

# **An Extinction Analysis for Lemurs using Random Forests**

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**Appendix: Database of Lemur Traits**

## **Abstract**

In order for conservation funds to be used both effectively and efficiently, there is often the need to prioritise species most in need of attention. I used a decision tree-based method to better understand the role that different lemur characteristics play in affecting the status of a species and then used the analysis to attempt to designate the status of a group of lemurs lacking a current threat status. The analysis suggests that external environmental conditions are the best predictors of extinction risk in lemurs, with a smaller role from slow life history traits, especially the length of gestation. I argue, however, that the results must be considered in light of the limitations of a narrow range study.

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## Introduction

Lemurs are a diverse group with varied characteristics and contain many threatened species (Richard & Dewar), making them an interesting case for extinction analyses. With limited resources, conservationists must often make difficult decisions about where their time, effort and resources would be best spent. Although not providing all of the answers, extinction analyses may be of practical help in focusing awareness on to particular species or regions that are in need of attention. Thus far the prioritisation of lemurs for conservation has mainly dealt with levels of relatedness between species and evolutionary differences (Lehman, 2005), promoting the idea that distantly related taxa should receive more attention. This is a feature which was integrated into the last lemur action plan in 1992 (Mittermeier, 1992).

Extinction analyses can be helpful in highlighting areas of concern relating to animal conservation, specifically as a means of:

1. Identifying intrinsic life history and ecological traits present among threatened species, as well as the most serious extrinsic environmental threats and human pressures they face.
2. Identifying species that at present are unthreatened, but which possess biological characteristics that predispose them to high risks of extinction. They can also draw notice to species that at present are threatened, but which are more similar in habit and life history to unthreatened species.
3. Providing species currently listed as data deficient or not evaluated with a predicted threat class.

The latter two points highlight one of the primary advantages of extinction analyses, in that they can pre-empt species becoming more threatened and highlight species currently without a threat status that are likely to be at a high risk of extinction. As Cardillo and Meijaard (2012) discussed, these types of analyses are best suited to proactive policies, for example where future potential threats are considered and species receive attention before they start to decline. They clearly have few uses in highly immediate reactive conservation.

My objective for this project was to discover the biological and ecological characteristics that threatened lemurs share so as to learn more about which variables most affect their survival. To do this I ran an extinction analyses for the lemurs, using Random Forest (Breiman, 2001), which is a classification algorithm, based upon a decision tree method. In addition the analysis was used to predict the status of a group of lemurs currently classified as data deficient or not evaluated

The two most common types of extinction analyses found in the literature are the phylogenetic comparative methods (PCM) and decision trees (DT). Although the pros and cons of both techniques have been discussed (Bielby et al, 2010), PCM appear to currently be of greater popularity, although DT seem to be an emerging new discipline in regards to biological and ecological studies (Sodhi et al, 2010), (Murray et al, 2010).

PCM consider the taxonomic relationships between two species in order to account for the non-independence between these species based upon traits that they share by common ancestry. Multiple regressions analyses (Wolf et al, 1998) or minimum adequate models are then run on this transformed data (Isaac & Cowlshaw, 2004). Bielby et al, 2010 have shown that PCM can have a high predictive value, when taxonomy is accounted for and that DT can in fact be unstable when only marginally different data is used.

DT takes a collection of cases, each with a set of variables and an assigned class; and passes them down through various branches that continually split and partition them into more homogenous or 'purer' nodes, based upon these variables. These groups progressively become more alike until the cases can no longer be split and the tree is fully grown, with each terminal node representing a class, each with a set of unifying variables. Clearly, decision trees will not always be capable of splitting cases into pure classes and thus there will be misclassifications (Quinlan, 1990). Sullivan et al. (2006) argue that DT methods are more easily interpretable to conservation practitioners and can be used to identify non-linear relationships, which may be missed by PCM. Jones et al (2006) contend that due to the fact that PCM use models derived through correlation, they have reduced predictive

value when there are many variables in use, owing to the many interactions between variables.

### **Random Forests (RF)**

Random Forests (Breiman, 2001) works by means of the creation of a group or 'forest' of decision trees, each using slightly different sets of data. Individual trees in the forest are grown via a resampling method known as bootstrap aggregation, whereby a sample of size equal to the number of cases is taken at random with replacement. In this sample, cases will appear more than once, with on average, 36% of cases not being present in the sample. These are known as out of bag data. Cases in the bootstrap sample are then used to create a tree whereby each node can only be split based upon a randomly chosen subset of variables, usually the square root of the number of variables. This method is then repeated to create a forest of trees. All cases in the out of bag data are then placed through their particular trees and a case is assigned to a class by means of majority 'vote', meaning the class where that case appears the most times out of all the classes. From this a proximity matrix is created, which displays the proportion of times a case appears in the same terminal node with another case and it can be used as a means to help replace missing data. Due to the fact that many different trees are created in the forest and that class assignment is based upon majority vote, this can smooth out inconsistencies with particular trees and overall, give a picture that is more reliable and replicable (Fielding, 2007) as well as less unstable compared with single decision trees (Bielby, 2010).

Two major methods can be used for assessing variable importance in an RF analysis. Mean decrease in accuracy is a permutation method, whereby, for a specific tree the values for one variable within the out of bag data are randomly permuted and then put through the tree. The measure is the increase in classification error compared with the original non-permuted data, normalised by the standard error (Kuhn et al, 2008). Clearly, for variables of importance, taking values away from their corresponding cases will increase classification error and therefore, higher scores relate to more important variables. Mean decrease in gini measure the increase in child node purity when a particular variable is used to split a parent node (Calle & Urrea, 2010). Variables of importance will create groups of data that are much

more homogenous and/or appear more often within a tree. This measure calculates the sum of all the increases in purity across all trees in the forest. There is some debate as to which measure is the better to use, with some in favour of accuracy (Nicodemus, 2011), arguing that mean decrease in gini leads to stable but incorrect placing of variables in the hierarchy of importance; and others arguing that gini is the better of the two (Calle & Urrea, 2010), suggesting that mean decrease in accuracy is unstable to small perturbations.

As Cutler et al (2007) discuss, RF analyses whilst being used in other scientific disciplines have been rarely used for ecological studies, despite the many advantages, such as classification accuracy and the ability to identify traits of importance. Davidson et al (2009) ran an extinction analysis on a mammal database and were able to identify risk in a number of data deficient species. Davidson et al (2011) also ran a study using RF to identify threats to marine mammals and areas of greatest risk.



## Method

### Database

The database of lemur life history, ecological and geographical traits was constructed using the 'Wilson and Reeder' 2005 version of the 'panTHERIA' database (Jones et al, 2009) of mammalian characteristics. This was updated with the names of the missing species and subspecies of lemur according to the taxonomy of the 'Lemurs of Madagascar: Third Edition' (Mittermeier et al, 2010). The database was then completed using a variety of scientific resources. Where more than one value was present in the literature for a particular trait, an average was taken for that species. As a result of the significant quantity of missing trait values, only the following were used in the RF analyses: adult body mass, adult head-and-body length, neonatal body mass, weaning age, age at sexual maturity, age at first birth, gestation length, inter-birth interval, litter size, litters per year, population group size (individuals living in close proximity), social group size (living in close proximity with social interactions), home range (individual or group), population density, activity cycle (period of time when active), diet breadth (number of food categories a species consumes), habitat breadth (number of types of habitat a species inhabits), trophic level, geographical range and human population density (population density within the species' range). For an extensive description of all traits see Jones et al, 2009.

### Analyses

Two main RF analyses were run; in both cases, 1000 trees were grown in the forest and the number of traits randomly selected for each node was 4. The first analysis involved only IUCN red list threatened and unthreatened species and subspecies, excluding *Microcebus sambiranensis*, *Phaner electromontis*, *Phaner furcifer* and *Phaner parienti*, due to a lack of trait data for these species. The individuals were classified into two groups based upon the level of threat, threatened for those with a status of vulnerable, endangered and critically endangered; and unthreatened for those classed as least concern and near threatened. This analysis was performed as a means to test which variables were the most important for classification and thus the best indicators of extinction. The red list categories were grouped

into two, due to the subjectivity of the status boundaries, particularly the threatened categories and in order to make a clearer distinction between which variables marked out the threatened from the unthreatened. Missing trait values were derived through a method of imputation based upon the RF analysis (Liaw & Wiener, 2012). This process first fills in gaps by simply taking the variable medians of the non-missing values for continuous variables and the most frequent values for categorical variables. An RF analysis is then performed on this completed dataset in order to generate a proximity matrix, which is then used to update the missing values. This is done for continuous variables by taking a weighted mean of the non-missing values, where the weights are the proximities of the missing values to each of the non-missing. For categorical variables an average of the proximities to the missing value is taken for each category, with the missing value given the category with the highest average. This process was put through five iterations to improve the accuracy of the values. Sodhi et al (2010) used an imputation method in conjunction with an RF analysis in their study

I also ran a series of correlations to explore the relationship between adult body mass, which forms the most comprehensive dataset (fewest missing values) and the most important life history traits as flagged up by the RF analysis of trait importance. Social group size was also correlated with population group size for similar reasons. This allows us to consider the robustness of the conclusions regarding trait importance derived from the investigation.

