**Methods**

Data

Survival estimates

We obtained survival estimates of raptor species reviewed by Newton, McGrady, and Oli (2016). We extracted information from their dataset to only include studies with estimates for adult birds obtained through formalized statistical methods (i.e., Methods 3-6: capture-mark-recapture or resight, joint live encounters-ring recoveries, radiotracking, multiple data types), and studies that reported sample sizes. We used age-, sex-, year-, area-, and group-specific estimates of survival when available. However, where separate estimates for different groups were provided but group-specific sample sizes were not, we used the arithmetic mean among all age groups (same as for sex, year, area, and other groupings). Then, we assigned each value of a survival estimate that was obtained through methods 3 and 5 as apparent survival estimate (1), and values obtained through methods 4 and 6 as true survival estimate (0).

For studies that do not explicitly report the number of dead birds (i.e., apparent survival estimates reported), we estimated these values using the equation:

ndead= n*j* - (n*j* \* p*i, j*) (Eqn. 1)

where n*j* is the sample size in study *j*, and p*i, j* is the survival estimate of species *i* reported in study *j.*

Species’ traits

We obtained species-specific attributes for the different raptor species from the EltonTraits 1.0 database and from the values reported by Ferguson-Lees and Christie (2001). Specifically, we used the average body mass (kg) of the adults of each species provided by Ferguson-Lees and Christie (2001). When sex-specific survival estimates were provided, we used the average body mass for the given sex of a given species. Otherwise, we used the arithmetic mean of the body mass for both males and females of a given species. We obtained values for the relative importance of invertebrates in species-specific diets and ground foraging for each species from the EltonTraits 1.0 database (Wilman et al., 2016).

Data Analysis

Beta-binomial model for evaluating survival-trait relationships

We evaluated the relationship between body mass, diet, and foraging strategy and the survival estimates of raptor species using a hierarchical beta-binomial model. This approach is used to evaluate the probabilities of observing successes (i.e., total number of survivors) given a number of trials (i.e., sample size), with the probabilities assumed to follow a beta distribution (i.e., survival estimates; Lee and Sabavala, 1987). This modelling framework has been widely used in the fields of epidemiology (Griffiths, 1973), medical diagnostics (Kuss, Hoyer, and Soms, 2014), mental testing (Lord, 1965), and human-environmental studies (Layton and Siikamäki, 2009). Here, we used a hierarchical beta-binomial model where the intercept was allowed to vary for each species, family and study. The model had the form:

(Eqn. 2)

(Eqn. 3)

(Eqn. 4)

In Eqn. 2, yi,j is the total number of survived species *i* in study *j* drawn from a binomial distribution with the parameters *n* (sample size)and *p* (probability of survival). The probability parameter *p* is drawn from a beta distribution with shape parameters (α1 and α2). Each shape parameter is modelled as a function of the estimated survival probability with variance parameter (; Eqn. 3). We modelled the *p* with the following parameters (Eqn. 4): β0 is the intercept for species *i* belonging to family *k* in study *j*, β1 is the slope estimate for the effect of body mass, β2 for the effect of the relative importance/proportion of invertebrates in their diet, β3 for the effect of ground foraging, and β4 for the effect of the type of survival estimate (i.e., apparent or true).

Model implementation and diagnostics

We implemented the model in a Bayesian framework and used weakly-informed priors for all parameters, except the variance term (for the shape parameters) which was informed using results obtained from preliminary assessments, and the effect of mass that was informed using the slope estimated in a previous study (Gelman et al., 2008, Newton, McGrady, and Oli, 2016; See Appendix for more details on the preliminary assessments conducted). We based parameter estimates from the beta-binomial model on four chains of 3000 iterations with 1000 used for warm-up period. We assessed model convergence and mixing of chains through visual inspection and by using the Gelman-Rubin (1992) diagnostic (R̂) and the effective sample size. We performed posterior predictive checks to evaluate deviations of model-generated data from the observed data. We then assessed the predictive performance of our model using k-fold cross validation methods. We interfaced to Stan using the ‘rstan’ package to fit our model in R ver 3.6.3 (Stan Development Team, 2019; R Core Team, 2018).

