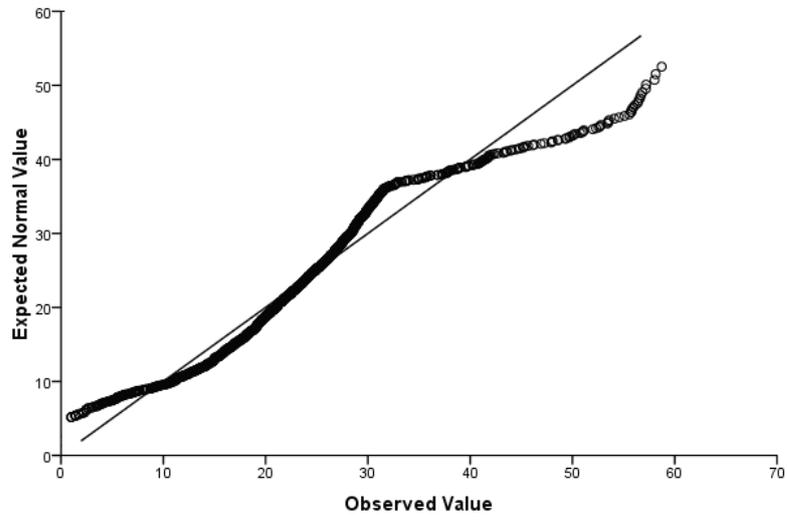
Appendix 7.1.3.1: Normal probability plot of the relative abundance of *Circaetus gallicus*.



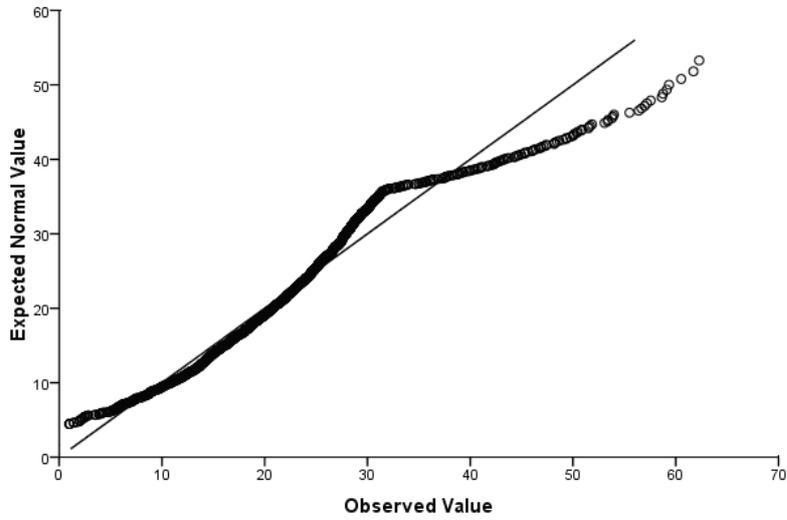
Appendix 7.1.3.2: Normal probability plot of the relative abundance of *Hemorrhoids hippocrepis*.



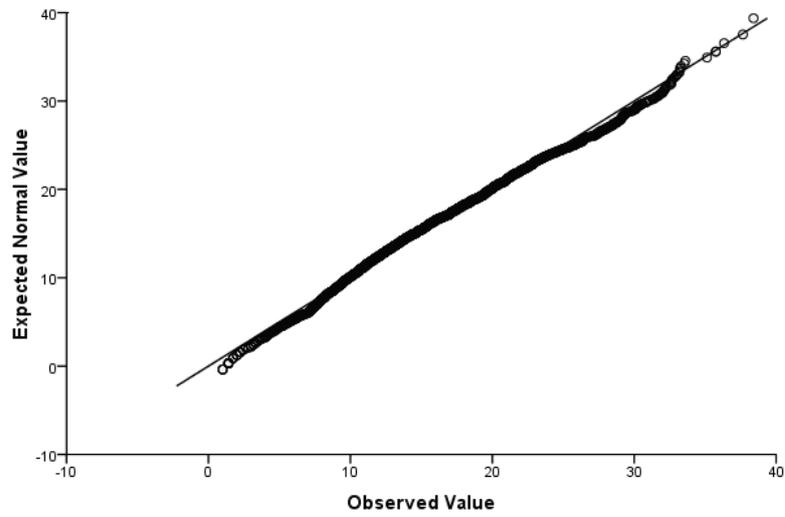
Appendix 7.1.3.3: Normal probability plot of the relative abundance of *Malpolon monspesulanus*.



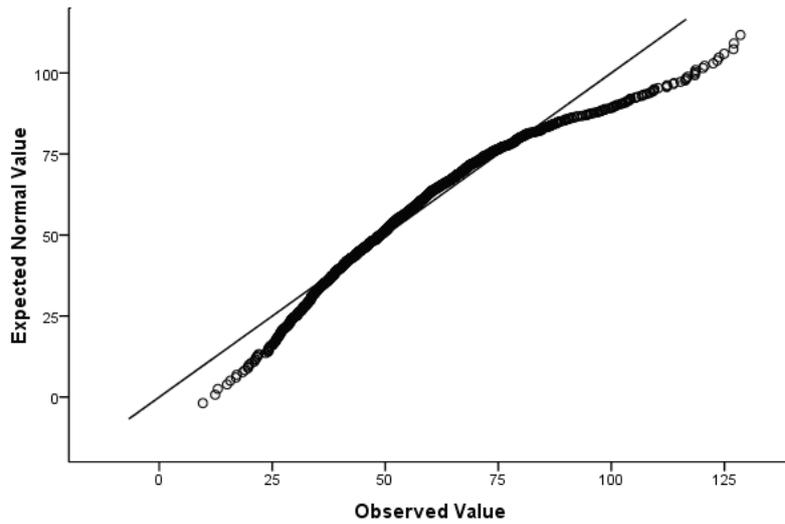
Appendix 7.1.3.4: Normal probability plot of the relative abundance of *Rhinechis scalaris*.



