SPI-IPM Code Manual

Chloé R. Nater

2021-09-30

Contents

A	bout	this manual	5
1	Pre	paring SPI-Birds data for Bayesian analysis	7
	1.1	Nest count data	8
	1.2	Clutch size data	8
	1.3	Fledgling count data	8
	1.4	Mark-recapture data	8
	1.5	Immigrant count data	8
	1.6	Auxiliary data on the sampling process	8
2	IPN	A Construction	9
	2.1	Open population model with 2 age classes	9
	2.2	Data likelihoods	11
	2.3	Priors and constraints	12
3	Modelling temporal variation		
	3.1	Random year variation	13
	3.2	Temporal covariates	13
	3.3	Notes on covariate selection	13
4	IPN	M Implementation	15
	4.1	Efficient implementation using NIMBLE	15
	4.2	Simulation of initial values	15
	4.3	Test runs and full runs: chains, iterations, burn-in, and thinning	15
	4.4	Trouble-shooting implementation issues	15

4 CONTENTS

5	\mathbf{Mo}	del Assessment	17
	5.1	Assessing chain convergence	17
	5.2	Plotting data vs. predictions	17
	5.3	Comparing estimates from integrated vs. independent analyses $$.	17
	5.4	"Reality check" using stochastic simulations	17
	5.5	Other approaches	17
6	Vis	ualizing and interpreting direct IPM outputs	19
	6.1	Population trajectories	19
	6.2	Within-population variation in vital rates	19
	6.3	Between-population variation in vital rates	19
	6.4	Covariate effects	19
7	Foll	ow-up Analyses	21
7	Fol! 7.1	ow-up Analyses Testing for time-trends	21 22
7		•	
7	7.1	Testing for time-trends	22
7	7.1 7.2	Testing for time-trends	22 22
7	7.1 7.2 7.3	Testing for time-trends	22 22 22
8	7.1 7.2 7.3 7.4 7.5	Testing for time-trends	22 22 22 22
	7.1 7.2 7.3 7.4 7.5	Testing for time-trends	22 22 22 22 22
	7.1 7.2 7.3 7.4 7.5	Testing for time-trends	222 222 222 222 223

About this manual

Briefly on the need for/value of standardized data and analyses.

Why IPMs are popular and what they are suitable for (Kéry and Schaub, 2011; Plard et al., 2019).

Overview over workflow, code repository & contents of manual (Figure 1).

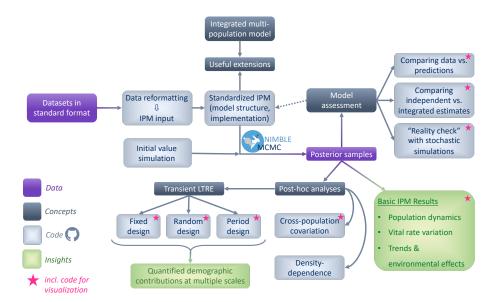


Figure 1: Schematic representation of the SPI-IPM workflow.

In no way complete: great if user's analyses/adaptations become part. How to cite.

6 CONTENTS

Preparing SPI-Birds data for Bayesian analysis

8CHAPTER 1. PREPARING SPI-BIRDS DATA FOR BAYESIAN ANALYSIS

- 1.1 Nest count data
- 1.2 Clutch size data
- 1.2.1 Nest level
- 1.2.2 Population level
- 1.3 Fledgling count data
- 1.3.1 Nest level
- 1.3.2 Population level
- 1.4 Mark-recapture data
- 1.4.1 Individual capture histories
- 1.4.2 M-array
- 1.5 Immigrant count data
- 1.6 Auxiliary data on the sampling process
- 1.6.1 Nest survey sampling effort
- 1.6.2 Capture probability proxies