The second main analysis was a predictive study, which used a similar RF to the one generated in the previous investigation of trait importance to assess the vulnerability to extinction of a group of 12 lemur species and subspecies that are listed as data deficient or have not been evaluated. The number of traits used to create the RF was smaller due to missing data and excluded neonatal body mass, weaning age, age at sexual maturity, age at first birth, inter-birth interval and population group size. The 12 cases put through the RF have the most comprehensive datasets, with the remainder lemurs without a threat status, lacking significant trait values for most variables, thus making questionable any conclusions regarding susceptibility to becoming extinct. Since no set of decision trees can be generated

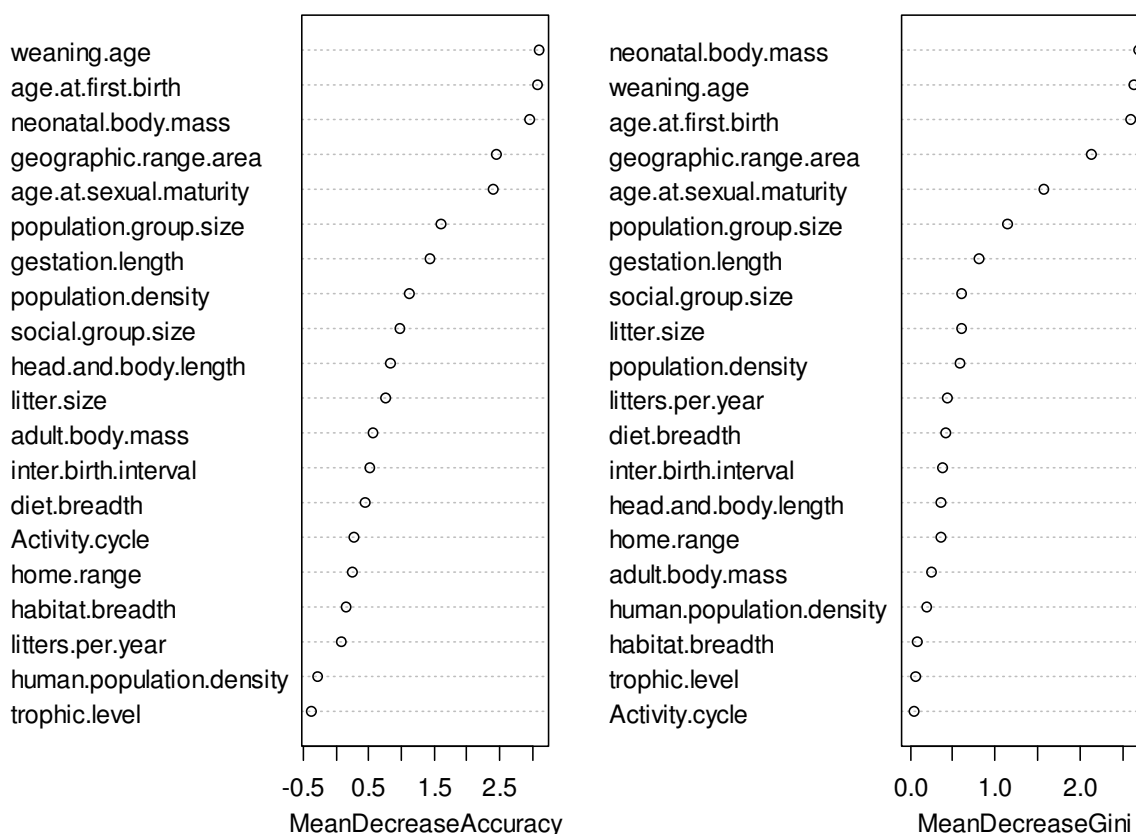
from classless data, a proximity matrix cannot be created for imputation and therefore, the formation of missing values for the 12 cases was performed by taking the medians for continuous variables and the most common values for categorical variables. Despite the limitations of this study, it demonstrates the value of RF in investigations of class prediction as well as some indication of the level of danger of extinction for the lemurs used in the analysis.

All decision tree analyses were carried out using the R version 2.15.1 (R Core Team, 2012) statistical programme with the randomForest 4.6-6 add-on package (Liaw & Wiener, 2002).

## Results

### Trait Importance

Since the method of data imputation and the random forest algorithm both have an inbuilt randomness, the results from analyses using the same dataset are always marginally different. Due to the fact that there are no clear guidelines regarding the interpretation of the two variable importance measures (Kuhn et al, 2008) and also, which index is likely to give more accurate outcomes, comparing and validating between the two may give a clearer picture. What is certain is that values  $<0$  for mean decrease in accuracy are not significant. Shih (2011) suggests, based upon the work of Dr Carolin Strobl, that traits which have a value that is less than the absolute value of the highest negative number are also insignificant. The results from the analysis of trait importance can be seen in the plots in Figure 1. These give an example of the values encountered.



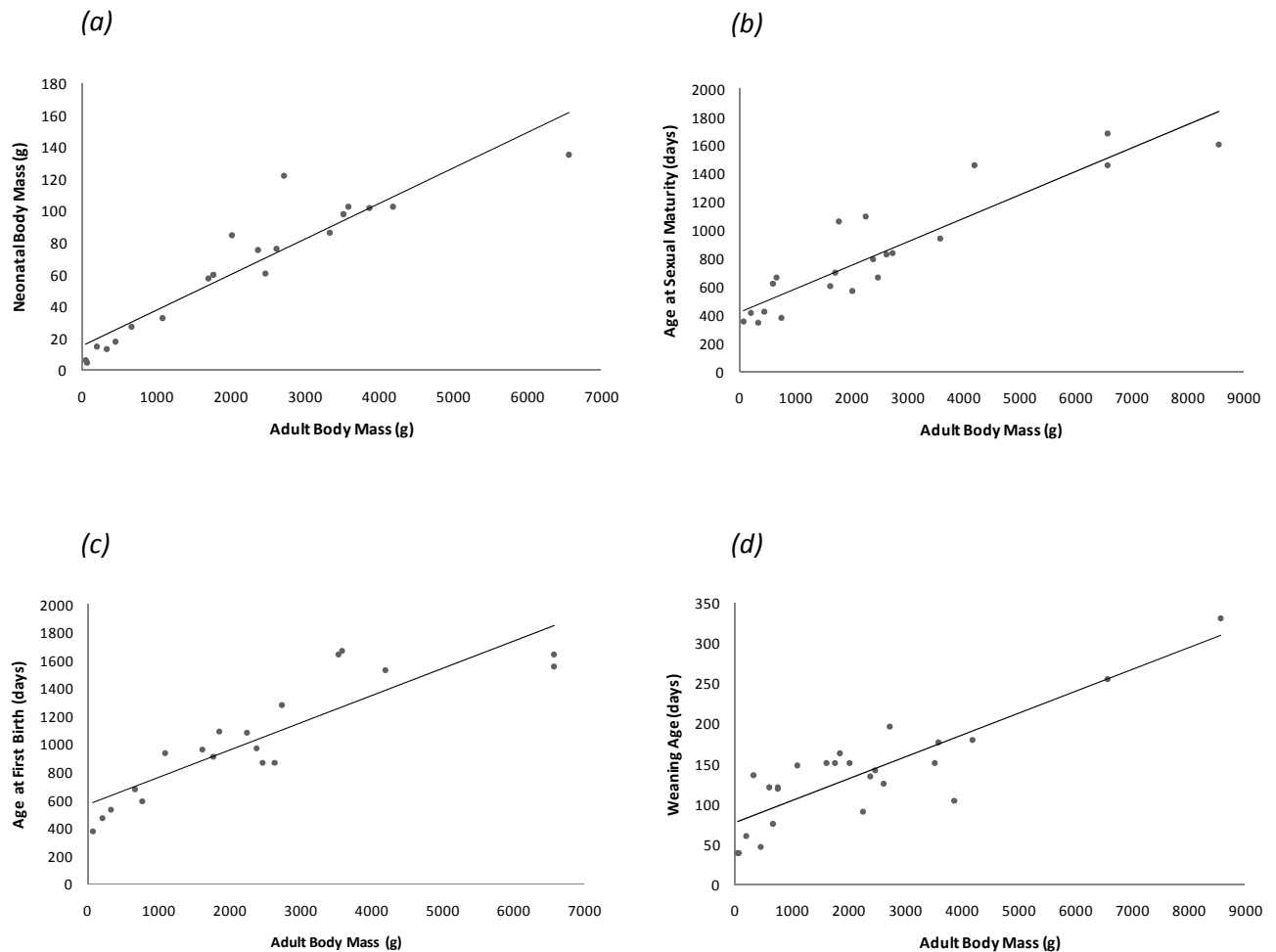
**Figure 1.** Plots of traits in descending order of importance, using mean decrease in accuracy and mean decrease in gini scores

Traits one to five in the hierarchy (age at first birth, weaning age, neonatal body mass, geographic range, age at sexual maturity) consistently appear preeminent throughout several repetitions of the RF analysis, using the same dataset, although their relative positions in the top five does vary. By taking averages, we can get an indication of the direction the variables take regarding threatened and unthreatened species. Threatened species on average are weaned (174 days, n=12), sexually mature (1011 days, n=11) and have their first births (1320 days, n=9) later than the unthreatened. In addition, threatened species have larger neonatal body masses (89g, n=10). Interestingly, unthreatened species sexually mature  $\approx$  1 year earlier (636 days, n=8) than threatened species and will have their first birth on average  $\approx$  6 months after maturation (815 days, n=8), whereas, threatened species give birth just over 10 months after reaching maturity. unthreatened species are also weaned only 2.3 months earlier (102 days, n=10) than threatened species. Threatened species also have smaller geographic ranges (14,968km<sup>2</sup>, n=9) than non-threatened (81,486km<sup>2</sup>, n=11).