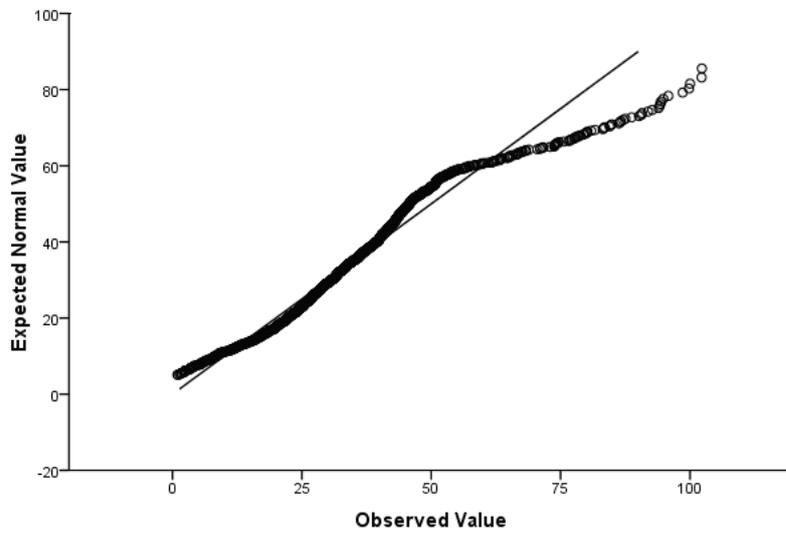
Appendix 7.1.3.5: Normal probability plot of the relative abundance of *Natrix natrix*.



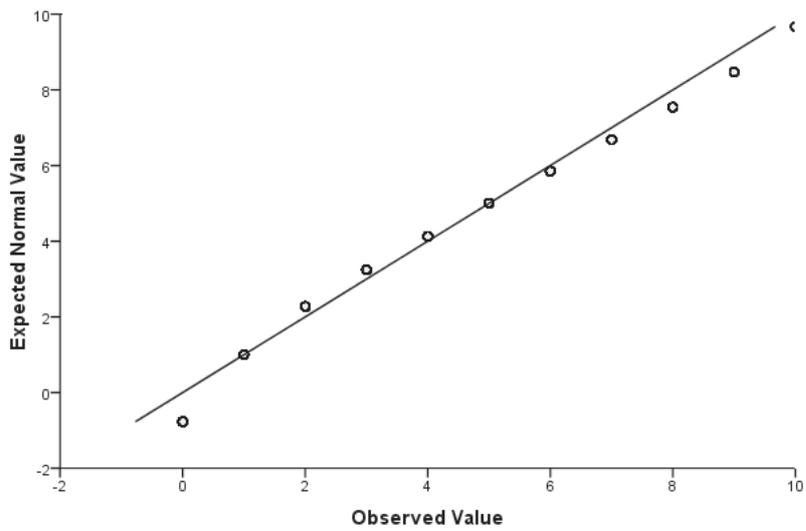
Appendix 7.1.3.6: Normal probability plot of the relative total abundance of snakes.



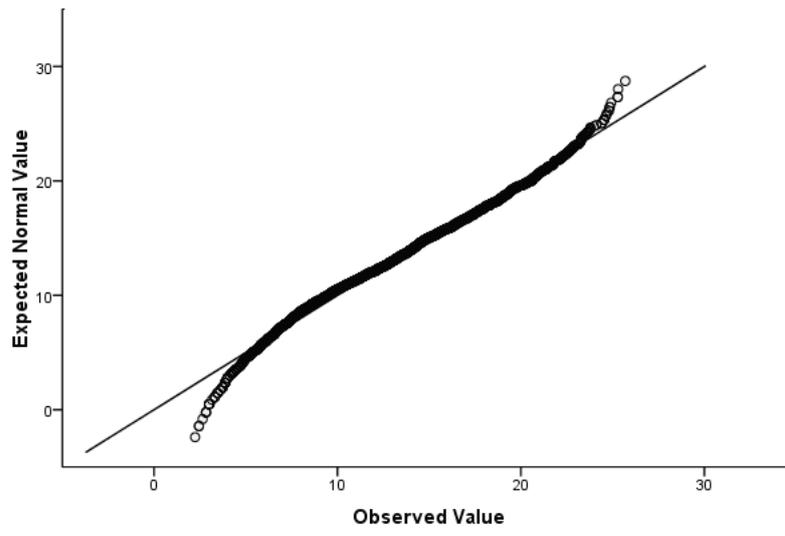
Appendix 7.1.3.7: Normal probability plot of the relative abundance of the 'main preys' of short-toed eagle.



Appendix 7.1.3.9: Normal probability plot of snake species richness.



Appendix 7.1.3.10: Normal probability plot of forest area.



Appendix 7.1.3.11: Shapiro-Wilk test for the explanatory variables.

Explanatory variables	Running procedure	Validation procedure
	P	P
R. A. of short-toed eagle	0.000	0.000
R. A. of <i>Hemorrhois hippocrepis</i>	0.000	0.000
R. A. of <i>Malpolon monspesulanus</i>	0.000	0.000
R. A. of <i>Rhinechis scalaris</i>	0.000	0.000
R. A. of <i>Natrix natrix</i>	0.035	0.041
R. A. of 'main preys' of <i>C. gallicus</i>	0.009	0.003
Relative total abundance of snakes	0.000	0.004
Snake species richness	0.001	0.000
Forest area	0.005	0.002

P = Level of significance

Appendix 7.1.3.12: Skewness of the explanatory variables.

