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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 9-88]

Following (McNew et al. 2012), I sample the mean vital-rate values from “random LTRE LL gpc.r” from Brett. I keep all values the same except for NEST probability (N.Prob) and RENEST Probability (Re.N.Prob), which I both set to 1.0 . I then calculate the yearling (F.Y) and adult (F.A) fecundities, create the Leslie matrix, and determine the population growth rate (LAMBDA.VR) from the dominant eigenvalue.

*Lek count data*

[Init\_GRPC.R 96-126]

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 128-160]

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 163-215]

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: “Standard” Vital Rate + Survey Count IPM**

[ipm\_1.GRPC.jags]

The first IPM 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 three different (female) subpopulations: Second-year (N.SY), after-second-year (N.ASY), and immigrant of unknown age (N.Imm). Priors for subpopulation sizes are initialized as a normal distribution with a mean of 50 for the first year for each population size. NOTE that I do not incorporate any additional information about stable age distribution from the vital rate matrix, as I’m not sure (yet) how that would function given the unknown age distribution of immigrants.

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 three things from this model:

1. In our initial fecundity calculation (in Part 1), we assume an even sex-ratio of fledglings.
2. Survival and Fecundity of Immigrants are currently taken as the mean Survival/Fecundity of SY and ASY adults. As with the stable age distribution issue, I’m not sure of the age-class of immigrants. Is it possible to get a sense of this to inform these parameters? Do we have empirical data on the survival and fecundity of new immigrant females?
3. Number of immigrants each year is drawn from a Poisson distribution of the estimated numImms parameter.

The observation space relates the subpopulation sizes to the lek count data with a Poisson distribution, including the proportion of leks surveyed for the year:

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

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**Part 3: λ-Diff IPM**

[ipm\_2.GRPC.jags]

This second model brings together the information through two *population growth rates*, one from the eigenvalue of the vital-rate matrix (λ.VR) and the other which integrates the lek count data (λ.lek). This model is drawn from (Davis et al. 2014). To be honest, I couldn’t keep up with some of their parameter subscripts (some of which I think may include typos!), and I understand this model far less well than the first one. However, I have included it here for the following reason:

(Davis et al. 2014) remark that their model, which draws a λ.VR from a vital-rate matrix and estimates a λ.lek after integrated population count data relates the two across *sexes*. In other words, the λ.VR represents the female population information, while the λ.lek (which, like our data, draws on male high-count data), represents the male population information. However, if we are to be sincere in taking our male high count data as representative of the female population size (or, alternatively, if we are to be sincere in believing that the sexes’ variation in rate of population change are closely correlated), then the parameters matching λ.VR to λ.lek (*a* and *b*, below), represent intercept and slope information about the influence of immigration.

This short model has complicated priors (see the code and the Davis paper), which do seem important to the results. I haven’t done thorough testing but there are big changes based on prior changes. However, the crux of the model is the linear mapping of λ.VR to λ.lek:

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This gives an output of λ.lek, *a*, *b*, and σ. The latter three parameters relate λ.lek to λ.VR, and therefore (I would argue) give us information about immigration.

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**Running the code**

Required packages: tidyverse, lubridrate, magrittr, jagsUI

jagsUI requires JAGS to run.

Navigate to the correct working direction (the GRPC folder containing Data/, Scripts/, and Output/)

The code should run easily if you run the “Run\_GRPC.R” script. This should load and initialize the data from the Data/ file, do the calculations in “Init\_GRPC.R”, run the model of your choice, and sort out some summary output.

You can specify the number of chains, thinning, burn-in, and iterations for either of the models at the top of the script. You also specify the model number, 1 or 2, at the top.

You can investigate the “out” R Object to view a summary output. This output is automatically saved into the Output/ folder. You can reload this output by using the command ‘load(“Output/out\_Model\_1”)’, for example.

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**References**

Davis, A. J., M. B. Hooten, M. L. Phillips, and P. F. Doherty. 2014. An integrated modeling approach to estimating Gunnison sage-grouse population dynamics: combining index and demographic data. Ecology and Evolution 4:4247–4257.

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

McNew, L. B., A. J. Gregory, S. M. Wisely, and B. K. Sandercock. 2012. Demography of greater prairie-chickens: Regional variation in vital rates, sensitivity values, and population dynamics. The Journal of Wildlife Management 76:987–1000.

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