

***An integrative approach to white-tailed deer management in Nova Scotia: Policy review and implementation
Final report to Nova Scotia Habitat Conservation Fund
2014-2015***

Executive Summary

In Nova Scotia, the Department of Natural Resources (NS DNR) has been collecting white-tailed deer (*Odocoileus virginianus*) data from hunters as well as through various programs in the last few decades till now. As numerous advanced sampling methodologies and statistical approaches have been published, local wildlife managers have more choices of methods to assist their management in data collection and demographic analysis. This project is helping to establish future management policies and regulative decisions for deer harvesting in Nova Scotia through looking at efficient survey methodologies and statistical analysis approaches.

The project reported is the last phase of a multi-year project (2012-2015). The goals of this three-year project are: (i) assessing current NS DNR deer management policy and suggesting necessary improvement; (ii) evaluating current deer data collection and identifying information gaps; (iii) investigating the development and application of population indices; (iv) investigating the development and application of population models.

For objective (i), a detailed review of deer management policy and statistical methodology has been completed with an associated report already submitted for 2012–2013 Habitat Conservation Fund. For objective (ii), the assessment of the effectiveness of Pellet Group Inventories (PGI's) for deer density and population estimates has been accomplished, and a new stochastic population dynamics (SPD) model to Pellet Group Inventories (PGI's) data has been evaluated and applied. A report summarizing this progress has been submitted for 2013–2014 Habitat Conservation Fund.

In this 2014–2015 report, to answer objective (iii) and (iv) we will report a summary of our final work involving three aspects: (a) the development and application of a new sampling mechanism to obtain sufficient and reliable age-at-harvest data (jawbone data); (b) the development and application of a new statistical mod-

eling approach, i.e. Beta Distribution Based Hierarchical (BDBH) model on estimating population age structure; and (c) an R package to implement the proposed methodologies in this report. Currently, age-at-harvest data (jawbones data) are collected as a voluntary sample. To ensure that the sample is representative of the total harvested deer jawbones, a new mandatory and data-oriented sampling mechanism has proposed in place of the old conventional one. Thus NS DNR can make use of the abundance estimates from the SPD model and employ our newly developed BDBH model to accurately estimate age structure of the deer population. The new mandatory sampling mechanism and the new BDBH model have been written as functions into the R package called *Wildlife*.

For the future research, we propose to build an add-on *user-friendly interface* based on *Wildlife* so that NS DNR can employ the statistical methods we developed to their applications without much extra effort.

Methods and Materials

A Sampling Mechanism for Collecting Jawbones Data

Taking measurements from jawbones is a routine method used by NS DNR to determine the age of deer. However, there are around 10,000 deer harvested every year. It is impossible to take measurements of all the jawbones from the harvested deer. On the other hand, jawbones returning will force extra work on hunters. Therefore it is possible that they are unwilling to carry this extra responsibility while enjoying their recreational hunting. Under these circumstances, the returning of jawbones has been voluntary so far.

Although the mechanism of voluntary jawbone returning offers less work, the jawbones collected constitute merely a convenient sample of the total harvest. A convenient jawbone sample will cause biases in recovering the age structure in the total harvested deer, as the will of the hunters who return jawbones is a subjective and uncontrollable factor. In order to produce a data-oriented random sample that is suitable for our future analysis, we highly suggest a new mandatory returning mechanism in replace of the old voluntary one.

The new mandatory returning mechanism includes a sampling method targeting on three-year consecutive successful hunters and setting up regulations for mandatory returns. Targeting on successful hunters is a reliable and efficient way of col-

lecting sufficient and representative jawbone samples. Successful hunters are the most experienced ones so that they would have stable harvest over the year, which should provides NS DNR a reliable source of collecting information. Analysis of viability of the deer will increase their chances of success in future hunting. We believe that the successful hunters are willing to turn in the jawbones they collect. The last but not least, these hunters can be easily reached since they have detailed registration in the local NS DNR office.