IPM Construction

2.1 Open population model with 2 age classes

2.1.1 Model description

Population dynamics are represented using a female-based age-structured open population model with a pre-breeding census in spring. At census, females are divided into two age classes: "yearlings" (1-year old birds hatched during the breeding season of the previous year) and "adults" (birds older than one year). The motivation underlying this distinction is that reproductive output often differs for these two age classes in passerine birds. The dynamics of the female segment of the population over the time-interval from census in year t to census in year t+1 can be described with classic matrix notation (Caswell, 2001) as:

$$N_{tot,t+1} = \begin{bmatrix} N_{Y,t+1} \\ N_{A,t+1} \end{bmatrix} = \begin{bmatrix} 0.5F_{Y,t}sJ_t & 0.5F_{A,t}sJ_t \\ sA_t & sA_t \end{bmatrix} \begin{bmatrix} N_{Y,t} \\ N_{A,t} \end{bmatrix} + \begin{bmatrix} Imm_{Y,t+1} \\ Imm_{A,t+1} \end{bmatrix}$$

 $N_{tot,t+1}$ represents the total number of yearling and adult females in the population upon arrival in the breeding areas in year t. The total female population size, $N_{tot,t+1}$, is the sum of the numbers of yearling and adult females in the population in year t+1 ($N_{Y,t+1}$ and $N_{A,t+1}$, respectively) and consists of local survivors and recruits from the previous breeding season, as well as immigrant yearling ($Imm_{Y,t+1}$) and adult ($Imm_{A,t+1}$) females.

 $F_{a,t}$ represents the expected number of fledglings produced by age class a females during the breeding season in year t and is the product of several vital rates. First, females in age class a may breed in a nestbox with probability $pB_{a,t}$ upon

arrival to breeding areas in year t. Each breeding female may then lay a clutch containing a certain number of eggs (expected number $=CS_{a,t}$), and each egg within the clutch may hatch and survive to fledging. The probability of an egg hatching and surviving to fledging is divided into an age-independent probability of nest success (pNS_t) , probability of complete clutch failure $=1-pNS_t)$ and a survival probability of every egg/chick to fledging provided that the nest has not failed entirely $(sN_{a,t})$, with a= age of the mother). Consequently, the expected number of fledglings produced by age class a females in year t is defined as:

$$F_{a,t} = pB_{a,t} \times CS_{a,t} \times pNS_t \times sN_{a,t} \tag{2.1}$$

Fledglings that survive to the next breeding season and remain within the population (probability = sJ_t) contribute to next year's yearling class ($N_{Y,t+1}$). Yearlings and adults that survive to the next breeding season and remain within the population (probability = sA_t) become part of next year's adult age class ($N_{A,t+1}$).

2.1.2 Code implementation including demographic stochasticity

Population process models within IPMs are typically implemented as stochastic models that account for randomness in the outcomes of demographic processes at the individual level ("demographic stochasticity", Caswell, 2001; Kéry and Schaub, 2011). The model described here is no different, meaning that the numbers of breeders, fledglings, and survivors are treated as binomial and Poisson random variables.

Reproduction is modelled via two sets of random variables: a binomial random variable representing the number of breeders in age class a in year t, $B_{a,t}$ and a Poisson random variable representing the number of fledlings produced by breeders of age class a in year t, $Juv_{a,t}$. The implementation in the BUGS language used in the SPI-IPM code (IPMSetup.R, lines 231-241) looks like:

```
for (t in 1:Tmax){
  for(a in 1:A){

    ## 1) Breeding decision
    B[a,t] ~ dbin(pB[a,t], N[a,t])

    ## 2) Offspring production
    Juv[a,t] ~ dpois(B[a,t]*CS[a,t]*pNS[t]*sN[a,t]*0.5)
}
```

Analogously, the numbers of local survivors – both fledglings surviving their first year and becoming yearlings, and yearlings and adults surviving to the next year – are implemented as binomial random variables (IPMSetup.R, lines 243-255):

```
for (t in 1:(Tmax-1)){

## 3) Annual survival of local birds

# Juveniles -> Yearlings
localN[1,t+1] ~ dbin(sJ[t], sum(Juv[1:A,t]))

# Yearlings/Adults -> adults
localN[2,t+1] ~ dbin(sA[t], sum(N[1:A,t]))

## 4) Immigration
for(a in 1:A){
   N[a,t+1] <- localN[a,t+1] + Imm[a,t+1]
}
</pre>
```

Immigrant numbers are also treated as outcomes of stochastic processes, and these are detailed in 2.2.5 Immigrant count data likelihood.