Model interpretation and forecasting

We report estimates on their original scale (i.e., survival estimate). We interpreted the effect of variables with the probability of direction (PD). PD describes the probability of the values of the coefficient estimates to be positive or negative (Makowski et al., 2019). Specifically, we quantified the probability of the effect of mass, diet, foraging strategy, and the estimate type (apparent or true) on the survival estimate.

We used the mean estimates for the main parameters of our model to predict the survival of other raptor species. We used the species-specific body mass of the adults of 523 species provided through the EltonTraits database (Wilman et al. 2016) and input them in the model equation to generate forecasted survival estimates for each species based on their mass, diet, and foraging strategy.

**Results**

We reviewed 65 journal articles on the survival estimates of 36 raptor species. Of these 65 references, 11 reported true survival of six raptor species. On average, adult raptors included in the analysis had a 65% survival probability. Moreover, the effect of estimate type was weakly negative (P (β2 < 0) = 0.57). This provides weak evidence that values obtained using methods yielding apparent survival estimates are generally lower.

Among the six families to which the raptor species were assigned, Cathartidae had the highest survival probability (94%). Other families, including Accipitridae (71%), Falconidae (74%), Pandionidae (64%), Strigidae (73%), and Tytonidae (65%) had much lower survival probabilities. Consistently, the top three species with the highest survival probabilities (94-99%) were vulture species including the Andean condor (*Vultur gryphus*)*,* Bearded vulture(*Gypaetus barbatus*), Griffon vulture (*Gyps fulvus*). Two species, including the boreal owl (*Aegolius funerus*)and the prairie falcon (*Falco mexicanus*) exhibited the lowest survival probabilities (<50%), at 46% and 49%, respectively.

Trait-survival relationships

Traits that we explored showed weak positive association with survival. Among the three, body mass exhibited the highest probability of being positively associated with species’ survival (P (β1 > 0) = 0.51). In fact, for species weighing <1.5 kg, the mean survival was around 69%, for species weighing from 1.6 to <6 kg, their mean survival was around 81%, and for larger-bodied species ( >6.1 kg), their mean survival was around 86%. Moreover, ground foraging strategy was only weakly associated with survival patterns (50%). On the other hand, degree of invertebrate diet specialization showed a moderately negative association with survival (P (β1 < 0) = 0.66). In other words, species less dependent on invertebrates as prey items tended to exhibit higher survival probabilities.

**Forecasted survival estimates**

**Appendix**

Preliminary assessment on survival and mass relationships

Beta regression model

We developed a beta regression model implemented in a Bayesian framework using the survival estimates of 40 raptor species (for both juveniles and adults) obtained from 77 journal articles reviewed by Newton, McGrady, and Oli (2016). We allowed the intercept to vary per species and study. Thus, the model had the form:

Eqn. 1

where β0 is the intercept for species *i* in study *j*, β1 is the slope for body mass, and β2 is the slope for the type of survival estimate (i.e., apparent or true). We obtained an estimate for the variance parameter from this model (= 7.3 [7.3, 7.4]) and used this to inform the mean of the variance parameter in the beta-binomial model.