Population group size and gestation length always appear in positions six and seven on the mean decrease in gini scale and frequently in these same positions according to mean decrease in accuracy. Thus, their importance as classifiers seems possible. Threatened species on average have larger population group sizes (7.4, n=11), albeit only slightly greater (unthreatened population group size=4.2, n=10) and slightly longer gestation lengths (135 days, n=23) than unthreatened (108 days, n=11). The remaining traits that follow in the list appear in diverse arrangements on both trait significance scales through separate repetitions. Their importance as characteristics that indicate high extinction risk is likely to be small if any.

### **Trait Correlations**

The series of correlations comparing adult body mass with traits two to seven in the importance hierarchy revealed this feature to strongly correlate positively with neonatal body mass ( $r^2=0.867$ , n=20), age at sexual maturity ( $r^2=0.833$ , n=21), and to a slightly lesser extent with age at first birth ( $r^2=0.768$ , n=19) and weaning age ( $r^2=0.735$ , n=25). See Figure 2.



**Figure 2.** A set of correlations between Adult body mass and (a) Neonatal body mass, (b) Age at Sexual Maturity, (c) Age at first birth and (d) Weaning age

These results put into serious doubt the significance of the traits as important indicators of species being threatened. It seems probable that due to the comprehensiveness of the adult body mass dataset, their high position in the table is an artefact of missing values, which has led to the variables being good classifiers of the data. Gestation length does not correlate well with body mass ( $r^2=0.275$ ,  $n=40$ ) and this dataset is more complete than those for the previous four traits, suggesting that this may be a relevant variable. Population group size, although correlating poorly with body mass, does strongly correlate positively with social group size ( $r^2=0.879$ ,  $n=21$ ), when the values for *Eulemur flavifrons* have been removed. It is likely that the figures for this species represent an extreme case considering that its population group size is considerably larger than the other members of its genus. This result brings the importance of this trait also into question.

## Species misclassifications

Several repetitions of the trait importance analysis revealed a group of five species that were consistently classified incorrectly. *Eulemur macaco* (vulnerable) was always classed as a non-threatened species. Conversely, non-threatened species classed as threatened were *Eulemur fulvus* (near threatened), *Eulemur rufifrons* (near threatened), *Daubentonia madagascariensis* (near threatened) and *Avahi laniger* (least concern). A further three species were sometimes classified incorrectly. These were *Mirza zaza* (vulnerable), *Lepilemur septentrionalis* (critically endangered) and *Lemur catta* (near threatened). Considering that the total number of least concern and near threatened species used in this study is twelve, this represents a classification error for this class that may reach to more than 40%. Conversely, threatened species have a much lower error of, which only ever reaches 5.26%. However, the difference in the quantity of species in each case must be noted, as the high error for the non-threatened category may be the result of the small number of species in this class. Additionally, the effects of the imputation of missing data and its role in misclassification must also be taken into consideration.

## Predicting Status

Table 1. shows an example the results of the predictive analysis, including the proportion of votes of the trees in the forest, for the predicted category (either threatened or non-threatened). All species apart from *Microcebus myoxinus* are threatened according to the analysis. *Allocebus trichotis* always wins its status by a small majority and separate repetitions of the RF analysis cause it to switch between status. The other species win their category by a higher percentage, especially *Hapalemur griseus ranomafanensis*. These results must be interpreted in light of the missing values and their simple replacements with variable medians for continuous variables and major classes for categorical variables, since proximity matrices cannot be developed.

**Table 1.** The list of species given a predicted status through the analysis. All species are data deficient apart from *Hapalemur griseus ranomafanensis*, which has not been evaluated.

Species Name	Predicted Status	Percentage of Votes for Winning Class
<i>Allocebus trichotis</i>	Threatened / Non-threatened	51.1% / 50.8% *
<i>Microcebus lehilahytsara</i>	Threatened	72.3%
<i>Microcebus myoxinus</i>	Non-threatened	69.1%
<i>Lepilemur dorsalis</i>	Threatened	76.5%
<i>Lepilemur leucopus</i>	Threatened	69.9%
<i>Lepilemur microdon</i>	Threatened	67.9%
<i>Lepilemur mustelinus</i>	Threatened	73.2%
<i>Lepilemur ruficaudatus</i>	Threatened	75.0%
<i>Lepilemur tymerlachsonorum</i>	Threatened	77.1%
<i>Eulemur rufus</i>	Threatened	60.5%
<i>Hapalemur griseus ranomafanensis</i>	Threatened	97.2%
<i>Avahi meridionalis</i>	Threatened	78.0%

\* For *Allocebus trichotis*, repetitions of the Random Forest analysis give a status of threatened or unthreatened depending on the run.



## Discussion

### Trait Importance

The 7 traits revealed to be of importance by the analysis (Geographic range, neonatal body mass, weaning age, age at sexual maturity, age at first birth, population group size and gestation length) are all to some extent discussed in the literature as being useful to distinguishing between high and low risk species. The high position of geographic range size, in the list of trait importance, is consistently supported by many large scale extinction analyses (Purvis et al, 2000), (Davidson et al, 2009), (Lee & Jetz, 2011). Moreover, the study of intrinsic and environmental factors and their relationship to extinction risk by Cardillo et al (2008) revealed that small geographic range is the most dependable feature present among threatened species across taxa and regardless of regional conditions. This is interesting, considering that geographic range is the only variable in my analysis that is controlled to a large extent by both the intrinsic biological traits of the species and external human-influenced habitat factors. For example, a species may be adapted to living within a restricted range, but this area in turn is affected by human induced pressures, which may further reduce its size. The prominence of geographic range in this sense, is also notable in light of the strong connections between adult body mass and the various major life history traits of significance derived from the RF analysis, which makes the importance of these features questionable.

Animals that are weaned at a late age, have long gestation lengths, sexually mature later and have their first births when older all fall along the slower end of what is termed the fast-slow continuum of life history (Read & Harvey, 1989). Bielby et al (2007) further suggested that in fact two axes probably exist; the first relates to the timing of reproduction, with fast species being weaned at an early age and maturing quickly and the second relating to reproductive yield, with fast species being those that have short gestation times and give birth to many offspring of a small neonate size. Generally, species with a slower set of life history traits are more at risk of extinction, since they are less capable of replenishing their numbers quickly, when the death rate increases (Purvis et al, 2000) and are therefore, more in danger of overexploitation (Reynolds et al, 2001). This supports my analysis regarding the

importance of these features to extinction. It is also intriguing to note that all these features are related to early age development and considering the fact that infant mortality appears to be especially high among lemurs, possibly twice as great as among monkeys (Wright, 1999) that these should be highlighted in the study. However, it must also be noted that the mortality rate of juveniles generally declines with increased gestation length (Kraus et al, 2005). With that said, Milne-Edwards sifaka (*Propithecus edwardsi*), which according to the database has a long gestation length compared with other lemurs, is also known to have high mortality rates for individuals that have not yet sexually matured, which suggests that this general rule may not be applicable to the lemurs and that infant mortality is an issue that may need to be considered in future conservation programmes. Work by Tecot (2010) on *Eulemur rubriventer* has shown how closely allied their breeding season is to the time at which trees fruit and how births even slightly out of synch lead to increased infant mortality rates. This suggests that changes to future weather and climate patterns, which could affect fruiting times, may have serious effects on lemur populations, all of whom appear to wean during this period (Wright, 2006).

Species with large group sizes are believed to be at a greater risk of extinction due to the fact that they require more feeding resources and thus are more susceptible to habitat destruction and degradation, which may reduce food availability (Isaac & Cowlishaw, 2004). Additionally, as Courchamp et al (1999) have shown, species that are dependent upon social interactions for their long term survival will become more threatened as individuals are removed from the population. Although it must be noted that social group size was not a significant trait according to this analysis. Likewise, home range did not emerge as an important feature, though presumably, larger groups will require more expansive areas over which to feed. Further, species living in bigger groups are more noticeable to hunters and thus, are more likely to suffer in this regard (Purvis et al, 2000). The importance of this trait is slightly unusual considering that lemurs naturally keep to relatively small group sizes compared with other primates and this includes the large diurnal lemurs (Richard & Dewar, 1991). It is possible that this represents the fine scale on which a decision tree can work.

In order to visualise the spread of the data across the forest and identify possible interactions between variables, I attempted to create single decision trees using the top five traits of importance, in the rpart add-on package in R. These all resulted in trees that were terminated after a single split. This consistently occurred as individual traits were removed from the group being used to create the trees, clearly indicating that all the most significant characteristics were able to partition the data into two classes, where further purification was impossible. These results highlight a potential advantage of RF over individual trees in that a hierarchy of traits based upon ability to classify cases can be created, showing traits by which to prioritise species for conservation.