Explanatory variables	Running procedure	Validation procedure
R. A. of short-toed eagle	1.297	1.124
R. A. of <i>Hemorrhois hippocrepis</i>	0.898	1.002
R. A. of <i>Malpolon monspesulanus</i>	0.233	0.211
R. A. of <i>Elaphe scalaris</i>	0.369	0.393
R. A. of <i>Natrix natrix</i>	0.257	0.183
R. A. of 'main preys' of short-toed eagle	0.933	0.950
Relative total abundance of snakes	0.453	0.433
Snake species richness	0.128	0.169
Density of forest patches	1.022	1.081

Appendix 7.1.3.13: Kurtosis of the explanatory variables.

Explanatory variables	Running procedure	Validation procedure
R. A. of short-toed eagle	3.703	2.882
R. A. of <i>Hemorrhois hippocrepis</i>	0.490	0.987
R. A. of <i>Malpolon monspesulanus</i>	1.596	1.661
R. A. of <i>Elaphe scalaris</i>	1.512	1.573
R. A. of <i>Natrix natrix</i>	-0.19	-0.336
R. A. of 'main preys' of short-toed eagle	1.560	1.879
Relative total abundance of snakes	-0.364	-0.180
Snake species richness	-0.684	-0.588
Density of forest patches	2.572	2.934

Appendix 7.1.4: VIF of explanatory variables:

Appendix 7.1.4.1: VIF of the whole set of explanatory variables.

Independent variables	Running procedure	Validation procedure
R. A. of <i>Hemorrhois hippocrepis</i>	28.571	26.316
R. A. of <i>Malpolon monspesulanus</i>	111.111	100.000
R. A. of <i>Rhinechis scalaris</i>	76.923	76.923
R. A. of <i>Natrix natrix</i>	4.082	4.098
R. A. of 'main preys' of short-toed eagle	500.000	500.000
Relative total abundance of snakes	13.889	12.821
Snake species richness	2.950	2.994
Forest area	2.096	2.000

Appendix 7.1.4.2: VIF of the explanatory variables to be included in models A and B, before removing collinearity.

Independent variables	Running procedure	Validation procedure
R. A. of <i>Hemorrhois hippocrepis</i>	3.185	2.857
R. A. of <i>Malpolon monspesulanus</i>	9.709	9.091
R. A. of <i>Rhinechis scalaris</i>	9.615	8.772
R. A. of <i>Natrix natrix</i>	4.082	4.098
Relative total abundance of snakes	12.821	11.905
Snake species richness	2.933	2.994
Forest area	2.079	1.976

Appendix 7.1.4.3: VIF of the explanatory variables to be included in model 1A.

Independent variables	Running procedure	Validation procedure
R. A. of <i>Hemorrhois hippocrepis</i>	3.165	2.857
R. A. of <i>Rhinechis scalaris</i>	4.975	4.630
R. A. of <i>Natrix natrix</i>	3.906	3.802
Relative total abundance of snakes	9.615	9.091
Snake species richness	2.933	2.907
Forest area	2.049	1.953

Appendix 7.1.4.4: VIF of the explanatory variables to be included in model 1B.

Independent variables	Running procedure	Validation procedure
R. A. of <i>Hemorrhois hippocrepis</i>	2.353	2.137
R. A. of <i>Rhinechis scalaris</i>	8.850	8.130
R. A. of <i>Natrix natrix</i>	1.996	2.132
R. A. of <i>Malpolon monspesulanus</i>	8.772	8.065
Snake species richness	2.725	2.833
Forest area	1.701	1.590

Appendix 7.1.4.5: VIF of the explanatory variables to be included in model 1C.

Independent variables	Running procedure	Validation procedure
R. A. of 'main preys' of short-toed eagle	5.208	4.695
Relative total abundance of snakes	6.803	6.667
Snake species richness	2.841	2.793
Forest area	1.901	1.773

Appendix 7.1.4.6: VIF of the explanatory variables to be included in “Additional model”.

Independent variables	Running procedure	Validation procedure
R. A. of <i>Hemorrhois hippocrepis</i>	3.155	2.849
R. A. of <i>Natrix natrix</i>	3.984	4.049
R. A. of <i>Malpolon monspesulanus</i>	5.000	4.831
Relative total abundance of snakes	9.709	9.434
Snake species richness	2.933	2.994
Forest area	1.946	1.838

7.2. Appendices for the path analysis procedure:

A description of the table headings is shown below:

SDE = Standardized direct effects.

SE = Standard errors of the regression coefficients.

CR = Critical ratios (Regression coefficient/standard error).

P = Significance level of the critical ratios.

Arrow = Proposed direct effect.

* = It indicates the proposed effect with lowest path coefficient.