*Beta-binomial model code*

|  |
| --- |
| data {  int<lower=0> N; // no.of obs  int <lower=0> y[N]; // survivors  int <lower=0> n[N]; // total  vector [N] mass;// ave.mass in kg  vector [N] diet; //invertebrate diet  vector [N] forage; //ground foraging strategy  int species[N]; //ID of each species  int family [N]; //ID of family  int study [N]; //ID of study  int Nsp; //no.of species  int Nst; //no.of studies  int Nfam;// no. of families  vector[N] death\_type;// direct/indirect  }    parameters {  real alpha;// global intercept  real mass\_eff; //slope mass  real est\_eff; //slope indirect effect  real diet\_eff;//slope diet  real for\_eff;// slope foraging strat  real<lower=0> sigma\_sp[Nsp];//errors for random effects  real<lower=0> sigma\_st[Nst];//errors for random effects  real<lower=0> sigma\_fam[Nfam];//errors for random effects  real <lower=0> phi;  real <lower=0, upper=1> pred\_surv[N] ;//survival per observation  }      transformed parameters{  vector <lower=0, upper=1> [N] surv\_mu; //mean estimated survival  vector <lower=0> [N] A;  vector <lower=0> [N] B;  vector [Nsp] alpha\_sp; //random intercept per species  vector [Nst] alpha\_st;// random intercept per study  vector [Nfam] alpha\_fam;// random intercept per family    for (j in 1:Nsp) {    alpha\_sp[j]= alpha+phi\*sigma\_sp[j];  }  for (k in 1:Nst) {    alpha\_st[k]= alpha+phi\*sigma\_st[k];  }    for (m in 1:Nfam) {    alpha\_fam[m]= alpha+phi\*sigma\_fam[m]; }      //model:    for (i in 1:N){    surv\_mu[i]= inv\_logit(alpha\_sp[species[i]]+alpha\_st[study[i]]+alpha\_fam[family[i]]+  mass\_eff\*mass[i]+est\_eff\*death\_type[i]+diet\_eff\*diet[i]+for\_eff\*forage[i]);  // mass\_fam[family[i]]+diet\_fam[family[i]]+for\_fam[family[i]]);  }    A = surv\_mu \* phi;  B = (1 - surv\_mu)\* phi;    }  model {  //priors  mass\_eff~ normal (0.1,1);  est\_eff~ normal (0,1);  diet\_eff~normal(0,1);  for\_eff~normal(0,1);  sigma\_sp~ normal(0,1);  sigma\_st~ normal(0,1);  sigma\_fam~ normal(0,1);    phi ~normal(7,1);// use info. from beta regression of all juv and adult    //model likelihood:    pred\_surv ~ beta(A, B); // survival estimate, beta dist.  y~binomial(n, pred\_surv); //no.of survivors drawn from binomial dist; based on sample size and reported survival estimate  }  generated quantities {    real pred\_y [N];//predictions on survival  real log\_lik [N];// for looic calculations    pred\_y = beta\_rng(A, B);    for (x in 1:N){  log\_lik[x]= beta\_lpdf(pred\_surv[x]| A[x], B[x]);}  } |

*Beta regression model code*

|  |
| --- |
| data{  int<lower=0> N; // no.of obs  real <lower=0, upper=1> survival[N]; //survival estimate  real <lower=0> mass[N];// ave.mass in kg  int species[N]; //ID of each species  int study [N]; //ID of study  int Nsp; //no.of species  int Nst; //no.of studies  int death\_type[N];// direct/indirect  }  parameters {  real <lower=0> alpha;// global intercept  real <lower=0> alpha\_sp[Nsp]; //random intercept per species  real <lower=0> alpha\_st [Nst];// random intercept per study  real <lower=0> beta1; //slope mass  real <lower=0> beta2; //slope indirect effect  real<lower=0> sigma\_sp;//errors for random effects  real<lower=0> sigma\_st;//errors for random effects  real <lower=0> phi;  }  transformed parameters{  vector <lower=0, upper=1> [N] surv\_mu; //estimated survival  vector <lower=0> [N] A;  vector <lower=0> [N] B;    for (i in 1:N){    surv\_mu[i]=  inv\_logit(alpha+beta1\*mass[i]+beta2\*death\_type[i]+alpha\_sp[Nsp]+alpha\_st[Nst]);  }    A = surv\_mu \* phi;  B = (1 - surv\_mu )\* phi;// look into this, if phi is not=1, relationship not hold  }    model {  //priors    alpha~ normal (0,1);  beta1~ normal (0,1);  beta2~ normal (0,1);  sigma\_sp ~normal(0,1);  sigma\_st~ normal(0,1);  phi~ normal(0,1);    for (i in 1:N){    survival[i]~ beta(A, B);  }    for(j in 1:Nsp){  alpha\_sp[j]~normal(0, sigma\_sp);  }  for (f in 1: Nst){  alpha\_st[f]~normal(0, sigma\_st);  }  }  generated quantities {  real log\_lik [N];//predictions  log\_lik = beta\_rng(A, B); } |