

# The VGAM Package for Capture–Recapture Data Using the Conditional Likelihood

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## Abstract

It is well known that using individual covariate information (such as body weight or gender) to model heterogeneity in capture–recapture (CR) experiments can greatly enhance inferences on the size of a closed population. Since individual covariates are only observable for captured individuals, complex conditional likelihood methods are usually required and these do not constitute a standard generalized linear model (GLM) family. Modern statistical techniques such as generalized additive models (GAMs), which allow a relaxing of the linearity assumptions on the covariates, are readily available for many standard GLM families. Fortunately, a natural statistical framework for maximizing conditional likelihoods is available in the Vector GLM and Vector GAM classes of models. We present several new R-functions (implemented within the **VGAM** package) specifically developed to allow the incorporation of individual covariates in the analysis of closed population CR data using a GLM/GAM-like approach and the conditional likelihood. As a result, a wide variety of practical tools are now readily available in the **VGAM** object oriented framework. We discuss and demonstrate their advantages, features and flexibility using the new **VGAM** CR functions on several examples.

*Keywords:* closed population size estimation, conditional likelihood, mark–capture–recapture, vector generalized additive model, **VGAM**.

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## 1. Introduction

Note: this vignette is essentially [Yee \*et al.\* \(2015\)](#).

Capture–recapture (CR) surveys are widely used in ecology and epidemiology to estimate population sizes. In essence they are sampling schemes that allow the estimation of both  $n$  and  $p$  in a Binomial( $n, p$ ) experiment ([Huggins and Hwang 2011](#)). The simplest CR sampling design consists of units or individuals in some population that are captured or tagged across several sampling occasions, e.g., trapping a nocturnal mammal species on seven consecutive nights. In these experiments, when an individual is captured for the first time then it is marked or tagged so that it can be identified upon subsequent recapture. On each occasion recaptures of individuals which have been previously marked are also noted. Thus each observed individual has a capture history: a vector of 1s and 0s denoting capture/recapture and

noncapture respectively. The unknown population size is then estimated using the observed capture histories and any other additional information collected on captured individuals, such as weight or sex, along with environmental information such as rainfall or temperature.

We consider closed populations, where there are no births, deaths, emigration or immigration throughout the sampling period (Amstrup *et al.* 2005). Such an assumption is often reasonable when the overall time period is relatively short. Otis *et al.* (1978) provided eight specific closed population CR models (see also Pollock (1991)), which permit the individual capture probabilities to depend on time and behavioural response, and be heterogeneous between individuals. The use of covariate information (or explanatory variables) to explain heterogeneous capture probabilities in CR experiments has received considerable attention over the last 30 years (Pollock 2002). Population size estimates that ignore this heterogeneity typically result in biased population estimates (Amstrup *et al.* 2005). A recent book on CR experiments as a whole is McCrea and Morgan (2014).

Since individual covariate information (such as gender or body weight) can only be collected on observed individuals, conditional likelihood models are employed (Pollock *et al.* 1984; Huggins 1989; Alho 1990; Lebreton *et al.* 1992). That is, one conditions on the individuals seen at least once through-out the experiment, hence they allow for individual covariates to be considered in the analysis. The capture probabilities are typically modelled as logistic functions of the covariates, and parameters are estimated using maximum likelihood. Importantly, these CR models are generalized linear models (GLMs; McCullagh and Nelder 1989; Huggins and Hwang 2011).

Here, we maximize the conditional likelihood (or more formally the positive-Bernoulli distribution) models of Huggins (1989). This approach has become standard practice to carry out inferences when considering individual covariates, with several different software packages currently using this methodology, including: MARK (Cooch and White 2012), CARE-2 (Hwang and Chao 2003), and the R packages (R Core Team 2015): **mra** (McDonald 2012), **RMark** (Laake 2013) and **Rcapture** (Baillargeon and Rivest 2014, 2007), the latter package uses a log-linear approach, which can be shown to be equivalent to the conditional likelihood (Cormack 1989; Huggins and Hwang 2011). These programs are quite user friendly, and specifically, allow modelling capture probabilities as linear functions of the covariates. So an obvious question is to ask why develop yet another implementation for closed population CR modelling?