Appendix 7.2.1. Model A

Appendix 7.2.1.1. Path coefficients of model 1A

Arrow	Running procedure				Validation procedure			
	SDE	SE	CR	P	SDE	SE	CR	P
1	-0.124	7.645	-2.926	0.003	-0.109	5.741	-3.154	0.002
2	-0.087	0.154	-1.959	0.050	-0.040	0.130	-0.942	0.346
3	0.122	6.772	0.929	0.353	0.228	6.233	1.977	0.048
5	0.077	2.922	2.179	0.029	0.133	2.651	4.295	<0.001
6	0.044	1.199	1.397	0.163	0.029	1.210	0.936	0.349
7*	-0.011	4.945	-0.185	0.853	-0.030	4.822	-0.559	0.576
8	0.097	0.013	3.234	0.001	0.004	0.014	0.130	0.896
9	0.215	0.024	5.716	<0.001	0.120	0.025	3.216	0.001
10	0.749	0.036	22.482	<0.001	0.723	0.036	21.042	<0.001
11	0.310	0.008	12.135	<0.001	0.356	0.008	14.621	<0.001
12	0.318	5.784	3.061	0.002	0.252	4.970	2.853	0.004

Appendix 7.2.1.2.: Path coefficients of model 2A

Arrow	Running procedure				Validation procedure			
	SDE	SE	CR	P	SDE	SE	CR	P
1	-0.191	3.707	-6.415	<0.001	-0.184	3.502	-6.497	<0.001
2	0.506	0.108	27.524	<0.001	0.460	0.112	23.621	<0.001
3	0.233	0.894	5.532	<0.001	0.275	0.848	6.949	<0.001
5	0.068	2.826	2.208	0.027	0.120	2.668	4.151	<0.001
6	0.059	0.794	2.296	0.022	0.048	0.812	1.981	0.028
8*	-0.033	0.018	-1.197	0.231	-0.057	0.018	-2.202	0.048
9	0.136	0.009	3.859	<0.001	0.109	0.009	3.126	0.002
10	0.406	0.046	21.592	<0.001	0.434	0.048	22.021	<0.001
11	0.532	0.009	25.433	<0.001	0.575	0.008	28.308	<0.001
12	0.360	1.833	10.199	<0.001	0.356	1.843	9.960	<0.001

Appendix 7.2.1.3.: Path coefficients of model 3A

Arrow	Running procedure				Validation procedure			
	SDE	SE	CR	P	SDE	SE	CR	P
1	-0.191	3.690	-6.456	<0.001	-0.189	3.487	-6.664	<0.001
2	0.506	0.107	27.753	<0.001	0.462	0.111	24.024	<0.001
3	0.233	0.893	5.542	<0.001	0.277	0.849	6.983	<0.001
5*	0.057	2.848	2.194	0.028	0.048	2.726	1.976	0.048
6	0.068	0.796	2.290	0.022	0.121	0.818	4.115	<0.001
9	0.121	0.009	3.655	<0.001	0.085	0.008	2.563	0.010
10	0.406	0.046	21.526	<0.001	0.432	0.048	21.843	<0.001
11	0.528	0.009	25.622	<0.001	0.569	0.008	28.559	<0.001
12	0.360	1.843	10.147	<0.001	0.357	1.860	9.918	<0.001

Appendix 7.2.1.4.: Path coefficients of model 4A

Arrow	Running procedure				Validation procedure			
	SDE	SE	CR	P	SDE	SE	CR	P
1	-0.185	3.776	-5.882	<0.001	-0.189	3.550	-6.378	<0.001
2	0.540	0.159	22.680	<0.001	0.475	0.170	17.981	<0.001
3	0.250	0.940	4.786	<0.001	0.284	0.967	5.480	<0.001
6*	0.004	0.931	0.151	0.880	0.007	0.940	0.267	0.790
9	0.546	0.012	19.104	<0.001	0.493	0.013	15.839	<0.001
10	0.397	0.065	18.244	<0.001	0.452	0.069	18.992	<0.001
11	0.559	0.009	26.680	<0.001	0.598	0.009	28.986	<0.001
12	0.409	2.198	10.085	<0.001	0.394	2.377	8.964	<0.001

Appendix 7.2.1.5.: Path coefficients of model 5A

Arrow	Running procedure				Validation procedure			
	SDE	SE	CR	P	SDE	SE	CR	P
1	-0.20	3.723	-6.233	<0.001	-0.204	3.540	-6.329	<0.001
2	0.789	0.130	51.333	<0.001	0.798	0.124	53.756	<0.001
3	0.556	0.451	16.894	<0.001	0.568	0.426	17.502	<0.001
9	0.860	0.012	35.618	<0.001	0.873	0.013	34.933	<0.001
10*	0.018	0.099	0.873	0.383	-0.005	0.112	-0.218	0.828
11	0.208	0.021	5.565	<0.001	0.184	0.025	4.428	<0.001
12	0.288	1.428	13.010	<0.001	0.283	1.469	12.711	<0.001

Appendix 7.2.1.6.: Path coefficients of model 6A

Arrow	Running procedure				Validation procedure			
	SDE	SE	CR	P	SDE	SE	CR	P
1	-0.20	3.722	-6.262	<0.001	-0.204	3.540	-6.326	<0.001
2	0.790	0.121	55.504	<0.001	0.798	0.117	56.931	<0.001
3	0.562	0.440	17.505	<0.001	0.567	0.424	17.572	<0.001
9	0.864	0.009	47.322	<0.001	0.872	0.009	48.414	<0.001
11*	0.192	0.018	5.803	<0.001	0.189	0.021	5.476	<0.001
12	0.287	1.422	13.043	<0.001	0.283	1.470	12.701	<0.001

Appendix 7.2.1.7.: Path coefficients of model 7

Arrow	Running procedure				Validation procedure			
	SDE	SE	CR	P	SDE	SE	CR	P
1*	-0.185	3.859	-5.758	<0.001	-0.193	3.687	-5.900	<0.001
2	0.778	0.128	53.182	<0.001	0.791	0.121	55.979	<0.001
3	0.573	0.433	18.255	<0.001	0.577	0.420	17.986	<0.001
9	0.873	0.007	67.704	<0.001	0.882	0.007	71.913	<0.001
12	0.283	1.521	12.443	<0.001	0.277	1.569	12.042	<0.001

