Report for the Irish Red Kite Project Development Group

Alan Fielding and Paul Haworth

Haworth Conservation

Potential impact of the removal of young birds on the Welsh red kite population

1. Aim

To assess the impact that the removal of 40-53 young red kites per year, over five years, would have on the Welsh population. The removals would begin in 2007.

2. Population modelling software

2.1 Modelling software

Models were implemented using the ULM (Unified Life Models) software (Version 4.4, May 2006) originally developed by Legendre and Clobert (1995) and developed further by Stéphane Legendre (http://www.biologie.ens.fr/~legendre/ulm/ulm.html). The ULM software models a wide range of population dynamics using a model description text file. The text file for the main model used in these analyses is listed in Appendix 1. Full details of the modelling procedure have been included so that interested parties can repeat or modify them.

2.2 Model structure

There are three main parameter categories used in the models. They are outlined below and a fuller description of the implementation is given later.

1. **Survival rates (*s1, s2 and v*)**: in this model it is assumed that the red kite population can be modelled as three age classes: 0-1, 1 – 2 and 3+ years. Age specific survival rates were obtained from Davies *et al* (2001): juvenile birds (from fledging to age 1) 0.66 (*s1*), all other age classes have an annual survival rate of 0.81 (*s2 and v*).

2. **Reproductive value (*f*)**: the reproductive output of the population is the number of females fledged per pair and depends on the sex ratio, the proportion of pairs that breed and the number of young raised by successful pairs. For birds in their third year and beyond the mean number fledged by a successful pair (*p*) was 1.44 and 62% of pairs (*gamma*) were assumed to be successful (38% failure rate). The sex ratio (*sigma*) is assumed to be 0.5 so the mean number of females fledged per pair (*f*) is *p.gamma.sigma* or *f* = 0.5 x 1.44 x 0.62 (0.45 females per pair). Second year females are assumed to breed at a rate which is one third of the older birds. If birds are removed for the Irish re-introduction this effectively

reduces the population's reproductive value. For example, in 2006 462 birds were fledged at a rate of 1.42 per successful pair. If 50 young birds are removed from nests the total fledged reduces to 412 and the rate reduces from 1.42 to 1.27.

3. **Initial population age structure ($n1$, $n2$ and $n3$)**: the starting values are based on the 2006 data recorded in Issue 18 (2006) of Boda Wennol (Newsletter of the Welsh Kite Trust). There were 340 pairs ($n3$) and 156 first year female birds ($n1$), using 66% survival of the 475 birds fledged in 2005 and an equal sex ratio. Finally, there were 104 second year female birds ($n2$), which are 81% of the 66% of survivors from the 390 young fledged in 2004.

The model is expressed in a matrix format with an associated vector of numbers per age class. $s1$ and $s2$ are survival rates for birds in their first and second years, v is the adult survival rate. fj and f are measures of reproductive output for second year and three+ year birds.

```
0,    fj,    f
s1,   0,     0
0,    s2,    v
```

2.3 Model parametization

In order to capture the annual variability in these vital rates a stochastic approach was used, combined with a montecarlo simulation. This is described below. Models were run for 50 years with 1000 simulated population trajectories. The key parameter of interest in these models is the population growth rate. As long as this is above one the population should continue to expand. The impact of the removals can be measured by comparing the mean population growth rates from the two models.

Survival rates

Survival rate (js) for first year birds	0.66
Standard deviation (jssd) for js used for the stochastic simulations	0.05
Upper limit for js (jsmax), the normal adult survival rate	0.81
Default survival rate (ads) for year 2 and 3+ birds	0.81
Upper limit for ads (asmax)	0.95

Instances for each simulation are obtained via a two-stage process. First a candidate survival value is drawn from a from a variant of the beta distribution which has a bell shape for the small standard deviations used in this study: for example: `defvar sa = beta1f(js, jssd)`, where js is the mean and jssd the standard deviation. The second stage checks to see if the random candidate value has exceeded the maximum, if it has it is capped at the maximum: for example,
`defvar s1 = if(sa>jsmax,jsmax,sa)`.
There is no lower limit to survival rate.