There are three key assumptions associated with random jawbones samples: (i) the success of a hunter is independent to the others; (ii) individual hunters have the same chance of a successful third kill; and (iii) the probability that a hunter is successful in the third year, given that he/she was successful in the previous two years, is constant over the time. The last assumption implies that hunting regulations are unchanged and hunters put equal efforts in their hunting over a consecutive three-year period. By employing this sampling method, NS DNR can draw a random sample that consists of hunters deemed to be the potential successful hunters in next hunting season, and then send letters to inform the selected hunters to return jawbones in advance of the next hunting season. The implementation of this sampling method has been integrated as a function called "reportsamp" in *Wildlife*.

Age Structure Estimation Using Jawbone Data

The Beta Distribution Based Hierarchical (BDBH) model is a continuation of development and application of population models, based on the new SPD model we developed (refer to 2013-2014 report) to estimate population abundances using PGI's data. This BDBH model requires age-at-harvest data (jawbones data) as primary input, and uses abundance estimates as auxiliary information. There are four key assumptions of this model: (i) the age structure of the deer population is stable across the time; (ii) harvest probabilities are only distinguishable between juveniles and adults; (iii) harvest probabilities are constant across the time; and (iv) the age-at-harvest data are randomly sampled from the total harvest deer. This model estimates not only the proportions taken by each age classes from the abundance but also the harvest probabilities upon juveniles and adults.

There are three majored advantages of this new modeling approach, listed as follows:

1. It solely uses existing routinely-collected deer harvest data by NS DNR instead of seeking new auxiliary information from other resources. It is attractive for its cost-effectiveness, in terms of both budgets and human efforts.

2. The model is robust to deer population with age-specific survivals, which is a common realistic assumption in wildlife demography. It is superior to many wildlife data analysis methods that make rigorous assumptions on survivals or need survival information as input.
3. We can incorporate random effects to take account of stochastic variability due to the environmental noises, such as a mild weather change or a light shortage of food. That is, this model is able to return robust deterministic estimates of age structure and harvest probabilities even in the case that there are departures from the model assumptions, given that the variation is not a systematical change. The implementation of this modeling method has been integrated as a function called "BDBH.model" in *Wildlife*.

Results

A Sampling Mechanism for Collecting Jawbones Data

We generated a list of hunters to be sampled in 2015 based on the hunters who have been consecutive successful in 2012–2014. By assuming there will be 65% of the successful hunters complying the mandatory request by NS DNR, NS DNR needs to sample at least 2629 hunters in order to receive a representative jawbones sample in 2015, which is 10% of the total harvested jawbones, with a 95% confidence level.

Age Structure Estimation Using Jawbone Data

We conducted a simulation study using our BDBH modeling approach to examine the model performance. This simulation study focused on the coverage of estimates, and the robustness to different sizes of the harvest sample and to population abundances estimated by three different methods. The population estimates are:

1. *Nran*, population abundance simulated by incorporating random effects
2. *PGI*, population abundance estimated by using PGI's index
3. *Nind*, population abundance simulated by a logarithm transformation

Figure 1 reported in the Appendix depicts the coverage of estimates of age proportions obtained from the BDBH model in the simulation. In the case of using *Nran*, it is evident that the estimates of age structures have satisfying coverage about their true values for four different sample sizes. In the case of using *PGI*, there exists an increasing degree of over-estimation in Class 1 (juveniles) as the

sample size increases. However, this over-estimation has been verified to be less than 5% of the population abundance. That is, for a population of 10000 deer we at most overestimate 200 deer in Class 1 (juveniles). The same phenomenon appears in the case of using *Nind*, but the over-estimation in Class 1 (juveniles) is far more severe than that in the case of using *PGI*. To conclude this simulation, it is encouraging that the use of abundance estimates from *PGI*'s is reliable for our BDBH model, but not all of the population abundance estimates are suitable for our BDBH model. Therefore, we need to investigate the selection of appropriate population abundance estimates for our model.

