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Preliminary GRPC IPM Work

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Brackets indicate line numbers in the code

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**Part 1: Data Wrangling**

*Vital rate data*

[Init\_GRPC.R 16-88]

I drew the pre- and post-construction lower level vital rates from the mean values reported in Table 4.3 in (Sandercock 2013). These mean values are considered deterministic parameters used to calculate fecundity values for pre- and post-construction years. NOTE that I could not find juvenile survival values in the DoE report, so I took the McNew et al. 2012 value (which is pre-construction only)

*Lek count data*

[Init\_GRPC.R 90-125]

I then turn to extracting population survey data from the lek counts (“lek\_metadata.csv”, formatted from the original “UK\_lek\_metadata\_tables.xlsx” file). These lek counts were used, I believe, in (Winder et al. 2015). I format a tidier dataset which contains the lek code (A, B, C, …), the year of the survey, the type of the survey (flush/trap), the total population count and, if present, the sex-differentiated count. All missing values are assigned *NA.*

[Init\_GRPC.R 127-160]

I then broadly follow (Winder et al. 2015) to determine female counts for each LEK and YEAR. First, I take *all* of the lek counts that have sex-differentiated counts. These include both flush and trap counts. I calculate a coefficient *discount*=N.M/N.TOT, and find a single mean value of this coefficient. I step through every row of lek data and discount the male counts: If there is a sex-differentiated N.M, I keep it; if there is only N.TOT, I calculate N.M for that count as N.TOT\**discount*.

[Init\_GRPC.R 162-215]

For each lek and year, I determine the proportion of surveys that were flush or trap counts. I find the *maximum* male count for each lek, year, and trap type, and then calculate a weighted mean as:

COUNT(lek, year) = MaximumFlushCount \* P.FlushCount + MaximumTrapCount \* P.TrapCount

I convert these to female counts directly. That is, Max\_N.F(lek, year) = Max\_N.F(lek,year). There are no further manipulations.

Finally, I calculate the summary lek count data: The total female counts per year, across all leks, and the proportion of leks surveyed each year.

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**Part 2: IPM**

[ipm\_grpc.jags]

The model combines the vital rate (i.e., age-specific fecundity and survival) and the summary lek count data to estimate an immigrant subpopulation size (Kéry and Schaub 2011). The model has only two subpopulations, as the pre- and post-construction vital rates are not separated by age-class: Returning adults (N.a) and immigrants (N.i). Priors for subpopulation sizes are initialized as a normal distribution with a mean of 150 (~ half each of the total 2007 population size given the ) for the first year for each population size. This initialization means that the subpopulation structure of the first year obviously does not carry useful information.

**Fecundity (f) is calculated within the model code for each year following the equation in McNew et al. 2012. Fecundity will differ deterministically in the pre- and post-construction periods, as the parameters differ only across those periods (with no other source of variance). Unlike in McNew et al. 2012, I use nest vs. renest differences in Hatching Success (as reported in Sandercock 2013).**

Immigrants are assumed to have the same annual survival rate as returning adults.

The number of immigrants for each year *t+1* (numImms) is estimated with a static mean μ and temporal variance ε[t], where:

ε[t]

The annual per-capita immigration rate, ω, is then derived as:

See (Schaub and Fletcher 2015) for further discussion on estimating immigration as a rate vs. a count.

The numImms μ parameter has a Uniform(0,100) prior, while the numImms ε[t] parameter has a Normal(0, τ) prior, where τ = 1 / Uniform(0,10)2 .

The state process links the subpopulation sizes and the information from the vital rates. Given the constant mean vital rates as simple inputs in this model, we draw fledgling population sizes for each year *t* from (t=2 to t=N.YEARS):

We then calculate the subpopulation sizes for that year:

**NOTE that the changing number of surveyed leks is accounted for relatively crudely, where the overall TRUE count is assumed to be the OBSERVED COUNT divided by PROPORTION OF SURVEY LEKS**

Finite rate of population growth, λ, is derived as the ratio of population sizes in years *t+1* and *t*:

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**References**

Kéry, M., and M. Schaub. 2011. Bayesian population analysis using WinBUGS: a hierarchical perspective. Academic Press.

Sandercock, B. K. 2013. Environmental Impacts of Wind Power Development on the Population Biology of Greater Prairie-Chickens. Final Technical Report, Department of Energy.

Schaub, M., and D. Fletcher. 2015. Estimating immigration using a Bayesian integrated population model: choice of parametrization and priors. Environmental and Ecological Statistics 22:535–549.

Winder, V. L., A. J. Gregory, L. B. McNew, and B. K. Sandercock. 2015. Responses of male Greater Prairie-Chickens to wind energy development. The Condor 117:284–296.