Appendix 7.2.1.8.: Path coefficients of model 8A

Arrow	Running procedure				Validation procedure			
	SDE	SE	CR	P	SDE	SE	CR	P
2	0.784	0.129	53.621	<0.001	0.796	0.122	56.377	<0.001
3	0.437	0.286	20.924	<0.001	0.430	0.266	21.030	<0.001
9	0.872	0.007	67.946	<0.001	0.882	0.007	72.067	<0.001
12*	0.308	1.505	13.574	<0.001	0.304	1.548	13.277	<0.001

Appendix 7.2.2. Models 1 to 8 B

Appendix 7.2.2.1.: Path coefficients of model 1B

Arrow	Running procedure				Validation procedure			
	SDE	SE	CR	P	SDE	SE	CR	P
1	-0.152	4.490	-6.066	<0.001	-0.156	3.887	-6.634	<0.001
2	-0.089	0.148	-2.093	0.036	-0.043	0.129	-1.012	0.312
4	-0.035	3.916	-0.723	0.469	-0.090	3.738	-1.959	0.050
5	0.028	3.969	0.580	0.431	0.031	4.009	0.653	0.513
6*	0.025	1.187	0.787	0.562	-0.013	1.214	-0.404	0.686
7	-0.033	3.806	-0.751	0.453	-0.066	3.772	-1.541	0.123
8	0.097	0.013	3.306	<0.001	0.004	0.014	0.148	0.882
9	0.215	0.023	5.915	<0.001	0.121	0.024	3.276	0.001
10	0.751	0.036	22.567	<0.001	0.726	0.036	21.049	<0.001
11	0.310	0.008	12.260	<0.001	0.356	0.008	14.635	<0.001
12	0.425	1.580	14.876	<0.001	0.449	1.596	15.686	<0.001

Appendix 7.2.2.2.: Path coefficients of model 2B

Arrow	Running procedure				Validation procedure			
	SDE	SE	CR	P	SDE	SE	CR	P
1	-0.154	4.624	-5.786	<0.001	-0.149	3.928	-6.067	<0.001
2	0.131	0.159	3.392	<0.001	0.209	0.136	5.533	<0.001
4	-0.085	4.151	-1.504	0.133	-0.155	4.128	-2.953	0.003
5*	-0.084	6.246	-1.241	0.215	-0.073	5.641	-1.168	0.243
7	-0.109	2.462	-3.066	0.002	-0.124	2.453	-3.559	<0.001
8	0.108	0.013	3.707	<0.001	0.014	0.014	0.483	0.429
9	0.262	0.026	5.653	<0.001	0.159	0.029	3.154	0.002
10	0.310	0.038	10.213	<0.001	0.267	0.038	8.469	<0.001
11	0.195	0.008	7.465	<0.001	0.233	0.009	9.128	<0.001
12	0.386	1.457	13.975	<0.001	0.410	1.492	14.686	<0.001

Appendix 7.2.2.3.: Path coefficients of model 3B

Arrow	Running procedure				Validation procedure			
	SDE	SE	CR	P	SDE	SE	CR	P
1	-0.169	4.410	-6.027	<0.001	-0.168	3.901	-6.159	<0.001
2	0.168	1.935	7.874	<0.001	0.120	1.660	8.189	<0.001
4	0.436	0.607	16.562	<0.001	0.379	0.623	13.495	<0.001
7	-0.163	2.218	-5.069	<0.001	-0.200	2.003	-6.494	<0.001
8*	-0.017	2.054	-1.065	0.945	-0.032	2.178	-2.065	0.910
9	0.803	0.016	47.686	<0.001	0.873	0.017	49.371	<0.001
10	-0.241	0.118	-5.294	<0.001	-0.271	0.111	-5.989	<0.001
11	-0.089	2.090	-2.091	0.231	-0.097	2.076	-3.013	0.048
12	0.279	1.207	11.535	<0.001	0.313	1.209	12.162	<0.001

Appendix 7.2.2.4.: Path coefficients of model 4B

Arrow	Running procedure				Validation procedure			
	SDE	SE	CR	P	SDE	SE	CR	P
1	-0.16	4.243	-6.007	<0.001	-0.160	3.711	-6.268	<0.001
2	0.457	0.187	19.655	<0.001	0.405	0.173	17.111	<0.001
4	0.440	0.595	17.063	<0.001	0.378	0.610	13.752	<0.001
7	-0.12	1.812	-4.315	<0.001	-0.145	1.553	-5.660	<0.001
9	0.932	0.013	58.936	<0.001	0.937	0.015	55.398	<0.001
10	-0.36	0.054	-17.787	<0.001	-0.453	0.049	-22.376	<0.001
11*	-0.07	0.008	-2.723	<0.001	-0.119	0.008	-4.785	<0.001
12	0.256	1.228	10.838	<0.001	0.289	1.235	11.329	<0.001

Appendix 7.2.2.5.: Path coefficients of model 5B

Arrow	Running procedure				Validation procedure			
	SDE	SE	CR	P	SDE	SE	CR	P
1	-0.159	4.261	-5.937	<0.001	-0.155	3.745	-6.105	<0.001
2	0.469	0.186	20.226	<0.001	0.420	0.174	17.313	<0.001
4	0.438	0.596	17.233	<0.001	0.372	0.611	13.896	<0.001
7*	-0.123	1.840	-4.357	<0.001	-0.143	1.546	-5.597	<0.001
9	0.930	0.014	57.625	<0.001	0.936	0.016	51.898	<0.001
10	-0.353	0.054	-17.342	<0.001	-0.449	0.048	-22.038	<0.001
12	0.257	1.221	11.024	<0.001	0.295	1.216	11.870	<0.001

