**Methods**

For 439 species, we used stated GL in years available from published IUCN Red List assessments (IUCN 2012a); for 822 additional species we derived GLs from data on species' reproductive life span and age at first reproduction (see Generation Length model, below). Life-history traits were obtained from PanTHERIA (Jones et al. 2009) and AnAge (Tacutu et al. 2013) . Moreover, for carnivores and ungulates, we applied a multiple imputation procedure to estimate missing values of life history variables (see below for a detailed description). We compiled the GL values of 3721 remaining species by assigning them the mean GL value of congeneric or confamilial species (when expert-based GL values of congeneric species were not available) in the same bin of log body mass (depending on data availability).

For the mammal body masses, we used PanTHERIA (Jones et al. 2009) as our main reference, and complemented the missing data with numerous other sources, including books and primary literature (see supplementary materials). For species that lacked body mass data (1047), we calculated the average body mass of congeneric or confamilial species.

For 315 species, lacking a congeneric or confamilial species in the same bin of log body mass, we assigned the mean GL value of congenerics or confamilials, irrespective of their body mass. For the remaining species (n=116, 2.1 % of the total), where no information was available for congeneric or confamilial species, we assigned the mean GL value of species in the same bin of log body mass, belonging to the same order, or simply the mean GL values of the order (2 species, *Ptilocercus lowii* and *Cyclopes didactylus*). We made an exception for the two species of Dermoptera and 9 species of small mammals (body mass < 100 g); since they were the only representatives of their orders, we estimated mean GLs from species belonging to the same bin of log body mass. In this way, we obtained a GL value for all existing 5426 mammals.

**Generation Length model**

We estimated GL for mammals from information on species age at first reproduction and reproductive life span, by applying the methodology described in the IUCN Red List Guidelines (IUCN 2013)

*[1]*

where *Rspan* is the species reproductive life span, calculated as the difference between the age at last reproduction and the age at first reproduction (AFR), and *z* is a constant “depending on survivorship and relative fecundity of young vs. old individuals in the population” (IUCN 2013). Generation length values in the Red List are typically provided for threatened species (Vulnerable to Critically Endangered) assessed under criteria A and C1 (IUCN, 2001). As largely discussed (e.g. Purvis 2000; Cardillo et al. 2005), threatened species are generally characterised by relatively slow life histories respect to non-threatened species (e.g. they are generally larger, have longer gestation times, smaller litter sizes etc.). This has a potential to bias the fitting of GL model parameter toward long-living species respect to short-living ones. Nonetheless, a moderate change in the z parameter, e.g. z=0.29 in our model (calculated as the slope of the linear regression between GL and Rspan for 221 species) vs the theoretical threshold of 0.5 proposed in IUCN guidelines, will have little influence on the calculation of a GL value for short-living species (such as most of rodents), e.g. their modelled GL will remain below 3.3 years in any case (i.e. the arbitrary threshold adopted for short-generation species in the Red List). For those 221 species with GL data reported in IUCN Red List assessments, we modelled the linear relationship between expert-based GL values and calculated GL values (from reproductive life span and age at first reproduction). We found a good fit (R2=0.84) and correlation (cor=0.92, p-value of the Pearson’s test < 2.2e-16) which indicate a good correspondence between reported and calculated GL values, and we are confident that this is a good validation of the overall validity of the GL data reported in the IUCN Red List for mammals. Discrepancies between the calculated GLs and the GLs IUCN might be a mix of process uncertainty (errors in the model) and observation uncertainty (errors in expert-based GL estimates), which are impossible to tease apart.

Since age at last reproduction is generally related to longevity in the wild (IUCN 2013), we assumed it to be equal to the maximum known longevity of the species. Even if published data on maximum longevity often refer to captive individuals, which might cause biases in Rspan estimates, we believe that these biases will probably influence only a limited number of large-bodied species. Moreover, since data on GL stated from experts were available for the majority of large-body species, we reduced the risk of using inaccurate data. We assumed AFR to be equal to age at first birth following IUCN guidelines (IUCN 2013). When information on age at first reproduction for a species was not available, we estimated it by summing gestation length and age at female sexual maturity. For species without empirical data on age at first reproduction for females, we used age at sexual maturity for males.

For carnivore and ungulate species, we completed missing data on maximum longevity and age at sexual maturity through a multiple imputation procedure (Rubin 1987). Carnivores and ungulates are generally characterized by lower levels of missing life-history data respect to other mammal groups (e.g. see Jones et al. 2009). Reproductive parameters used in our analyses were available for over 50% of species among Carnivora, Cetartiodactyla and Perissodactyla. Missing life-history traits were imputed, separately for carnivores and ungulates, following the procedure described in Di Marco et al. (2012). In both datasets, all missing data were imputed 10 times in order to obtain 10 complete datasets for each group. Finally, a median value was calculated for all imputed data for maximum longevity and sexual maturity for each species. Multiple imputation analyses were conducted in R using the package MICE (van Buuren & Groothuis-Oudshoorn 2010).

**Dataset description**

The dataset includes generation lengths of 5426 species mammals. Fields given are:

1. TaxID: identification number of species;
2. Order;
3. Family;
4. Genus;
5. ScientificName;
6. AdultBodyMass\_g: body mass of species in grams;
7. Sources\_AdultBodyMass: AnAge, Animal Diversity, Encyclopedia of Life (eol.org/), Nowak and Paradiso 1999, PanTHERIA, Smith et al. 2003, Verde Arregoitia et al. 2013, Mean congenerics, Mean\_confamilials;
8. Max\_longevity\_d: maximum longevity (days) mediated from PanTHERIA, AnAge and Carn\_Ung (multiple imputation for carnivores and ungulates);
9. Sources\_Max\_longevity: AnAge, Carn\_ung (multiple imputation for ungulates and carnivores) and PanTHERIA;
10. CalculatedRspan\_d: reproductive life span (days) calculated from maximum longevity and age at first reproduction;
11. AFR\_d; age at first reproduction (days);
12. Data\_AFR: calculated or published data;
13. CalculatedGL\_d: GL (days) calculated from reproductive life span and age at first reproduction;
14. GenerationLength\_d: best known estimate of GL (days), including information taken from IUCN database, calculated data and mean estimates;
15. Sources\_GL:

* GMA (IUCN Red List data);
* Rspan-AFB (GL calculated as the difference between reproductive life span and age at first birth);
* Rspan-AFR(SM+Gest) (when data on age at first reproduction were not available, we calculated this parameter as the sum between age at female sexual maturity and gestation length);
* Rspan-ASMmales (GL calculated with age at sexual maturity for males, when data on age at first reproduction for females were not available);
* Mean\_congenerics\_same\_body\_mass (mean GL calculated from congeneric species in the same bin of log body mass);
* Mean\_congenerics (mean GL calculated from congeneric species, irrespective of body mass);
* Mean\_family\_same\_body\_mass (mean GL calculated from confamilial species in the same bin of log body mass);
* Mean\_family (mean GL calculated from confamilial species, irrespective of body mass);
* Mean\_order\_same\_mass (for species with unknown parameter estimates, we assigned the mean GL value of species in the same bin of log body mass and belonging to the same order);
* Mean\_order (mean GL calculated from species belonging to the same order, irrespective of body mass);
* Mean\_all\_orders\_same\_body\_mass (species for which we estimated mean GL from species belonging to the same bin of log body mass).

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