We also fitted our BDBH model outlined in the previous section to the male jaw-bone data in 2010–2013. Figure 2 reported in the Appendix displays the trend of age proportion estimations obtained from the BDBH model. Except for year 2011, the estimates of other three years (2010, 2012 and 2013) constitute three healthy distribution curves that are consistent with our expectation to the deer population dynamics. Among all the age classes, Class 1 (juveniles) takes the largest proportion, which is approximately equal to 40%–50% of the total abundance. Starting from class 2 (yearlings), the proportion estimate declines gradually as age goes up and it approaches 0 after Class 6. The harvest probabilities of juveniles and adults are estimated as 0.03 and 0.53, respectively. The estimate of juvenile harvest is reasonable as juveniles are seldom harvested by hunters, but that of adult is much higher than usual acknowledged amount. However, it is still encouraging that the order of the harvest probabilities' estimates are well preserved.

Our BDBH model has the potential to be developed into a generic model capable of specifically analyzing the age structure of other wildlife mammal species besides deer, since the internal beta distribution used in our model has a good approximation to the survivorship function of other mammal species. Though harvest behavior for different species can vary, we may adjust our generic BDBH model parameters to match the harvest situation of other mammal species of interest.

An R Package *Wildlife*

Since we used the computer software, R, to implement our methods, we integrated all the methods as R functions into an R package called *Wildlife*. Figure 3 in the Appendix displays a table of content of functions in the package, and Figure 4–8 exhibits the individual help file of each main function.

The R package currently has 5 main functions: “DownRe”, “SAKRe”, “lesproj”, “reportsamp” and “BDBH.model”. The function “DownRe” and “SAKRe” implement the population reconstruction based on harvest tables by using Downing reconstruction method and Sex-Age-Kill (SAK) reconstruction method respectively. The function “lesproj” allows users to project population growth based on the inputted harvest, survival and fecundity parameters. The function “reportsamp” carries out the sampling method presented in this report, returning a desirable sample size and automatically generating an excel file containing a list of hunters to be sampled. The function “BDBH.model”, as its name suggests, implements the BDBH model proposed in this report, returning the estimates of age proportions of each age classes and the estimates of the harvest probabilities. A help file is attached to each function so as to guide the user in successfully employing the function.

Recommendations

We have successfully accomplished all the goals we proposed, that has brought a real impact on wildlife data management and policy making in Nova Scotia. NS DNR has implemented our mandatory sampling mechanism in 2015 jawbone data collection. It is necessary to transfer all our findings into the reality. The computer program *Wildlife* has implemented all methods we researched. The program is written in R. In order to use it, some R background and computing skills are needed. Therefore for the future work, we propose to develop an add-on *user-friendly interface*. The interface will be wizard-like, which allows users simply choosing options from the menu and typing numbers into blanks. With the new interface, NS DNR can conduct their own analyses without much R computing experience. Detailed information about how to develop this interface can be found in our proposal for Habitat Conservation Fund 2015-2016.