Appendix 7.2.2.6.: Path coefficients of model 6B

Arrow	Running procedure				Validation procedure			
	SDE	SE	CR	P	SDE	SE	CR	P
1	-0.17	3.790	-5.223	<0.001	-0.169	3.566	-5.066	<0.001
2	0.767	0.133	50.166	<0.001	0.777	0.126	52.873	<0.001
4	0.565	0.764	17.279	<0.001	0.561	0.760	16.618	<0.001
9	0.888	0.008	65.383	<0.001	0.901	0.007	68.789	<0.001
10*	-0.06	0.082	-3.626	<0.001	-0.087	0.084	-5.044	<0.001
12	0.161	1.526	6.527	<0.001	0.161	1.548	6.403	<0.001

Appendix 7.2.2.7.: Path coefficients of model 7B

Arrow	Running procedure				Validation procedure			
	SDE	SE	CR	P	SDE	SE	CR	P
1*	-0.163	3.939	-4.770	<0.001	-0.161	3.765	-4.587	<0.001
2	0.778	0.128	52.675	<0.001	0.791	0.122	55.576	<0.001
4	0.562	0.813	16.492	<0.001	0.562	0.831	15.743	<0.001
9	0.883	0.007	69.540	<0.001	0.895	0.007	73.338	<0.001
12	0.189	1.633	7.526	<0.001	0.188	1.712	7.227	<0.001

Appendix 7.2.2.8.: Path coefficients of model 8B

Arrow	Running procedure				Validation procedure			
	SDE	SE	CR	P	SDE	SE	CR	P
2	0.789	0.128	53.878	<0.001	0.801	0.121	56.625	<0.001
4	0.433	0.508	20.299	<0.001	0.429	0.502	19.860	<0.001
9	0.878	0.007	68.877	<0.001	0.890	0.007	72.730	<0.001
12*	0.213	0.493	9.035	<0.001	0.212	1.552	8.741	<0.001

Appendix 7.2.3.: Model 1 C

Appendix 7.2.3.1.: Path coefficients of model 1C

Arrow	Running procedure				Validation procedure			
	SDE	SE	CR	P	SDE	SE	CR	P
1	-0.20	3.732	-6.583	<0.001	-0.188	3.520	-6.593	<0.001
2	0.552	0.103	31.824	<0.001	0.523	0.104	29.331	<0.001
3	0.260	0.792	6.903	<0.001	0.287	0.747	8.131	<0.001
4-6*	0.008	5.687	0.488	0.626	0.011	7.724	-0.748	0.454
8	-0.07	0.016	-3.129	0.002	-0.110	0.017	-4.819	<0.001
9	0.166	0.007	6.016	<0.001	0.139	0.006	5.101	<0.001
10	0.341	0.041	19.613	<0.001	0.356	0.042	19.856	<0.001
11	0.516	0.008	26.234	<0.001	0.545	0.008	28.506	<0.001
12	0.355	1.455	12.016	<0.001	0.366	1.429	12.630	<0.001

Appendix 7.2.4. “Additional model”

Appendix 7.2.4.1.: Path coefficients of model 1

Arrow	Running procedure				Validation procedure			
	SDE	SE	CR	P	SDE	SE	CR	P
1	-0.114	8.1	-4.21	0.024	-0.118	7.9	-2.34	0.021
2	0.284	0.300	8.495	<0.001	0.262	0.226	7.888	<0.001
3	0.084	7.226	0.878	0.380	0.091	8.272	1.003	0.316
4	0.070	2.992	0.989	0.322	0.014	3.132	0.190	0.850
6*	0.018	1.402	0.575	0.630	0.004	1.490	0.091	0.927
7	-0.023	3.218	-0.502	0.616	-0.065	3.193	-1.414	0.157
8	-0.310	0.010	-6.506	<0.001	-0.288	0.010	-6.844	<0.001
9	0.301	0.134	2.935	0.003	0.288	0.145	3.290	<0.001
10	0.250	0.010	6.448	<0.001	0.291	0.011	7.999	<0.001
11	0.304	0.079	8.224	<0.001	0.289	0.077	8.190	<0.001
12	0.310	4.889	3.540	<0.001	0.314	5.405	3.222	0.001

The path coefficient of the proposed effect 6 had a confidence interval of -0.040 to 0.051 in the running procedure, and -0.053 to 0.037 in the validation procedure, using a confidence level of 99%. A new model was re-specified deleting the proposed effect 6.

Appendix 7.2.4.2.: Path coefficients of model 2

Arrow	Running procedure				Validation procedure			
	SDE	SE	CR	P	SDE	SE	CR	P
1	-0.144	3.805	-5.805	<0.001	-0.142	4.416	-5.182	<0.001
2	0.270	0.559	8.742	<0.001	0.412	1.854	8.246	<0.001
3	0.426	0.213	3.788	<0.001	0.368	2.100	3.456	<0.001
4	0.025	2.142	0.270	0.787	0.117	2.186	1.269	0.205
7*	0.017	1.290	0.182	0.811	0.012	2.050	0.092	0.928
8	-0.068	3.043	-1.524	0.127	-0.040	3.325	-0.863	0.388
9	0.680	0.037	37.580	<0.001	0.628	0.016	37.871	<0.001
10	-0.068	3.043	-1.524	0.137	-0.081	2.741	-1.792	0.241
11	-0.266	0.111	-5.973	<0.001	-0.238	0.118	-5.263	<0.001
12	0.354	1.395	12.400	<0.001	0.313	1.368	11.787	<0.001

The path coefficient of the proposed effect 7 had a confidence interval of -0.036 to 0.045 in the running procedure, and -0.056 to 0.033 in the validation procedure, using a confidence level of 99%. A new model was re-specified deleting the proposed effect 7.