Similar calculations are used to obtain values for s2 and v, except that the maximum value is 0.95.

Reproductive characteristics

The proportion of breeders, *gamma*, is obtained as a random value from a modified beta distribution with a mean of 0.62 (62% breeders) and a standard deviation of 0.05:

```
defvar gamma  = beta1f(0.62,0.05)
```

The mean number fledged per successful pair, *p*, used in a particular simulation is drawn randomly from a gaussian distribution with a mean of 1.44 and a standard deviation of 0.05.

```
defvar p = gaussf(1.44,0.05).
```

Similarly, the sex ratio used in a particular simulation is drawn randomly from a beta distribution with a mean of 0.5 (equality) and a standard deviation of 0.05.

```
defvar sigma = beta1f(0.5,0.05)
```

The fecundity or reproductive value (*f*) is obtained as the product of these three parameters: *p.gamma.sigma.*

Simulated Harvesting for the re-introduction

If young birds are removed ('harvested') for the proposed re-introduction programme it can be simulated by reducing the number of young fledged per pair. However, this reduction will only take place for the first five years. In 2006 462 young were fledged by 325 successful pairs, giving a mean per pair of 1.42 (462/325). If 50 of these newly fledged birds are removed the number fledged reduces to 412, which means that the mean number fledged by successful pairs reduces to 1.27 (412/325). In these simulations the reduction is achieved by calculating two values for *p* (*p1* & *p2*), where *p1* is the value with no removals and *p2* is the value after 50 young have been reduced.

```
defvar p1 = gaussf(1.44,0.05)
```

```
defvar p2 = gaussf(1.27,0.05)
```

A value for *f* is calculated as above but using *p1* for the first five years and *p2* after the remaining 45 years.
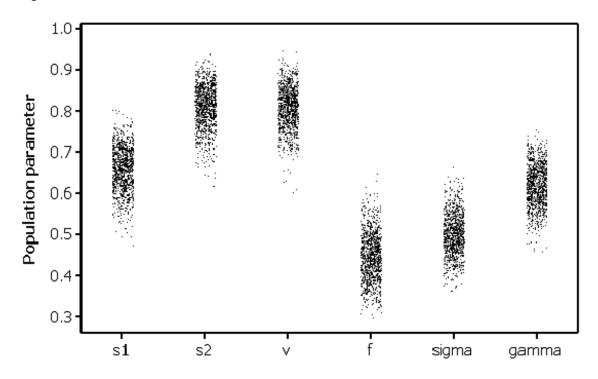
```
defvar p = if(t<6,p2,p1)
```

The level of noise introduced by this stochastic approach is shown in Table 1 and Figure 1. The mean values in Table 1 show that the desired values were achieved during the siumations.

Table 1. Summary statistics for six population vital rates from 1000 simulations.

Variable	Mean	SE	SD	Minimum	Maximum
s1	0.65858	0.00166	0.05235	0.47490	0.80460
s2	0.81246	0.00159	0.05042	0.61630	0.93910
v	0.80856	0.00159	0.05021	0.60190	0.94770
f	0.44567	0.00183	0.05785	0.29820	0.64860
sigma	0.50063	0.00158	0.04982	0.36470	0.66520
gamma	0.61761	0.00158	0.05009	0.45730	0.75410

Figure 1. Individual values for six of the vital rates from 1000 simulations.

3. Results

The removal of 50 newly fledged red kites each year for five years has minimal impacts on the Welsh population's future trajectory.

The mean population growth rates with and without removals are 1.048 and 1.048 (standard errors for both are <0.00025). Therefore, over the 50 year simulation both populations are predicted to expand by approximately 5% each year. During the five years when removals are taking place the mean population growth rate declines to approximately 1.028, which still allows the population to expand by approximately 3% per year.

Similarly, the mean scaled population structures are very similar being 26.34% (n1), 16.75% (n2) and 56.90% (n3) for the unharvested population and 26.50% (n1), 16.72% (n2) and 56.78% (n3) for the harvested population.