In addition to the traits of importance it is perhaps interesting to consider the biological variables that the analysis fails to find of significance but which one might think to be of relevance. Adult body mass is perhaps the most discussed biological trait in regards to extinction risk. Matthews et al (2011) found that among extant primates, large body size was indicative of high risk of extinction; although the link between mass and historic patterns of extinction was less clear. Cardillo et al (2005) found that body mass was likely to be a very significant factor influencing extinction risk, as they showed that mammals above 3kg in size were made more susceptible by both their intrinsic biological features and the external environment. Species below 3kg were only affected by extrinsic factors. However, Purvis et al (2000) found that for a range of extinction analyses, body mass was not ubiquitous among them. The main issue stems from the fact that body size strongly correlates with a variety of features, such as slow life history traits and hunting pressure, as well as interacting with a variety of other features that encourage species to become more threatened (Cardillo et al, 2008). Therefore, disentangling them to discover the true vulnerability of a species to extinction is problematic. McKinney (1997) relates that the range of results concerning body mass and extinction are due to differences in the taxonomic and scalar focus of studies.

The fact that this analysis found that adult body mass was not a good indicator of extinction risk in lemurs may be due to a historic human-induced extinction filter that has removed larger bodied species (Balmford, 1996). Catlett et al (2010) states that all lemurs above 10kg

have become extinct and their study showed that large body size was a strong contributory factor in the extirpation of prehistoric lemurs, through hunting and environmental change. This was regardless of their life history, which appeared to be quite variable. Cardillo and Bromham (2001) suggest that a similar filter likely is the reason why body mass is not a good indicator of vulnerability among extant large Australian mammals due to the Pleistocene extinction event on that continent. This conclusion receives a certain level of support from the study by Fritz et al (2009), where body mass was not considered a good indicator of extinction in regions that had received high levels of historic habitat modification, identified primarily as temperate areas. Body mass was, however, significant in the tropics and it is, therefore, interesting to note that Madagascar may be a good example of recent large scale megafaunal extinctions in a tropical region. There is also some evidence from north-eastern Madagascar that size is not necessarily always the main driver of hunting pressure, as it has been shown that locals may be more likely to take the smaller dwarf lemurs (*Cheirogaleus*) over larger woolly lemurs (*Avahi*) due to taste preferences (Mittermeier et al, 2010). Nevertheless, it was also noted that larger species are still overall likely to be the greatest targets for hunters. However, Godfrey and Irwin (2007) have shown that whereas hunting played the major role in the extinction of historic lemurs, current species are more likely at risk from habitat disturbance.

Assuming that the correlation between adult body mass and the life history traits flagged up as being of importance in the analysis as well as the relationship between social and population group size are correct, then this is a strong indication that geographic range is the best determinant of extinction risk in lemurs regardless of their biological characteristics; with perhaps a small influence from gestation length. The idea that the biological characteristics of a species are less important than extrinsic factors is supported by the study of Cardillo et al (2008) who found that among primates very little if any variation in the risk of extinction could be explained through intrinsic life history or ecological variables. It is also possible that the effects of the environment are more intense on islands, where they overwhelm any of the biological characteristics of species. Although Madagascar is a large island with varied habitats and geography, it has lost much of its natural environment to habitat destruction and conversion (Mittermeier et al, 2010), likely

leading to a reduction in the ranges of many species of lemur, which is the primary trait of importance in my analysis.

Alternatively, the lack of an effect of intrinsic biological traits on extinction may be a product of the narrow scope of this study, in the sense that it only dealt with a relatively small taxonomic group. Invariably, small scale studies will involve closely related species that either have many traits in common or possess features that differ only within a limited range of values. The natural variability of traits among related species within a small array of possible values would inevitably lead to studies where few characteristics of significance are found. As discussed previously this may well be the case for a number of the traits used in the analysis, especially, litter size. This drawback is noted by Jones et al (2003) in their investigation of extinction among bats. Additionally, as Cardillo (2003) points out in his study, one possible issue is the small number of cases for a particular class. In my analysis of trait importance, there were only twelve values for the non-threatened category, compared with 38 for the threatened group. This low number may make it difficult to determine relationships in the data or at least, make conclusions less robust. Furthermore, the lack of data for many variables may confound results, either through the formation of patterns that are not actually present, such as may have occurred in this study, shown through the correlations between different traits or through the inability to find relationships between variables and extinction risk, which may actually exist in nature but are not revealed due to missing values. Cardillo et al (2008) also expressed some apprehension over the use of narrow studies with small datasets. My results indicate that there is likely an optimum scale on which to base an extinction analysis. Too narrow a range and the analysis may find it difficult to identify traits of importance and partition species into classes.

One final possibility is that lemurs have life history traits that are flexible to a certain degree. This can be attested to in the literature in regards to differences in population density in *Lemur catta* across variable habitats and between disturbed and undisturbed areas (Gould, 2006). Likewise, lemurs have been shown to have highly variable diets and activity cycles (Richard & Dewar, 1991), which suggests why these traits are not considered important by the analysis. When these characteristics are taken as averages across the

geographic range of a species, extreme values will be reduced, possibly also removing patterns in the data. Conversely, if a species has received little attention in terms of biological research, then its trait data may contain extreme values, since studies may have been limited to a particular region. For example, *Eulemur flavifrons* in the database has a population group size of 20 compared with other members of its genus, which range between 4 and 9.5. This phenomenon clearly could also create problems for the analysis.

### **Misclassified Species and Predictions**

The out of bag error rate for the RF analysis that measures trait importance is 14%, which means that 86% of cases are correctly classified. Cohen's kappa ( $k$ ) = 0.58, which measures the extent to which data is partitioned (1 = perfect splitting, 2 = splitting that is no better than random) is moderately low and this stems from the large classification error of the unthreatened group, where 5 out of the 12 species are classed as threatened.

Misclassified species are those where their trait data is not in agreement with their current status. It is important to note that this study measures susceptibility to extinction and not the contemporary situation that a species might be facing. Therefore, species presently classed on the red list as unthreatened, but which have been misclassified according to the analysis are those that possess biological traits that predispose them to a high risk of extinction, but which are not facing imminent pressures from their external environment. *Daubentonia madagascariensis* (near threatened), with a predicted status of threatened, has a highly unusual set of life history traits compared with other lemurs (Catlett et al, 2010), including late weaning, sexual maturation and first births as well as a very long gestation length. However, it is also very broadly distributed across a range of habitats (Duckworth, 1993), which is primarily the reason for its current status as a non-threatened species. It is interesting to note that the large geographic range of *D. madagascariensis* does not seem to affect the results of the analysis, suggesting that slow life history traits do play some role in extinction risk; perhaps in circumstances where they are particularly extreme.

Similarly, *Avahi laniger* (least concern) according to the database has a weaning age and age at first birth that is above average for non-threatened species. In addition they also gestate

for a period of time more akin to threatened lemurs. They are, however, distributed widely, including within a number of protected areas and are believed to not be under any major threats (red list). Like with *D. madagascariensis*, this species also has a large range, which clearly did not strongly influence results. The reasons for the designation of both *Eulemur fulvus* (near threatened) and *Eulemur rufifrons* (near threatened) as threatened and *Eulemur macaco* (vulnerable) as non-threatened are more obscure. Although, *E. macaco* sexually matures at an earlier age than the other two species, many of their other traits are very similar. This may be suggestive of fine scale differentiation between species in the analysis, but it is probably more likely the result of missing data and the effects of imputation.

Species that are currently threatened but through the analysis emerge as part of the non-threatened class are those that have biological characteristics that would imply that they are more similar to non-threatened species. This suggests that they may be facing external pressures that are pushing them into a higher endangerment category regardless of their traits. *E. macaco* suffers from deforestation and hunting within its range and is known to be particularly susceptible to these threats (Bayart & Simmen, 2005).

Species that are never always designated into a particular class are likely to be those with a combination of features, which make it difficult for the RF analysis to make a concrete decision as to their placement. *Lepilemur septentrionalis* (critically endangered) is a good example of this, sexually maturing well below the average for a non-threatened species, but gestating for the same length of time as the average for the threatened lemurs; its weaning age intermediate between threatened and non-threatened. *Lemur catta* (near threatened), likewise has a mix of traits, with a high gestation length, but a relatively low age at first birth. The inability of the analysis to successfully classify *Mirza zaza* (vulnerable) is almost certainly due to a lack of data, with gestation length being the only trait of importance with a value.

I investigated the high error of the unthreatened group by splitting it into least concern and near threatened and kept the threatened species clumped together to create three groups

for classification. An RF analysis was run using the same variables and data, with imputation of missing values as in the study of trait importance. This investigation was performed to check where most misclassifications were occurring and to test the efficacy of the RF method for correctly predicting when a species was likely to be threatened. The results can be seen in Table 2.

		Predicted Status			Classification Error
		Least Concern	Near Threatened	Threatened	
Actual Status	Least Concern	6	0	1	14.29%
	Near Threatened	1	0	4	100%
	Threatened	0	0	38	0%

**Table 2.** The number of correct and incorrect predicted classifications for the different classes

What is clear is that the analysis strongly predicts threatened species, with repetitions only ever misclassifying one of the cases. Likewise, least concern species appear to generally be correctly classified, with the moderately high error likely the result of the small number of cases in this category. However, what is also clear is that not one near threatened species is ever correctly classified by the analysis and the fact that they are classified as being either more or less threatened, with not one correct classification, suggests that the ultimate causes relating to why a species is at risk of extinction are primarily derived from external environmental factors, since clearly, near threatened species do not share a unifying set of intrinsic traits.