Appendix 7.2.4.3.: Path coefficients of model 3

Arrow	Running procedure				Validation procedure			
	SDE	SE	CR	P	SDE	SE	CR	P
1	-0.218	3.745	-6.730	<0.001	-0.213	3.563	-6.552	<0.001
2	0.802	0.292	23.260	<0.001	0.808	0.312	21.712	<0.001
3	0.448	0.675	9.079	<0.001	0.498	0.704	9.262	<0.001
4	0.152	1.343	3.010	0.003	0.095	1.428	1.706	0.088
8*	-0.042	0.024	-0.413	0.680	-0.030	0.026	-0.264	0.792
9	0.862	0.013	33.492	<0.001	0.013	0.013	33.987	<0.001
10	0.206	0.021	5.455	<0.001	0.181	0.023	4.782	<0.001
11	0.009	0.101	0.398	0.690	-0.013	0.112	-0.566	0.571
12	0.248	1.668	9.629	<0.001	0.258	1.768	9.622	<0.001

The path coefficient of the proposed effect 8 had a confidence interval of -0.093 to 0.038 in the running procedure, and -0.078 to 0.014 in the validation procedure,

using a confidence level of 99%. A new model was re-specified deleting the proposed effect 8.

Appendix 7.2.4.4.: Path coefficients of model 4

Arrow	Running procedure				Validation procedure			
	SDE	SE	CR	P	SDE	SE	CR	P
1	-0.21	3.581	-6.519	<0.001	-0.218	3.778	-6.671	<0.001
2	0.798	0.118	56.417	<0.001	0.789	0.123	54.228	<0.001
3	0.498	0.693	9.408	<0.001	0.448	0.662	9.259	<0.001
4	0.094	1.428	1.705	0.088	0.152	1.344	3.009	0.003
9	0.873	0.008	56.503	<0.001	0.858	0.008	54.767	<0.001
10	0.184	0.017	6.392	<0.001	0.207	0.015	7.522	<0.001
11*	0.005	0.087	-0.265	0.791	0.019	0.081	1.116	0.268
12	0.258	1.762	9.658	<0.001	0.249	1.658	9.687	<0.001

The path coefficient of the proposed effect 11 had a confidence interval of -0.065 to 0.054 in the running procedure, and -0.021 to 0.128 in the validation procedure, using a confidence level of 99%. A new model was re-specified deleting the proposed effect 11.

Appendix 7.2.4.5.: Path coefficients of model 5B

Arrow	Running procedure				Validation procedure			
	SDE	SE	CR	P	SDE	SE	CR	P
1	-0.213	3.582	-6.517	<0.001	-0.218	3.774	-6.679	<0.001
2	0.798	0.116	57.499	<0.001	0.790	0.120	55.709	<0.001
3	0.498	0.688	9.475	<0.001	0.449	0.680	9.017	<0.001
4*	0.094	1.427	1.707	0.088	0.154	1.349	2.997	0.003
9	0.872	0.007	60.454	<0.001	0.862	0.008	59.116	<0.001
10	0.189	0.017	6.676	<0.001	0.191	0.015	6.955	<0.001
12	0.258	1.764	9.645	<0.001	0.249	1.650	9.735	<0.001

The path coefficient of the proposed effect 4 had a confidence interval of -0.033 to 0.145 in the running procedure, and 0.088 to 0.204 in the validation procedure, using

a confidence level of 99%. A new model was re-specified deleting the proposed effect 4.

Appendix 7.2.4.6.: Path coefficients of model 6

Arrow	Running procedure				Validation procedure			
	SDE	SE	CR	P	SDE	SE	CR	P
1*	-0.20	3.721	-6.264	<0.001	-0.204	3.539	-6.327	<0.001
2	0.790	0.120	55.722	<0.001	0.798	0.116	57.503	<0.001
3	0.562	0.437	17.625	<0.001	0.567	0.423	17.612	<0.001
9	0.864	0.008	59.091	<0.001	0.872	0.007	60.437	<0.001
10	0.192	0.015	7.012	<0.001	0.189	0.017	6.699	<0.001
12	0.287	1.422	13.045	<0.001	0.283	1.470	12.702	<0.001

The path coefficient of the proposed effect 1 had a confidence interval of 0.129 to 0.276 in the running procedure, and 0.133 to 0.278 in the validation procedure, using a confidence level of 99%. A new model was re-specified deleting the proposed effect 1.

Appendix 7.2.4.7.: Path coefficients of model 7

Arrow	Running procedure				Validation procedure			
	SDE	SE	CR	P	SDE	SE	CR	P
2	0.797	0.121	56.290	<0.001	0.804	0.117	58.056	<0.001
3	0.411	0.274	20.254	<0.001	0.411	0.260	20.487	<0.001
9	0.863	0.008	59.079	<0.001	0.872	0.007	60.398	<0.001
10*	0.184	0.015	6.597	<0.001	0.181	0.017	6.316	<0.001
12	0.285	1.431	12.705	<0.001	0.282	1.479	12.450	<0.001

Observing the squared multiple correlation of the relative abundance of short-toed eagle, in model 7, can be observed that having eliminated the proposed effect 1 improved the squared multiple correlation of the relative abundance of short-toed eagle from 0.277 to 0.287 in the running procedure, and from 0.276 to 0.285 in the validation procedure. In other words, snake species richness had no significant effect on the relative abundance of short-toed eagle. Path coefficient of the proposed effect 10 had a confidence interval of 0.126 to 0.231 in the running procedure, and 0.133

to 0.235 in the validation procedure, using a confidence level of 99%. A new model was re-specified deleting the proposed effect 10.