Firstly, nonlinearity arises quite naturally in many ecological applications, (Schluter 1988; Yee and Mitchell 1991; Crawley 1993; Gimenez *et al.* 2006; Bolker 2008). In the CR context, capture probabilities may depend nonlinearly on individual covariates, e.g., mountain pygmy possums with lighter or heavier body weights may have lower capture probabilities compared with those having mid-ranged body weights (e.g., Huggins and Hwang 2007; Stoklosa and Huggins 2012). However, in our experience, the vast majority of CR software does not handle nonlinearity well in regard to both estimation and in the plotting of the smooth functions. Since GAMs (Hastie and Tibshirani 1990; Wood 2006) were developed in the mid-1980s they have become a standard tool for data analysis in regression. The nonlinear relationship between the response and covariate is flexibly modelled, and few assumptions are made on the functional relationship. The drawback in applying these models to CR data has been the difficult programming required to implement the approach.

Secondly, we have found several implementations of conditional likelihood slow, and in some

instances unreliable and difficult to use. We believe our implementation has superior capabilities, and has good speed and reliability. The results of Section ?? contrast our software with some others. Moreover, the incorporation of these methods in a general, maintained statistical package will result in them being updated as the package is updated.

Standard GLM and GAM methodologies are unable to cope with the CR models considered in this article because they are largely restricted to one linear/additive predictor  $\eta$ . Fortunately however, a natural extension in the form of the vector generalized linear and additive model (VGLM/VGAM) classes do allow for multiple  $\eta$ s. VGAMs and VGLMs are described in Yee and Wild (1996) and Yee and Hastie (2003). Their implementation in the **VGAM** package (Yee 2008, 2010, 2014) has become increasingly popular and practical over the last few years, due to large number of exponential families available for discrete/multinomial response data. In addition to flexible modelling of both VGLMs and VGAMs, a wide range of useful features are also available:

- smoothing capabilities;
- model selection using, e.g., AIC or BIC (Burnham and Anderson 1999);
- regression diagnostics and goodness-of-fit tools;
- reduced-rank regression (Yee and Hastie 2003) for dimension reduction;
- computational speed and robustness;
- choice of link functions;
- offsets and prior weights; and
- (specifically) when using R: generic functions based on object oriented programming, e.g., `fitted()`, `coef()`, `vcov()`, `summary()`, `predict()`, `AIC()`, etc.

Our goal is to provide users with an easy-to-use object-oriented **VGAM** structure, where four family-type functions based on the conditional likelihood are available to fit the eight models of Otis *et al.* (1978). We aim to give the user additional tools and features, such as those listed above, to carry out a more informative and broader analysis of CR data; particularly when considering more than one covariate. Finally, this article primarily focuses on the technical aspects of the proposed package, and less so on the biological interpretation for CR experiments. The latter will be presented elsewhere.

An outline of this article is as follows. In Section 2 we present the conditional likelihood for CR models and a description of the eight Otis *et al.* (1978) models. Section 3 summarizes pertinent details of VGLMs and VGAMs. Their connection to the CR models is made in Section 4. Software details are given in Section 5, and examples on real and simulated data using the new software are demonstrated in Section 6. Some final remarks are given in Section 7. The two appendices give some technical details relating to the first and second derivatives of the conditional log-likelihood, and the means.

## 2. Capture–recapture models

Symbol	Explanation
$N$	(Closed) population size to be estimated
$n$	Total number of distinct individuals caught in the trapping experiment
$\tau$	Number of sampling occasions, where $\tau \geq 2$
$\mathbf{y}_i$	Vector of capture histories for individual $i$ ( $i = 1, \dots, n$ ) with observed values 1 (captured) and 0 (noncaptured). Each $\mathbf{y}_i$ has at least one observed 1
“ $h$ ”	Model $\mathcal{M}$ subscript, for heterogeneity
“ $b$ ”	Model $\mathcal{M}$ subscript, for behavioural effects
“ $t$ ”	Model $\mathcal{M}$ subscript, for temporal effects
$p_{ij}$	Probability that individual $i$ is captured at sampling occasion $j$ ( $j = 1, \dots, \tau$ )
$z_{ij}$	= 1 if individual $i$ has been captured before occasion $j$ , else = 0
$\boldsymbol{\theta}$	Vector of regression coefficients to be estimated related to $p_{ij}$
$\boldsymbol{\eta}$	Vector of linear predictors (see Table 3 for further details)
$g$	Link function applied to, e.g., $p_{ij}$ . Logit by default

Table 1: Short summary of the notation used for the positive-Bernoulli distribution for capture–recapture (CR) experiments. Additional details are in the text.