The results of the predictions from the group of data deficient and not evaluated species are somewhat obscure. In a number of cases data was lacking, especially for the two most important traits, geographic range and gestation length. The potential of what missing values can do to an analysis are illustrated by the fact that *Avahi meridionalis* should win its class by such a high number of votes when only a few trait values are present. This suggests



the danger of attempting predictive extinction analyses with non comprehensive datasets as well as the limits of value imputation.

Misclassification is an essential tool for an extinction analysis, in that it brings to attention species that may become threatened in the future should their external environment be changed and through highlighting species that are clearly under intense pressure in their habitat, that even with a preferential set of life history traits continue to face extinction. This is a point supported by Jones et al (2006) and is one of the major advantages of the decision tree method. The results from the analysis separating the non-threatened category into least concern and near threatened, showed firstly that the analysis was very successful in classifying threatened species, such that from a predictive perspective, Type II errors, which in this sense, would refer to a species wrongly classified as non-threatened are low. Type I errors, where a species is wrongly classified as threatened are also relatively low. Arguably, Type II errors are more serious than Type I, in that what is at risk from Type I, is the money and effort spent to investigate a species potentially at risk, whereas as a Type II error could result in extinction (Jones pers. comm.). Secondly, it showed that the analysis had trouble classifying near threatened species, which would suggest that future prioritisations should examine this class of species carefully and individually.

## **Conclusions**

As a means to clarify what has been discussed in the previous section in a more concise and practical framework, I set down the following points that have been learnt:

1. The first priorities for lemur conservation are those species with the most restricted distributions, regardless of their life history or ecological traits. Secondly, species with 'slow' life history traits, best indicated by gestation length such as *D. madagascariensis* and *A. Laniger*, should be the focus, as these are species that are susceptible to extinction and could very quickly become threatened, should their natural habitat become less hospitable.
2. The extinction analyses generated using Random Forest was successful at designating least concern and threatened species, but failed at assigning the near

threatened to their correct class. This would suggest that near threatened species should be investigated in more depth during status assessments.

3. The fact that early stage life history traits have emerged as being potentially of some importance to extinction risk, combined with the fact that lemurs are seasonal breeders, with breeding seasons coinciding with fruiting periods, may be cause for concern. Should climate patterns change in the future, reproductive cycles may be disrupted and infant mortality increase to even higher levels than it already is. This suggests the need for a pre-emptive study to investigate this idea further.
4. The narrow scope of this study, simply focusing on the lemurs, combined with the fact that there were not only a limited number of overall cases but also a significant number of missing values, suggests that future extinction analyses should be very carefully considered to ensure that the results are applicable and also, so that a workable scale can be developed, which can not only identify and prioritise species but also be robust to statistical analysis.

Future analyses should involve more focus on human-based pressures, such as levels of hunting and acute habitat loss experienced by different species, in order to gain a greater understanding of the interactions between intrinsic and extrinsic factors.

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## **Appendix**

Database of Lemur Traits, taken from 'PanTHERIA' (Jones et al, 2009) and other source, including 'Lemurs of Madagascar: Third Edition' (Mittermeier et al, 2010).



Case	Family	Genus	Species	Binomial
1	Cheirogaleidae	<i>Mirza</i>	<i>coquereli</i>	<i>Mirza coquereli</i>
2	Cheirogaleidae	<i>Mirza</i>	<i>zaza</i>	<i>Mirza zaza</i>
3	Cheirogaleidae	<i>Allocebus</i>	<i>trichotis</i>	<i>Allocebus trichotis</i>
4	Cheirogaleidae	<i>Cheirogaleus</i>	<i>major</i>	<i>Cheirogaleus major</i>
5	Cheirogaleidae	<i>Cheirogaleus</i>	<i>medius</i>	<i>Cheirogaleus medius</i>
6	Cheirogaleidae	<i>Cheirogaleus</i>	<i>crossleyi</i>	<i>Cheirogaleus crossleyi</i>
7	Cheirogaleidae	<i>Cheirogaleus</i>	<i>minusculus</i>	<i>Cheirogaleus minusculus</i>
8	Cheirogaleidae	<i>Cheirogaleus</i>	<i>sibreei</i>	<i>Cheirogaleus sibreei</i>
9	Cheirogaleidae	<i>Microcebus</i>	<i>murinus</i>	<i>Microcebus murinus</i>
10	Cheirogaleidae	<i>Microcebus</i>	<i>rufus</i>	<i>Microcebus rufus</i>
11	Cheirogaleidae	<i>Microcebus</i>	<i>berthae</i>	<i>Microcebus berthae</i>
12	Cheirogaleidae	<i>Microcebus</i>	<i>bongolavensis</i>	<i>Microcebus bongolavensis</i>
13	Cheirogaleidae	<i>Microcebus</i>	<i>danfossorum</i>	<i>Microcebus danfossorum</i>
14	Cheirogaleidae	<i>Microcebus</i>	<i>griseorufus</i>	<i>Microcebus griseorufus</i>
15	Cheirogaleidae	<i>Microcebus</i>	<i>jollyae</i>	<i>Microcebus jollyae</i>
16	Cheirogaleidae	<i>Microcebus</i>	<i>lehilahytsara</i>	<i>Microcebus lehilahytsara</i>
17	Cheirogaleidae	<i>Microcebus</i>	<i>mamiratra</i>	<i>Microcebus mamiratra</i>
18	Cheirogaleidae	<i>Microcebus</i>	<i>mittermeieri</i>	<i>Microcebus mittermeieri</i>
19	Cheirogaleidae	<i>Microcebus</i>	<i>myoxinus</i>	<i>Microcebus myoxinus</i>
20	Cheirogaleidae	<i>Microcebus</i>	<i>ravelobensis</i>	<i>Microcebus ravelobensis</i>
21	Cheirogaleidae	<i>Microcebus</i>	<i>sambiranensis</i>	<i>Microcebus sambiranensis</i>
22	Cheirogaleidae	<i>Microcebus</i>	<i>simmonsi</i>	<i>Microcebus simmonsi</i>
23	Cheirogaleidae	<i>Microcebus</i>	<i>tavaratra</i>	<i>Microcebus tavaratra</i>
24	Cheirogaleidae	<i>Microcebus</i>	<i>margotmarshae</i>	<i>Microcebus margotmarshae</i>
25	Cheirogaleidae	<i>Microcebus</i>	<i>arnholdi</i>	<i>Microcebus arnholdi</i>
26	Cheirogaleidae	<i>Microcebus</i>	<i>macarthurii</i>	<i>Microcebus macarthurii</i>
27	Cheirogaleidae	<i>Phaner</i>	<i>electromontis</i>	<i>Phaner electromontis</i>
28	Cheirogaleidae	<i>Phaner</i>	<i>furcifer</i>	<i>Phaner furcifer</i>
29	Cheirogaleidae	<i>Phaner</i>	<i>pallescens</i>	<i>Phaner pallescens</i>
30	Cheirogaleidae	<i>Phaner</i>	<i>parienti</i>	<i>Phaner parienti</i>
31	Lepilemuridae	<i>Lepilemur</i>	<i>dorsalis</i>	<i>Lepilemur dorsalis</i>
32	Lepilemuridae	<i>Lepilemur</i>	<i>edwardsi</i>	<i>Lepilemur edwardsi</i>
33	Lepilemuridae	<i>Lepilemur</i>	<i>leucopus</i>	<i>Lepilemur leucopus</i>
34	Lepilemuridae	<i>Lepilemur</i>	<i>microdon</i>	<i>Lepilemur microdon</i>
35	Lepilemuridae	<i>Lepilemur</i>	<i>mustelinus</i>	<i>Lepilemur mustelinus</i>
36	Lepilemuridae	<i>Lepilemur</i>	<i>ruficaudatus</i>	<i>Lepilemur ruficaudatus</i>
37	Lepilemuridae	<i>Lepilemur</i>	<i>aeecelis</i>	<i>Lepilemur aeecelis</i>
38	Lepilemuridae	<i>Lepilemur</i>	<i>ahmansonorum</i>	<i>Lepilemur ahmansonorum</i>
39	Lepilemuridae	<i>Lepilemur</i>	<i>ankaranensis</i>	<i>Lepilemur ankaranensis</i>
40	Lepilemuridae	<i>Lepilemur</i>	<i>betsileo</i>	<i>Lepilemur betsileo</i>
41	Lepilemuridae	<i>Lepilemur</i>	<i>fleuretae</i>	<i>Lepilemur fleuretae</i>
42	Lepilemuridae	<i>Lepilemur</i>	<i>grewcockorum</i>	<i>Lepilemur grewcockorum</i>
43	Lepilemuridae	<i>Lepilemur</i>	<i>hubbardorum</i>	<i>Lepilemur hubbardorum</i>
44	Lepilemuridae	<i>Lepilemur</i>	<i>jamesorum</i>	<i>Lepilemur jamesorum</i>
45	Lepilemuridae	<i>Lepilemur</i>	<i>milanoii</i>	<i>Lepilemur milanoii</i>
46	Lepilemuridae	<i>Lepilemur</i>	<i>mittermeieri</i>	<i>Lepilemur mittermeieri</i>
47	Lepilemuridae	<i>Lepilemur</i>	<i>otto</i>	<i>Lepilemur otto</i>
48	Lepilemuridae	<i>Lepilemur</i>	<i>petteri</i>	<i>Lepilemur petteri</i>
49	Lepilemuridae	<i>Lepilemur</i>	<i>randrianasoloi</i>	<i>Lepilemur randrianasoloi</i>
50	Lepilemuridae	<i>Lepilemur</i>	<i>sahamalazensis</i>	<i>Lepilemur sahamalazensis</i>
51	Lepilemuridae	<i>Lepilemur</i>	<i>seali</i>	<i>Lepilemur seali</i>
52	Lepilemuridae	<i>Lepilemur</i>	<i>septentrionalis</i>	<i>Lepilemur septentrionalis</i>
53	Lepilemuridae	<i>Lepilemur</i>	<i>tymerlachsonorum</i>	<i>Lepilemur tymerlachsonorum</i>
54	Lepilemuridae	<i>Lepilemur</i>	<i>wrightae</i>	<i>Lepilemur wrightae</i>
55	Lepilemuridae	<i>Lepilemur</i>	<i>hollandorum</i>	<i>Lepilemur hollandorum</i>
56	Lepilemuridae	<i>Lepilemur</i>	<i>scottorum</i>	<i>Lepilemur scottorum</i>