2.2 Data likelihoods

IPMs obtain information on the population model's parameters (population sizes and vital rates) from several different data sets. Information in each data set is channeled into model parameters via one or multiple data likelihoods. The SPI-IPM contains five data modules consisting of a total of eight data likelihoods: nest count data (one likelihood), clutch size data (two likelihoods), fledgling count data (three likelihoods), mark-recapture data (one likelihood), and immigrant count data (one likelihood). The likelihoods contained in each data module are described in detail in the following sub-chapters. The underlying data sets are introduced in Chapter 1 of the manual.

- 2.2.1 Nest count data likelihood
- 2.2.2 Clutch size data likelihoods
- 2.2.3 Fledgling count data likelihoods
- 2.2.4 Mark-recapture data likelihood
- 2.2.5 Immigrant count data likelihood
- 2.3 Priors and constraints

Modelling temporal variation

- 3.1 Random year variation
- 3.2 Temporal covariates
- 3.2.1 Continuous variables
- 3.2.2 Categorical variables
- 3.2.3 Imputation of missing covariate values
- 3.3 Notes on covariate selection

IPM Implementation

4.1 Efficient implementation using NIMBLE

We use the fantastic **nimble** package (de Valpine et al., 2017)!

- 4.2 Simulation of initial values
- 4.3 Test runs and full runs: chains, iterations, burn-in, and thinning
- 4.4 Trouble-shooting implementation issues

Model Assessment

- 5.1 Assessing chain convergence
- 5.2 Plotting data vs. predictions
- 5.3 Comparing estimates from integrated vs. independent analyses
- 5.4 "Reality check" using stochastic simulations
- 5.5 Other approaches

Running for additional years and comparing to non-included data, PPCs, etc.

Visualizing and interpreting direct IPM outputs

- 6.1 Population trajectories
- 6.2 Within-population variation in vital rates
- 6.2.1 Age-class-specific averages
- 6.2.2 Year-by-year variation
- 6.3 Between-population variation in vital rates
- 6.3.1 Population-specific averages
- 6.3.2 Year-by-year variation
- 6.4 Covariate effects

20 CHAPTER~6.~~VISUALIZING~AND~INTERPRETING~DIRECT~IPM~OUTPUTS

Follow-up Analyses

- 7.1 Testing for time-trends
- 7.2 Testing for density-dependence
- 7.3 Investigating cross-population covariation
- 7.4 Quantifying demographic contributions to short term population dynamics
- 7.4.1 Year-by-year variation in population growth rate (random design LTRE)
- 7.4.2 Year-to-year differences in population growth rate (fixed design LTRE)
- 7.5 Quantifying demographic contributions to long-term population trends
- 7.5.1 Differences in population trajectories between time periods (period design LTRE)
- 7.5.2 Differences in population trajectories between locations (period design LTRE with time-by-space substitution)

Useful extensions and outlook

- 8.1 Adapting the population model for your species/population
- 8.1.1 Accounting for multiple broods per bird per year
- 8.1.2 Altering age structure
- 8.1.3 Individual heterogeneity beyond age: sex, traits, and more
- 8.2 Including additional data and informative priors
- 8.2.1 Including partially observed age information
- 8.2.2 Making the most of auxiliary knowledge about immigrants/dispersers
- 8.2.3 Letting published values help with estimation when data is sparse
- 8.3 Building on the multi-population perspective
- 8.3.1 Joint analysis of data from several populations
- 8.3.2 Modelling cross-population covariation
- 8.3.3 Estimating hyper-parameters in large-scale analyses
- 8.3.4 Unlocking the secrets of dispersal

Bibliography

- Caswell, H. (2001). Matrix population models: construction, analysis, and interpretation. Sunderland, Mass.: Sinauer Associates.
- de Valpine, P., Turek, D., Paciorek, C. J., Anderson-Bergman, C., Lang, D. T., and Bodik, R. (2017). Programming with models: writing statistical algorithms for general model structures with nimble. *Journal of Computational and Graphical Statistics*, 26(2):403–413.
- Kéry, M. and Schaub, M. (2011). Bayesian population analysis using WinBUGS: a hierarchical perspective. Academic Press.
- Plard, F., Fay, R., Kéry, M., Cohas, A., and Schaub, M. (2019). Integrated population models: powerful methods to embed individual processes in population dynamics models. *Ecology*, page e02715.