Acknowledgement

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Appendix

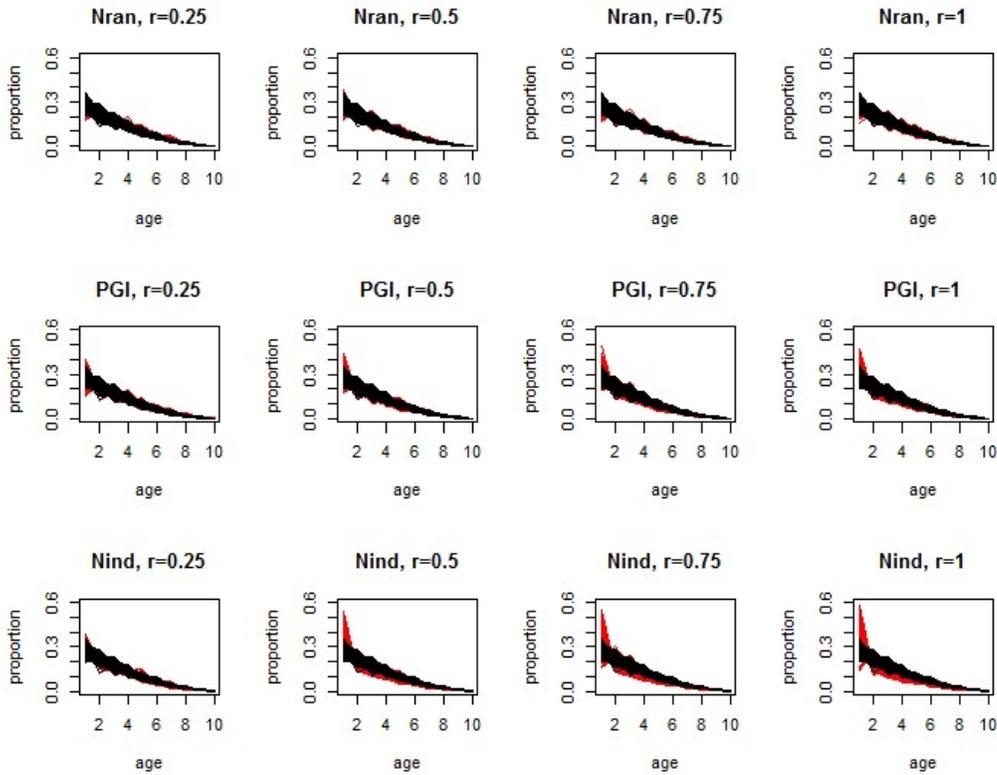


Figure 1: Age distribution curves produced by the estimates of age proportion from the BDBH model under the simulation study of using different size of harvest sample and difference inputted estimates of population abundance. Three estimates are: *Nran*, population abundance simulated by incorporating random effects; *PGI*, population abundance estimated by using PGI's index and *Nind*, population abundance simulated by a logarithm transformation. The red lines represents for the estimates, and the black lines represents for the true value.

Age distribution of male deer, 2010-2013

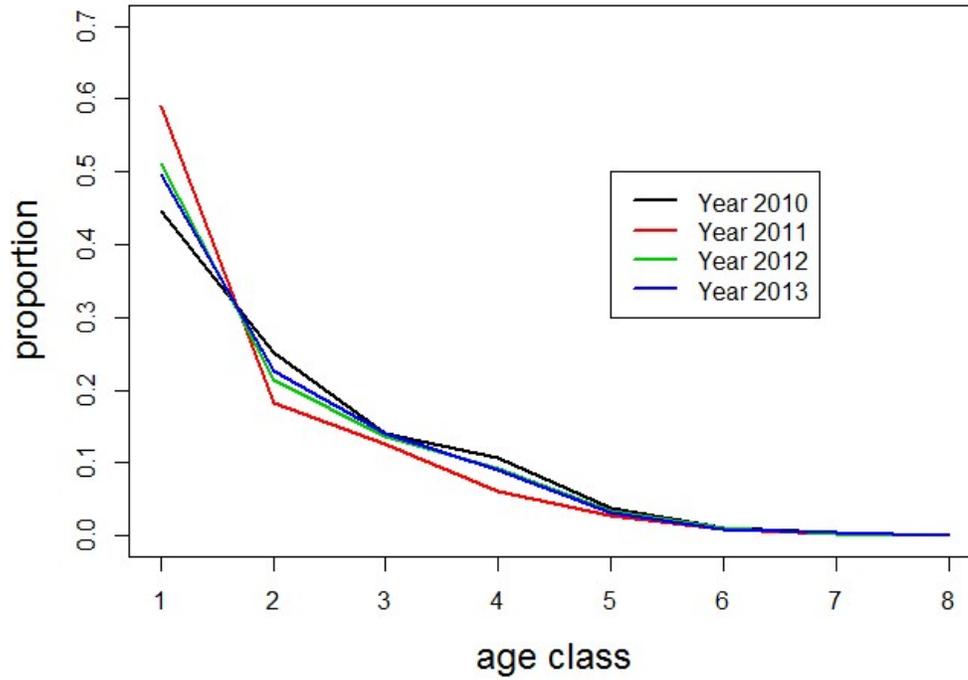


Figure 2: The fitting of BDBH model to the male age-at-harvest data in 2010-2013 in Nova Scotia.

Wildlife Demographic Analysis Method Collection and Application



Documentation for package 'Wildlife' version 1.0

- [DESCRIPTION file](#).