Case	Common Name	IUCN Status
1	<i>Mirza coquereli</i> (Coquerel's Giant Mouse Lemur)	Near Threatened ver 3.1
2	<i>Mirza zaza</i> (Northern Giant Mouse Lemur)	Vulnerable B2ab(ii,iii) ver 3.1
3	<i>Allocebus trichotis</i> (Hairy-eared Dwarf Lemur)	Data Deficient ver 3.1
4	<i>Cheirogaleus major</i> (Geoffroy's Dwarf Lemur)	Least Concern ver 3.1
5	<i>Cheirogaleus medius</i> (Western Fat-tailed Dwarf Lemur)	Least Concern ver 3.1
6	<i>Cheirogaleus crossleyi</i> (Furry-eared Dwarf Lemur)	Data Deficient ver 3.1
7	<i>Cheirogaleus minusculus</i> (Lesser Iron-grey Dwarf Lemur)	Data Deficient ver 3.1
8	<i>Cheirogaleus sibreei</i> (Sibree's Dwarf Lemur)	Data Deficient ver 3.1
9	<i>Microcebus murinus</i> (Grey Mouse-lemur)	Least Concern ver 3.1
10	<i>Microcebus rufus</i> (Rufous Mouse Lemur)	Least Concern ver 3.1
11	<i>Microcebus berthae</i> (Madame Berthe's Mouse Lemur)	Endangered B1ab(iii) ver 3.1
12	<i>Microcebus bongolavensis</i> (Bongolava Mouse Lemur)	Data Deficient ver 3.1
13	<i>Microcebus danfossi</i> (Danfoss' Mouse Lemur)	Data Deficient ver 3.1
14	<i>Microcebus griseorufus</i> (Grey-brown Mouse Lemur)	Least Concern ver 3.1
15	<i>Microcebus jollyae</i> (Jolly's Mouse Lemur)	Data Deficient ver 3.1
16	<i>Microcebus lehilahytsara</i> (Goodman's Mouse Lemur)	Data Deficient ver 3.1
17	<i>Microcebus mamiratra</i> (Claire's Mouse Lemur)	Data Deficient ver 3.1
18	<i>Microcebus mittermeieri</i> (Mittermeier's Mouse Lemur)	Data Deficient ver 3.1
19	<i>Microcebus myoxinus</i> (Peters' Mouse Lemur)	Data Deficient ver 3.1
20	<i>Microcebus ravelobensis</i> (Golden-brown Mouse Lemur)	Endangered B1ab(iii) ver 3.1
21	<i>Microcebus sambiranensis</i> (Sambirano Mouse Lemur)	Endangered B1ab(iii) ver 3.1
22	<i>Microcebus simmonsii</i> (Simmons' Mouse Lemur)	Data Deficient ver 3.1
23	<i>Microcebus tavaratra</i> (Tavaratra Mouse Lemur)	Endangered B1ab(iii) ver 3.1
24	<i>Microcebus margotmarshae</i> (Margot Marsh's Mouse Lemur)	Not Evaluated
25	<i>Microcebus arnholdi</i> (Montagne d'Ambre Mouse Lemur)	Not Evaluated
26	<i>Microcebus macarthurii</i> (Anjahely Mouse Lemur)	Not Evaluated
27	<i>Phaner electromontis</i> (Montagne D' Ambre Fork-marked Lemur)	Vulnerable B1ab(iii) ver 3.1
28	<i>Phaner furcifer</i> (Masoala Fork-marked Lemur)	Least Concern ver 3.1
29	<i>Phaner pallescens</i> (Pale Fork-marked Lemur)	Least Concern ver 3.1
30	<i>Phaner parienti</i> (Sambirano Fork-marked Lemur)	Vulnerable B1ab(iii) ver 3.1
31	<i>Lepilemur dorsalis</i> (Gray's Sportive Lemur)	Data Deficient ver 3.1
32	<i>Lepilemur edwardsi</i> (Milne-edwards's Sportive Lemur)	Vulnerable B1ab(iii,v) ver 3.1
33	<i>Lepilemur leucopus</i> (White-footed Sportive Lemur)	Data Deficient ver 3.1
34	<i>Lepilemur microdon</i> (Small-toothed Sportive Lemur)	Data Deficient ver 3.1
35	<i>Lepilemur mustelinus</i> (Weasel Sportive Lemur)	Data Deficient ver 3.1
36	<i>Lepilemur ruficaudatus</i> (Red-tailed Sportive Lemur)	Data Deficient ver 3.1
37	<i>Lepilemur aeeclis</i> (Antafia Sportive Lemur)	Data Deficient ver 3.1
38	<i>Lepilemur ahmansonorum</i> (Ahmanson's Sportive Lemur)	Data Deficient ver 3.1
39	<i>Lepilemur ankaranensis</i> (Ankarana Sportive Lemur)	Endangered B1ab(iii,v) ver 3.1
40	<i>Lepilemur betsileo</i> (Betsileo Sportive Lemur)	Data Deficient ver 3.1
41	<i>Lepilemur fleuretae</i> (Fleurette's Sportive Lemur)	Data Deficient ver 3.1
42	<i>Lepilemur grewcockorum</i> (Grewcock's Sportive Lemur)	Data Deficient ver 3.1
43	<i>Lepilemur hubbardorum</i> (Hubbard's Sportive Lemur)	Data Deficient ver 3.1
44	<i>Lepilemur jamesorum</i> (James' Sportive Lemur)	Data Deficient ver 3.1
45	<i>Lepilemur milanoii</i> (Daraina Sportive Lemur)	Data Deficient ver 3.1
46	<i>Lepilemur mittermeieri</i> (Mittermeier's Sportive Lemur)	Data Deficient ver 3.1
47	<i>Lepilemur otto</i> (Otto's Sportive Lemur)	Data Deficient ver 3.1
48	<i>Lepilemur petteri</i> (Petter's Sportive Lemur)	Data Deficient ver 3.1
49	<i>Lepilemur randrianasoloi</i> (Randrianasolo's Sportive Lemur)	Data Deficient ver 3.1
50	<i>Lepilemur sahamalazensis</i> (Sahamalaza Peninsula Sportive Lemur)	Data Deficient ver 3.1
51	<i>Lepilemur seali</i> (Seal's Sportive Lemur)	Data Deficient ver 3.1
52	<i>Lepilemur septentrionalis</i> (Sahafary Sportive Lemur)	Critically Endangered C2a(i) ver 3.1
53	<i>Lepilemur tymerlachsonorum</i> (Nosy Be Sportive Lemur)	Data Deficient ver 3.1
54	<i>Lepilemur wrightae</i> (Wright's Sportive Lemur)	Data Deficient ver 3.1
55	<i>Lepilemur hollandorum</i> (Mananara-Nord Sportive Lemur)	Not Evaluated
56	<i>Lepilemur scottorum</i> (Masoala Sportive Lemur)	Not Evaluated