In this section we give an outline for closed population CR models under the conditional likelihood/GLM approach. For further details we recommend [Huggins \(1991\)](#) and [Huggins and Hwang \(2011\)](#). The notation of Table 1 is used throughout this article.

## 2.1. Conditional likelihood

Suppose we have a closed population of  $N$  individuals, labelled  $i = 1, \dots, N$  and  $\tau$  capture occasions labelled  $j = 1, \dots, \tau$ . We make the usual assumptions that individuals in the population behave independently of each other, individuals do not lose their tags, and tags are recorded correctly. Let  $y_{ij} = 1$  if the  $i$ th individual was caught on the  $j$ th occasion and be zero otherwise, and let  $n$  be the number of distinct individuals captured.

Let  $p_{ij}$  denote the probability of capturing individual  $i$  on occasion  $j$ . As noted in Section 1, [Otis \*et al.\* \(1978\)](#) describe eight models for the capture probabilities, see Section 2.2 for further details. Label the individuals captured in the experiment by  $i = 1, \dots, n$  and those never captured by  $i = n + 1, \dots, N$ . The full likelihood is given by

$$\begin{aligned}
 L_f &= K \prod_{i=1}^N \prod_{j=1}^{\tau} p_{ij}^{y_{ij}} (1 - p_{ij})^{1 - y_{ij}} \\
 &= K \left\{ \prod_{i=1}^n \prod_{j=1}^{\tau} p_{ij}^{y_{ij}} (1 - p_{ij})^{1 - y_{ij}} \right\} \cdot \left\{ \prod_{i=n+1}^N \prod_{j=1}^{\tau} (1 - p_{ij}) \right\} \quad (1)
 \end{aligned}$$

where  $K$  is independent of the  $p_{ij}$  but may depend on  $N$ . The RHS of (1) requires knowledge of the uncaptured individuals and in general cannot be computed. Consequently no MLE of  $N$  will be available unless some homogeneity assumption is made about the noncaptured individuals. Instead, a conditional likelihood function based only on the individuals observed at least once is

$$L_c \propto \prod_{i=1}^n \frac{\prod_{j=1}^{\tau} p_{ij}^{y_{ij}} (1 - p_{ij})^{1 - y_{ij}}}{1 - \prod_{s=1}^{\tau} (1 - p_{is}^{\dagger})}. \quad (2)$$

Capture history	Joint probability			
	$\mathcal{M}_0/\mathcal{M}_h$	$\mathcal{M}_b/\mathcal{M}_{bh}$	$\mathcal{M}_t/\mathcal{M}_{th}$	$\mathcal{M}_{tb}/\mathcal{M}_{tbb}$
01	$(1-p)p$	$(1-p_c)p_c$	$(1-p_1)p_2$	$(1-p_{c1})p_{c2}$
10	$p(1-p)$	$p_c(1-p_r)$	$p_1(1-p_2)$	$p_{c1}(1-p_{r2})$
11	$p^2$	$p_c p_r$	$p_1 p_2$	$p_{c1} p_{r2}$
00	$(1-p)^2$	$(1-p_c)^2$	$(1-p_1)(1-p_2)$	$(1-p_{c1})(1-p_{c2})$
$M \equiv \dim(\boldsymbol{\eta})$	1	2	2 ( $= \tau$ )	3 ( $= 2\tau - 1$ )

Table 2: Capture history sample space and corresponding probabilities for the eight models of Otis *et al.* (1978), with  $\tau = 2$  capture occasions in closed population CR experiment. Here,  $p_{cj}$  = capture probability for unmarked individuals at sampling period  $j$ ,  $p_{rj}$  = recapture probability for marked individuals at sampling period  $j$ , and  $p$  = constant capture probability across  $\tau = 2$ . Note that the “00” row is never realized in sample data.

is used. Here  $p_{is}^\dagger$  are the  $p_{ij}$  computed as if the individual had not been captured prior to  $j$  so that the denominator is the probability individual  $i$  is captured at least once. This conditional likelihood (2) is a modified version of the likelihood corresponding to a positive-Bernoulli distribution (Patil 1962).