Help Pages

Wildlife-package	Wildlife Demographic Analysis Method Collection and Application
BDBH_model	A Beta-Distribution Based Hierarchical Model Estimating Age distributions.
DownRe	Downing Population Reconstruction
DownRe.default	Downing Population Reconstruction
lesproj	Leslie Matrix Simulation
lesproj.default	Leslie Matrix Simulation
print.DownRe	Downing Population Reconstruction
print.lesproj	Leslie Matrix Simulation
print.SAKRe	A Sex-Age-Kill (SAK) Population Reconstruction
reportsamp	Sample Size Estimation for Collecting Age Information
SAKRe	A Sex-Age-Kill (SAK) Population Reconstruction
SAKRe.default	A Sex-Age-Kill (SAK) Population Reconstruction
Wildlife	Wildlife Demographic Analysis Method Collection and Application

Figure 3: An overall glance of the structure of our R package "Wildlife".

Downing Population Reconstruction

Description

Reconstruct population Using Downing's Method (Downing 1980)

Usage

```
DownRe(x, ...)
```

```
## Default S3 method:  
DownRe(x)  
## S3 method for class 'DownRe'  
print(object, ...)
```

Arguments

x a numeric data matrix or dataframe of harvest data, with row representing time and column representing age classe.
object an object of class "DownRe", i.e. a fitted model.
... not used.

Value

An object of class `DownRe`, a list including elements

harvest.M a copy of the input harvest table
reconstructed.M reconstructed population table

Author(s)

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References

Davis, M. L., Berkson, J., Steffen, D., & Tilton, M. K. (2007). Evaluation of accuracy and precision of Downing population reconstruction. *The Journal of Wildlife Management*, 71(7), 2297- 2303.

Examples

```
M <- matrix(1:12,3,4)
```

Figure 4: The first page of the help file of function "DoweRe" in our package

A Sex-Age-Kill (SAK) Population Reconstruction

Description

Reconstruct population Using SAK Method

Usage

```
SAKRe(m, f, ...)

## Default S3 method:
SAKRe(m, f, PH=NULL, PM=NULL, PF=NULL, RJF=NULL, theta=NULL)
## S3 method for class 'SAKRe'
print(object, ...)
```

Arguments

m a numeric data matrix of male harvest table, with row representing time and column of length 3 representing "Juvenile", "Yearling" and "Adult" respectively.

f a numeric data matrix of female harvest table. Format and dimension have to the same of **m**.

PH a numeric vector, representing yearly proportion of harvest mortality taken from total (harvest+natural) mortality. The default value is `null`, and will be set to 1 in the model if no evaluations are given.

PM a numeric vector, representing yearly proportion of yearling males taken from non-juvenile (yearling + adult) males. The default value is `null`, and will be calculated by using the input male and female harvest table (i.e. **m** and **f**) if no evaluations are given.

PF Refer to **PM**, regarding to female.

RJF a numeric vector, representing yearly ratio of total (male + female) juveniles to non-juvenile (yearling + adult) females. The default value is `null`, and will be calculated by using the input male and female harvest table (i.e. **m** and **f**) if no evaluations are given.

theta a numeric vector, representing yearly sex ratio of fetal male:female. The default value is `null`, and will be calculated by using the input male and female harvest table (i.e. **m** and **f**) if no evaluations are given.

object an object of class "SAKRe", i.e. a fitted model.

... not used.

Value

An object of class `SAKRe`, a list including an element

`Recon.table` reconstructed population table

Figure 5: The first page of the help file of function "SAKRe" in our package.

Leslie Matrix Simulation

Description

construct either density-independent or density-dependent Leslie matrix and use leslie matrix to simulate population growth.