In reality, it is highly unlikely that the 4.8% growth rates would be maintained for 50 years, if it was the populations would rise to approximately 3,500 pairs. It is much more likely that density dependent mechanisms would begin to regulate the population. Figure 2 shows the predicted population trajectories for both simulated populations. The removal of 250 young over a five year period has created a lag in the harvested population, suggesting the eventual maximum population size will be delayed by a few years.
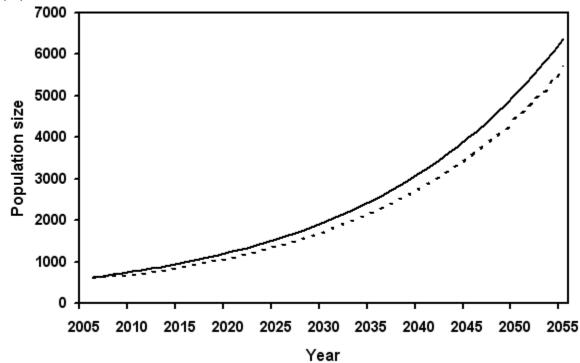
Figure 2. Simulated population trajectories (all age classes combined). The harvested population has a dotted line.

How do the 'normal' results compare with actual population growth of the Welsh population? Using the number of pairs between 1980 and 2000 the actual mean population growth rate was 1.094 compared with the 1.048 obtained for these simulations. The observed rate can be achieved in the model if v (adult survival) is increased to 0.88.

4. References

Davis, P., Cross, T. and Davis, J. 2001. Movement, settlement, breeding and survival of red kites *Milvus milvus* marked in Wales. *Welsh Birds,* 3:18-43.

Legendre, S and Clobert, J. 1995. ULM, a software for conservation and evolutionary biologists. *Journal of Applied Statistics,* **22:**817-834. (Version 4.4. downloaded from http://www.biologie.ens.fr/~legendre/ulm/ulm.html).

Appendix 1 Model description file for the harvesting simulation

```
{ Matrix for welsh red kite, uses 2006 values and
{ 3 age classes.

defmod redkite(3)
mat : a
vec : w

defvec w(3)
n1, n2, n3

{ ---------------------------------------------------------------
{ Set the initial values for the number of individuals in each
{ age class

{66% of 475 fledged in 2005, half are female
defvar n1 = 156

{81% of (390 x 0.66) / 2 for females
defvar n2 = 104

defvar n3 = 340

defvar n = n1 + n2 + n3

{ ---------------------------------------------------------------
{ Set the initial values for the survival rates

{ ads is adult survival rate
defvar ads = 0.81

{ immature (year 1) survival rates with sd and maximum values:
defvar js = 0.66

defvar jssd = 0.05

defvar jsmax = ads

defvar sa = beta1f(js, jssd)

defvar s1 = if(sa>jsmax,jsmax,sa)

{ second year birds with sd and maximum values
defvar imsd = 0.05

defvar immsmax = 0.95

defvar sc = beta1f(ads, imsd)
```

```
defvar s2 = if(sc>immsmax,immsmax,sc)

{ adult survival rate
defvar adsd = 0.05

defvar adsmax = 0.95

defvar sd = beta1f(ads, adsd)

defvar v = if(sd>adsmax,adsmax,sd)

{ --------------------------------------------------------------
{ Set the initial values for reproductive output

{ proportion of breeders
defvar gamma  = beta1f(0.62,0.05)

{ with no harvesting only line needed is:
{ defvar p = gaussf(1.44,0.05)

{ output reduced for 50 removals
defvar p1 = gaussf(1.44,0.05)

{ fecundity
defvar p2 = gaussf(1.27,0.05)

{only harvest for first 5 years
defvar p = if(t<6,p2,p1)

{ sex ratio
defvar sigma = beta1f(0.5,0.05)

{ fertility
defvar f = sigma*p*gamma

{ early breeders, set at 33% of f
defvar  fj = f/3

{ --------------------------------------------------------------
{ Model structure

defmat a(3)
 0,  fj,   f
 s1,  0,   0
 0,  s2,   v

{ end of description file
```