Case	litter size	litters per year	maximum longevity (month)	teat number	population group size	social group size	home range (km2)	individual home range (km2)	population density (n/km2)	Activity cycle	terrestriality	diet breadth	habitat breadth	trophic level	basal metabolic rate (mL o2/hour)	basal metabolic rate mass (g)	aetmean	petmean
1	1.71	1.1	183.6	4	4.5	1	0.03	0.04	107.17	2	2	5	2					
2						1	0.01355	0.0115	735.5	1	2	5	1	2				
3	1	1			2	1	0.1845	0.104		2	2	6	1	2			1388.2	1653.7
4	2.26	1	180	4	1	1	0.02	0.04	68	1	2	5	1	2			1207.3	1567.8
5	2.04	1.1	231.6	4	1	1	0.02	4.78E-03	221.44	1	2	6	1	2	195	300	899.72	1625.8
6									90		2							
7											2							
8											2							
9	2	1.1	186		3.5	1	0.01	0.01	461	1	2	5	1	2	125.84	101.05	897.1	1624.7
10	2.52	1	144		3.25	1	0.01	0.01	167.8	1	2	5	1	2			1319.6	1595.2
11						1		0.037	65	1	2	5		2				
12											2							
13									397		2							
14	1.68	1				1		0.005925	325	1	2	4		2				
15											2							
16						1			110	1	2	3	1	2				
17											2							
18											2							
19	2					1				1	2	4	1	2				
20						1		0.005738	927.5	1	2	4		2				
21											2							
22											2							
23									144.883		2							
24											2							
25											2							
26											2							
27											2							
28											2							
29	1.01		144		1.5	1	0.02	0.03	205	2	2	4	1	2				
30											2							
31	1.01			2		1				1	2	3	1	1			1240.4	1623.7
32	1			2	1	1	8.34E-03	9.53E-03	70.98	1	2	5	1	2			963.15	1571.2
33	1.01	1	103	2	1	1	2.00E-03	2.14E-03	504.99	1	2	2	1	1			803.16	1741.5
34				2	1	1			36.05	1	2	4	1	2			1311.1	1556.5
35	1	1	144	2		1	2.73E-03	3.87E-03	255.1	1	2	3	1	1	225	693	1388.5	1668.7
36	1.02	1		2		1		0.008	260	1	2	2	1	1			789.13	1602.6
37											2							
38											2							
39						1		0.01	350		2	3		1				
40											2							
41											2							
42											2							
43											2							
44											2							
45									131.3		2							
46											2							
47											2							
48											2							
49											2							
50									28	2	2							
51											2							
52	1	1		2		1	7.06E-03	0.01	154.26	1	2	3	1	1				
53	1	1									2	2		1				
54											2							
55											2							
56											2							



Case	Family	Genus	Species	Binomial
57	Lemuridae	<i>Eulemur</i>	<i>coronatus</i>	<i>Eulemur coronatus</i>
58	Lemuridae	<i>Eulemur</i>	<i>fulvus</i>	<i>Eulemur fulvus</i>
59	Lemuridae	<i>Eulemur</i>	<i>macaco</i>	<i>Eulemur macaco</i>
60	Lemuridae	<i>Eulemur</i>	<i>mongoz</i>	<i>Eulemur mongoz</i>
61	Lemuridae	<i>Eulemur</i>	<i>rubriventer</i>	<i>Eulemur rubriventer</i>
62	Lemuridae	<i>Eulemur</i>	<i>albifrons</i>	<i>Eulemur albifrons</i>
63	Lemuridae	<i>Eulemur</i>	<i>cinereiceps</i>	<i>Eulemur cinereiceps</i>
64	Lemuridae	<i>Eulemur</i>	<i>collaris</i>	<i>Eulemur collaris</i>
65	Lemuridae	<i>Eulemur</i>	<i>flavifrons</i>	<i>Eulemur flavifrons</i>
66	Lemuridae	<i>Eulemur</i>	<i>rufifrons</i>	<i>Eulemur rufifrons</i>
67	Lemuridae	<i>Eulemur</i>	<i>rufus</i>	<i>Eulemur rufus</i>
68	Lemuridae	<i>Eulemur</i>	<i>sanfordi</i>	<i>Eulemur sanfordi</i>
69	Lemuridae	<i>Lemur</i>	<i>catta</i>	<i>Lemur catta</i>
70	Lemuridae	<i>Hapalemur</i>	<i>aureus</i>	<i>Hapalemur aureus</i>
71	Lemuridae	<i>Hapalemur</i>	<i>griseus ssp. gilberti</i>	<i>Hapalemur griseus ssp. gilberti</i>
72	Lemuridae	<i>Hapalemur</i>	<i>griseus ssp. griseus</i>	<i>Hapalemur griseus ssp. griseus</i>
73	Lemuridae	<i>Hapalemur</i>	<i>griseus ssp. Ranomafanensis</i>	<i>Hapalemur griseus ssp. ranomafanensis</i>
74	Lemuridae	<i>Hapalemur</i>	<i>alaotrensis</i>	<i>Hapalemur alaotrensis</i>
75	Lemuridae	<i>Hapalemur</i>	<i>meridionalis</i>	<i>Hapalemur meridionalis</i>
76	Lemuridae	<i>Hapalemur</i>	<i>occidentalis</i>	<i>Hapalemur occidentalis</i>
77	Lemuridae	<i>Prolemur</i>	<i>simus</i>	<i>Prolemur simus</i>
78	Lemuridae	<i>Varecia</i>	<i>variegata ssp. editorum</i>	<i>Varecia variegata ssp. Editorum</i>
79	Lemuridae	<i>Varecia</i>	<i>variegata ssp. subcincta</i>	<i>Varecia variegata ssp. Subcincta</i>
80	Lemuridae	<i>Varecia</i>	<i>variegata ssp. variegata</i>	<i>Varecia variegata ssp. Variegata</i>
81	Lemuridae	<i>Varecia</i>	<i>rubra</i>	<i>Varecia rubra</i>
82	Daubentoniidae	<i>Daubentonia</i>	<i>madagascariensis</i>	<i>Daubentonia madagascariensis</i>
83	Indridae	<i>Avahi</i>	<i>laniger</i>	<i>Avahi laniger</i>
84	Indridae	<i>Avahi</i>	<i>betsileo</i>	<i>Avahi betsileo</i>
85	Indridae	<i>Avahi</i>	<i>cleesei</i>	<i>Avahi cleesei</i>
86	Indridae	<i>Avahi</i>	<i>meridionalis</i>	<i>Avahi meridionalis</i>
87	Indridae	<i>Avahi</i>	<i>occidentalis</i>	<i>Avahi occidentalis</i>
88	Indridae	<i>Avahi</i>	<i>peyrierasi</i>	<i>Avahi peyrierasi</i>
89	Indridae	<i>Avahi</i>	<i>ramanantsoavanai</i>	<i>Avahi ramanantsoavanai</i>
90	Indridae	<i>Avahi</i>	<i>unicolor</i>	<i>Avahi unicolor</i>
91	Indridae	<i>Avahi</i>	<i>mooreorum</i>	<i>Avahi mooreorum</i>
92	Indridae	<i>Propithecus</i>	<i>diadema</i>	<i>Propithecus diadema</i>
93	Indridae	<i>Propithecus</i>	<i>tattersalli</i>	<i>Propithecus tattersalli</i>
94	Indridae	<i>Propithecus</i>	<i>verreauxi</i>	<i>Propithecus verreauxi</i>
95	Indridae	<i>Propithecus</i>	<i>candidus</i>	<i>Propithecus candidus</i>
96	Indridae	<i>Propithecus</i>	<i>coquereli</i>	<i>Propithecus coquereli</i>
97	Indridae	<i>Propithecus</i>	<i>coronatus</i>	<i>Propithecus coronatus</i>
98	Indridae	<i>Propithecus</i>	<i>deckenii</i>	<i>Propithecus deckenii</i>
99	Indridae	<i>Propithecus</i>	<i>edwardsi</i>	<i>Propithecus edwardsi</i>
100	Indridae	<i>Propithecus</i>	<i>perrieri</i>	<i>Propithecus perrieri</i>
101	Indridae	<i>Indri</i>	<i>indri</i>	<i>Indri indri</i>