Usage

```
lesproj(init, h, s, f, t, ...)

## Default S3 method:
lesproj(init, h, s, f, t, den.dp=FALSE, b=10^-7)
## S3 method for class 'lesproj'
print(object, ...)
```

Arguments

init a numeric size-of-aged vector that initiates the population simulation.

h a numeric vector of age-specific harvest probabilities.

s a numeric vector of age-specific natural survival probabilities.

f a numeric vector of age-specific fecundities.

t a number specifying how many years of data to simulate.

den.dp a logical indicating whether a density-independent or a density-dependent Leslis matrix should be used. The default value is set to FALSE (i.e. a default density-independent matrix). You can specify just the initial letter.

b the strength of density dependence on fecundities. This agrument only works when **den.dp=TRUE**. The default value is set to 10^{-7} .

object an object of class "lesproj", i.e. a fitted model.

... not used.

Value

An object of class `lesproj`, a list including elements

growth.rate If **den.dp=FALSE**, returns a numeric value of the growth rate under the density-independent Leslie matrix. If **den.dp=TRUE**, returns a vector of groth rates between consecutive years.

Leslie.Matrix a density-independent Leslie matrix. This exists only when **den.dp=FALSE**.

N.table a matrix that stores the simulation result of Leslis matrix projection.

Figure 6: The first page of the help file of function "reportsamp" in our package.

Sample Size Estimation for Collecting Age Information

Description

An application to wildlife management about estimating the size of sample to draw from hunter population in order to obtain sufficient information of harvest for analysis. Based on the previous three consecutive years successful hunters' information, predicts the 95 percent quantile of sample size to draw in the next year. A detailed random sample will be drawn along with the function.

Usage

```
reportsamp(Nt_2, Nt_1, Nt, sample.rate = 0.1, total.jawbone = 10000, response.rate = 0.65)
```

Arguments

`Nt_2` a $m \times 2$ dataframe of hunters' information of year $t-2$, where m is the number of observations. The first column indicates the ID's of hunters, and it should be numeric. The second column indicates the names of hunters, and it should be characters.

`Nt_1` a $n \times 2$ dataframe of hunters' information of year $t-1$, where n is the number of observations. Structure refers to `Nt_2`.

`Nt` a $l \times 2$ dataframe of hunters' information of year t , where l is the number of observations. Structure refers to `Nt_2`.

`sample.rate` The proportion of sample that you want to draw next year from jawbones that potentially produced by the hunters' population.

`total.jawbone` The number of jawbones that potentially produced by the hunter population.

`response.rate` The rate of hunters that are willing to comply reporting.

Value

Instead of returning values, this function will prompt the number of ideal (i.e. default 95 percent quantile) sample size that needs to be drawn in next year. However, a random sample will be drawn and stored as a csv file in the current directory

Author(s)

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Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##-- or do help(data=index) for the standard data sets.
```

Figure 7: The first page of the help file of function "lesproj" in our package.

A Beta-Distribution Based Hierarchical Model Estimating Age distributions.

Description

An new approach for analyzing age distributions based on harvest table and population indices. By assuming "stable-stationary age distribution" and "constant harvest over year" assumption, it estimates the proportions taken by each age class from the total population and jointly estimates age-specific (juvenile and non-juvenile distinguishable only) harvest probabilities. Models are fitted via "Just Another Gibbs Sampler"(JAGS) by package "rjags".

Usage

```
BDBH.model(hmat, Nindex, r = 1)
```

Arguments

`hmat` a $Y \times A$ harvest numeric data matrix, where Y indicates how many years and A indicates how many age classes.

`Nindex` a numeric vector of yearly population indices of length Y .

`r` a numeric value representing the reporting rate of jawbones returning. If there is no reporting issue, `r` takes default value 1.

Details

In order to run this function, you need to install the software "Just Another Gibbs sampler"(JAGS) and two R packages "rjags" and "dclone".

Value

An `mcmc.list` object returned by "jags.fit". For detailed information, see `?jags.fit`

Author(s)

Entao Chen

References

Lynch, H. J., & Fagan, W. F. (2009). Survivorship curves and their impact on the estimation of maximum population growth rates. *Ecology*, 90(4), 1116-1124.

Plummer, M., Stukalov, A., Denwood, M., & Plummer, M. M. (2015). Package "rjags"™. update, 16, 1.

SÃyimos, P. (2010). dclone: Data Cloning in R. *The R Journal*, 2(2), 29-37.

Figure 8: The first page of the help file of function "BDBH.model" in our package.