Appendix 7.2.4.8.: Path coefficients of model 8

Arrow	Running procedure				Validation procedure			
	SDE	SE	CR	P	SDE	SE	CR	P
2	0.784	0.129	53.621	<0.001	0.796	0.122	56.377	<0.001
3	0.437	0.286	20.924	<0.001	0.430	0.266	21.030	<0.001
9	0.872	0.007	67.946	<0.001	0.882	0.007	72.067	<0.001
12	0.308	1.505	13.574	<0.001	0.304	1.548	13.277	<0.001

The squared multiple correlation of snake species richness in model 7A is 0.034 in the running procedure and 0.033 in the validation procedure, which indicates that around 3% of the variability of snake species richness was accounted for by forest area. In other words, forest area had no significant effect on snake species richness.

The final “Additional model” is the same 8A model.

Appendix 7.3. Pictures and average sizes of the 13 snake species of Spain



Figure 8 - 1: *Hemorrhois hippocrepis*
(100 cm)



Figure 8 - 2: *Hierophis viridiflavus*
(100 cm)



Figure 8 - 3: *Coronella austriaca*
(50 cm)



Figure 8 - 4: *Coronella girondica*
(50 cm)



Figure 8 - 5: *Macroprotodon brevis*
(30 cm)



Figure 8 - 6: *Zamenis longissimus*
(110 cm)



Figure 8 - 7: *Rhinechis scalaris*
(100 cm)



Figure 8 - 8: *Malpolon monspesulanus*
(120 cm)



Figure 8 - 9: *Natrix maura*
(40 cm)



Figure 8 - 10: *Natrix natrix*
(100 cm)



Figure 8 - 11: *Vipera aspis*
(60 cm)



Figure 8 - 12: *Vipera latastei*
(55 cm)



Figure 8 - 13: *Vipera seoanei*
(55 cm)

Image source:

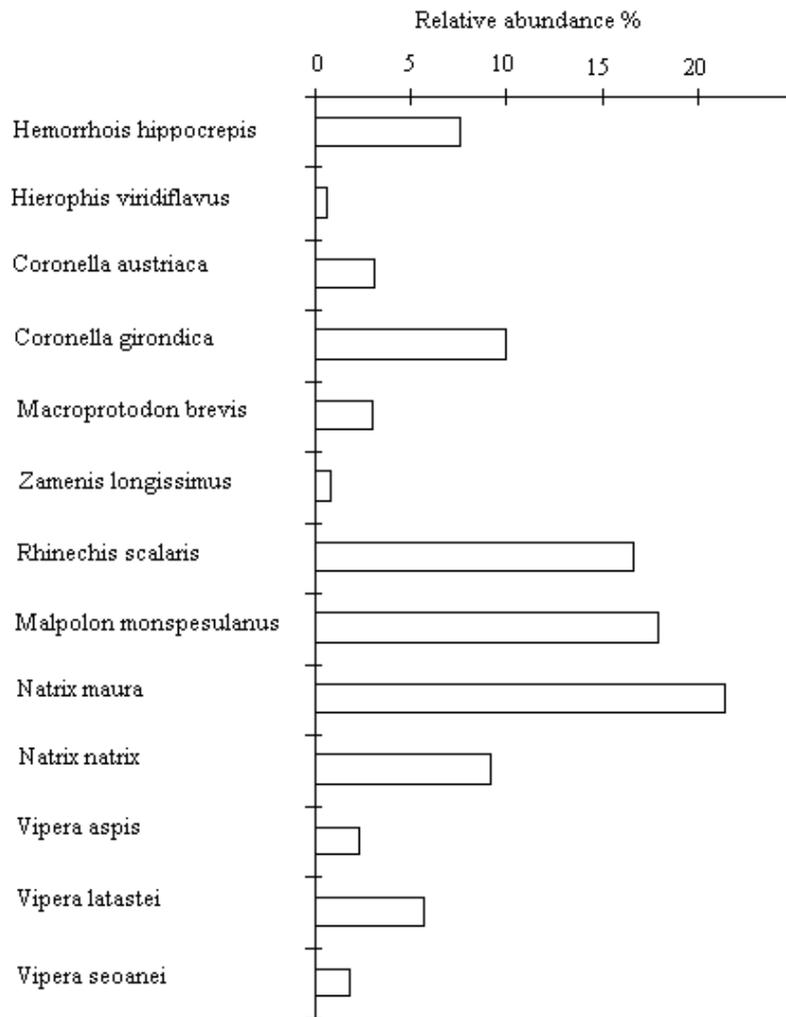
http://www.mma.es/secciones/biodiversidad/inventarios/inb/anfibios_reptiles

Average size source:

Virtual encyclopedia of Spanish vertebrates: <http://www.vertebradosibericos.org>

Ministry of Environment of Spain: <http://www.mma.es>.

Appendix 7.4. Relative abundances of the 13 snake species of Spain, estimated using kernel density.



Appendix 7.5. Additional analysis:

Arrow	Running procedure				Validation procedure			
	SDE	SE	CR	P	SDE	SE	CR	P
9!	0.702	0.000	43.325	<0.001	0.711	0.000	44.757	<0.001

The relative abundances of all the snakes except *M. monspesulanus* were added up. Arrow 9! is the possible effect of the relative total abundance of snakes, except *M. monspesulanus*, on the relative abundance of *M. monspesulanus*.