Case	Common Name	IUCN Status
57	<i>Eulemur coronatus</i> (Crowned Lemur)	Vulnerable B1ab(i,ii,iii,v) ver 3.1
58	<i>Eulemur fulvus</i> (Common Brown Lemur)	Near Threatened ver 3.1
59	<i>Eulemur macaco</i> (Black Lemur)	Vulnerable B1ab(i,ii,iii,v) ver 3.1
60	<i>Eulemur mongoz</i> (Mongoose Lemur)	Vulnerable B1ab(i,ii,iii,v) ver 3.1
61	<i>Eulemur rubriventer</i> (Red-bellied Lemur)	Vulnerable A2cd ver 3.1
62	<i>Eulemur albifrons</i> (White-fronted Brown Lemur)	Vulnerable A2cd ver 3.1
63	<i>Eulemur cinereiceps</i> (White-collared Lemur)	Endangered B1ab(i,ii,iii,v) ver 3.1
64	<i>Eulemur collaris</i> (Collared Brown Lemur)	Vulnerable A2cd ver 3.1
65	<i>Eulemur flavifrons</i> (Blue-eyed Black Lemur)	Critically Endangered A4cd ver 3.1
66	<i>Eulemur rufifrons</i> (Red-fronted Brown Lemur)	Near Threatened ver 3.1
67	<i>Eulemur rufus</i> (Red Brown Lemur)	Data Deficient ver 3.1
68	<i>Eulemur sanfordi</i> (Sanford's Brown Lemur)	Endangered B1ab(i,ii,iii,v) ver 3.1
69	<i>Lemur catta</i> (Ring-tailed Lemur)	Near Threatened ver 3.1
70	<i>Hapalemur aureus</i> (Golden Bamboo Lemur)	Endangered B1ab(iii,v) ver 3.1
71	<i>Hapalemur griseus ssp. gilberti</i> (Gilbert's Lesser Bamboo Lemur)	Data Deficient ver 3.1
72	<i>Hapalemur griseus ssp. griseus</i> (Grey Lesser Bamboo Lemur)	Vulnerable A2cd ver 3.1
73	<i>Hapalemur griseus ssp. ranomafanensis</i> (Ranomafana Bamboo Lemur)	Not Evaluated
74	<i>Hapalemur alaotrensis</i> (Lake Alaotra Gentle Lemur)	Critically Endangered B1ab(iii,v) ver 3.1
75	<i>Hapalemur meridionalis</i> (Rusty-gray Lesser Bamboo Lemur)	Vulnerable B1ab(iii,v) ver 3.1
76	<i>Hapalemur occidentalis</i> (Sambirano Lesser Bamboo Lemur)	Vulnerable A2cd ver 3.1
77	<i>Prolemur simus</i> (Greater Bamboo Lemur)	Critically Endangered C1+2a(i) ver 3.1
78	<i>Varecia variegata ssp. editorum</i> (Southern Ruffed Lemur)	Critically Endangered A2cd ver 3.1
79	<i>Varecia variegata ssp. subcincta</i> (White-belted Ruffed Lemur)	Critically Endangered A2cd ver 3.1
80	<i>Varecia variegata ssp. variegata</i> (Black And White Ruffed Lemur)	Critically Endangered A2cd ver 3.1
81	<i>Varecia rubra</i> (Red Ruffed Lemur)	Endangered B1ab(iii,v) ver 3.1
82	<i>Daubentonia madagascariensis</i> (Aye-aye)	Near Threatened ver 3.1
83	<i>Avahi laniger</i> (Gmelin's Woolly Lemur)	Least Concern ver 3.1
84	<i>Avahi betsileo</i> (Betsileo Woolly Lemur)	Data Deficient ver 3.1
85	<i>Avahi cleesei</i> (Bemaraha Woolly Lemur)	Endangered B1ab(i,ii,iii) ver 3.1
86	<i>Avahi meridionalis</i> (Southern Woolly Lemur)	Data Deficient ver 3.1
87	<i>Avahi occidentalis</i> (Lorenz Von Liburnau's Woolly Lemur)	Endangered B1ab(iii) ver 3.1
88	<i>Avahi peyrierasi</i> (Peyrieras' Woolly Lemur)	Data Deficient ver 3.1
89	<i>Avahi ramanantsoavanai</i> (Ramantsoavana's Southern Woolly Lemur)	Data Deficient ver 3.1
90	<i>Avahi unicolor</i> (Sambirano Woolly Lemur)	Data Deficient ver 3.1
91	<i>Avahi mooreorum</i> (Masoala Woolly Lemur)	Not Evaluated
92	<i>Propithecus diadema</i> (Diademmed Sifaka)	Endangered A2cd ver 3.1
93	<i>Propithecus tattersalli</i> (Golden-crowned Sifaka)	Endangered B1ab(ii,iii,v) ver 3.1
94	<i>Propithecus verreauxi</i> (Verreaux's Sifaka)	Vulnerable A2cd ver 3.1
95	<i>Propithecus candidus</i> (Silky Sifaka)	Critically Endangered C2a(i) ver 3.1
96	<i>Propithecus coquereli</i> (Coquerel's Sifaka)	Endangered A2cd ver 3.1
97	<i>Propithecus coronatus</i> (Crowned Sifaka)	Endangered A2cd ver 3.1
98	<i>Propithecus deckenii</i> (Van Der Decken's Sifaka)	Vulnerable A2c ver 3.1
99	<i>Propithecus edwardsi</i> (Milne-Edward's Sifaka)	Endangered A2cd+3cd ver 3.1
100	<i>Propithecus perrieri</i> (Perrier's Sifaka)	Critically Endangered C2a(ii) ver 3.1
101	<i>Indri indri</i> (Indri)	Endangered A2cd ver 3.1

Case	Status	adult body mass (g)	forearm length (mm)	head and body length (mm)	neonatal body mass (g)	neonatal head and body length (mm)	weaning body mass (g)	weaning head and body length (mm)	age at eye opening (day)	weaning age (day)	dispersal age (day)	age at sexual maturity (day)	age at first birth (day)	gestation length (day)	inter birth interval (day)
57	4	1699.85		352.27	57.81							701.52		124.04	
58	3	2376.99		469.62	74.99					134.64		791.75	970.9	120.83	547.5
59	4	2470.43		397.11	60.5					143.28		660.75	868.7	127.49	365
60	4	1771.13		354.85	59.48	100				151.13		1060.7	916.15	129	
61	4	2015.4		404.72	84.97					151.22		566.36		126.99	730
62	4	2000		405										120	
63	5	2397.37		395											
64	4	2375		395										120	
65	6	1850		420						164.5			1095	120	358
66	3	2250		440						92		1095	1080	120	
67	1	2394.62		457.01											
68	5	2394.03		390										120	
69	3	2626.48		425	75.8					126.51		831.62	866.87	134.74	468.41
70	5	1562.41		305.08										142.5	365
71	1	967		280											
72	4	775		300											
73	0	775		300										138.5	365
74	6	1616.83		400						151.67		600	962.273	145.5	
75	4	855													
76	4	1017		275										138.5	365
77	6	2030.41		370										140	365
78	6	3350		500											
79	6	3350		500											
80	6	3350		500	86.433										
81	5	3872.6		525	101.733					105				102	365
82	3	2731.37		400	121.79		1535			197.7		834.72	1277.5	166.48	760.41
83	2	1092.28		275	32.97	89.99				149.15			941.7	136.15	365
84	1	1050		285.5											
85	5	1025		270											
86	1	1175		260											
87	5	828.98		286											
88	1	1050		289											
89	1	1050		275											
90	1	850		270											
91	0	920		307											
92	5	6568.99		501.74	134.99					256.27		1683.65	1553.07	152.08	745.2
93	5	3531.39		475	97.47					152.13			1642.5	149	
94	4	3588.26		472.49	102.65					177.83		943.94	1668.05	149.77	365
95	6	5500		510										180	609.55
96	5	4189.27		460	102.45					180.96		1460	1533	140.99	365
97	5	3900		420											912.5
98	4	3750		450											
99	5	6573.27		470							1825	1460	1642.5	179	569.4
100	6	4650		450											
101	5	8565.48		734.99						331.34		1605.69		136.5	912.5



Case	litter size	litters per year	maximum longevity (month)	teat number	population group size	social group size	home range (km2)	individual home range (km2)	population density (n/km2)	Activity cycle	terrestriality	diet breadth	habitat breadth	trophic level	basal metabolic rate (mL O2/hour)	basal metabolic rate mass (g)	actmean	petmean
57	1.53		220.8			6.95	0.05		101.98	2	2	4	2	2			1253.3	1528
58	1.1	0.89	444	3	9.25	9.15	0.05	8.75E-03	221	2	2	3	1	1	746	2374.5	1139.2	1586.2
59	1.04	1	360		9.5	9.2	0.03		53.85	2	2	5	1	2			1188.6	1717.6
60	1.11	1	360		4	2.7	0.05	0.07	346.7	2	2	4	1	2			932.21	1603.7
61	1.01	1			4.75	3.3	0.13		30	2	2	4	1	2			1344	1575.5
62						9.027	0.131		14.5	2	2	4	2	2				
63						6	0.489		15.943	2	2	3	2	1				
64						9.5	0.7		14	2	2	4	2	1				
65	1.048				20	7.233	0.0671		42	2	2	4	2	2				
66	1					8.5	0.5335		571	2	2	3	2	1				
67						9.5				2	2							
68						7.7	0.15		4.45	2	2	4		2				
69	1.18	1	360		15	16.45	0.05	0.14	215	2	2	5	2	2				
70	1.01	1.1			4	3	0.21	0.36	2.04	2	2	3	2	1			1321.4	1516.9
71											2							
72							0.08		54.5	2	2							
73	1	1				4.5	0.175		18.25	2	2	4	2	1				
74	1.4					3.665	0.02			2	2	2	3	1				
75						5.7				2	2	3	2	1				
76	1	1								2	2							
77	1	1	144		4	7.5	0.62			2	2	4	2	2				
78					5		1.97		12.753		2	4	2	1				
79						2.8			36	2	2		2	1				
80											2	4	2	1				
81	2.165				18		0.405		23.5	1	2	3	2	1				
82	1.01	0.42	291.6	2	1	1	0.06	0.11	39.79	1	2	6	2	2			1216.3	1601.3
83	1.01	1		2	2	2	0.01	0.01	84.85	2	2	3	2	1			1272.9	1597.8
84											2							
85								0.02		1	2	1		1				
86						2		0.0272	176		2	2		1				
87	1.02					3	0.01	0.02	66.99	2	2	3	1	1				
88									29.81		2							
89											2							
90											2							
91											2							
92	1.01	0.76		2		4.95	0.21	0.35	5.65	3	2	4	2	1			1342.6	1582.5
93				2		3.85	0.06		68.083	2	2	4	2	1			1149	1476
94	1.02	1	247.2	2	7.5	6.3	0.03	0.05	150	3	2	4	2	1	670	3350	881.86	1632.2
95	1					4.7	0.405		65	3	2	4	2	1				
96	1	1.1				5.5	0.065		60	3	2	3	2	1				
97	1					5	0.0135		236.3	3	2	3	2	1				
98						8			9.2	3	2		2					
99	1					6	1.75		8	3	2	4	2	1				
100						4.5	0.3		8.622	3	2	3	2	1				
101	1.01	0.42		2	3.5	3.1	0.12	0.17	10.62	3	2	4	2	1				