## 2.2. The eight models

Models which allow capture probabilities to depend on one or a combination of time, heterogeneity or behavioural effects are defined using appropriate subscripts, e.g.,  $\mathcal{M}_{th}$  depends on time and heterogeneity. These eight models have a nested structure of which  $\mathcal{M}_{tbb}$  is the most general. The homogeneous model  $\mathcal{M}_0$  is the simplest (but most unrealistic) and has equal capture probabilities for each individual  $H_0 : p_{ij} = p$ , regardless of the sampling occasion. All eight models are GLMs, since the conditional likelihood (2) belongs to the exponential family (Huggins and Hwang 2011).

To illustrate the approach, we use the following toy example throughout, consider a CR experiment with two occasions—morning and evening (i.e.,  $\tau = 2$ ), with capture probabilities varying between the two occasions. Furthermore, suppose we have collected some individual covariates—weight and gender. The joint probabilities of all the eight models are listed in Table 2. It can be seen that all but the positive-Binomial model ( $\mathcal{M}_0/\mathcal{M}_h$ ) require more than one probability and hence more than one linear predictor, so that the original Nelder and Wedderburn (1972) GLM framework is inadequate. Further, there are two noteworthy points from Table 2 which apply for any  $\tau \geq 2$ :

- first, for  $\mathcal{M}_t$ -type models, as  $\tau$  increases so will the number of linear predictors and hence the potential number of parameters;
- secondly, it is evident that there are four main categories consisting of non-heterogeneity models ( $\mathcal{M}_0$ ,  $\mathcal{M}_b$ ,  $\mathcal{M}_t$  and  $\mathcal{M}_{tb}$ ), which are paired with a heterogeneity sub-model (respectively  $\mathcal{M}_h$ ,  $\mathcal{M}_{bh}$ ,  $\mathcal{M}_{th}$  and  $\mathcal{M}_{tbb}$ ).

The four heterogeneity models allow for each individual to have their own probability of capture/recapture. In our toy example, the capture probabilities are dependent on an individual’s

weight and gender. We discuss these models further in Section 3.1. It is natural to consider individual covariates such as weight and gender as linear/additive predictors. Let  $x_i$  denote a covariate (either continuous or discrete) for the  $i$ th individual, which is constant across the capture occasions  $j = 1, \dots, \tau$ , e.g., for continuous covariates one could use the first observed value or the mean across all  $j$ . If there are  $d - 1$  covariates, we write  $\mathbf{x}_i = (x_{i1}, \dots, x_{id})^\top$  with  $x_{i1} = 1$  if there is an intercept. Also, let  $g^{-1}(\eta) = \exp(\eta)/\{1 + \exp(\eta)\}$  be the inverse logit function. Consider model  $\mathcal{M}_{tbh}$ , then the capture/recapture probabilities are given as [notation follows Section 3.3]

$$\begin{aligned} p_{ij}^\dagger &= g^{-1}\left(\beta_{(j+1)1}^* + \mathbf{x}_{i[-1]}^\top \boldsymbol{\beta}_{1[-1]}\right), & j = 1, \dots, \tau, \\ p_{ij} &= g^{-1}\left(\beta_{(1)1}^* + \beta_{(j+1)1}^* + \mathbf{x}_{i[-1]}^\top \boldsymbol{\beta}_{1[-1]}\right), & j = 2, \dots, \tau, \end{aligned}$$

where  $\beta_{(1)1}^*$  is the behavioural effect of prior capture,  $\beta_{(j+1)1}^*$  for  $j = 1, \dots, \tau$  are time effects, and  $\boldsymbol{\beta}_{1[-1]}$  are the remaining regression parameters associated with the covariates. Computationally, the conditional likelihood (2) is maximized with respect to all the parameters (denote by  $\boldsymbol{\theta}$ ) by the Fisher scoring algorithm using the derivatives given in Appendix A.

### 2.3. Estimation of $N$

In the above linear models, to estimate  $N$  let  $\pi_i(\boldsymbol{\theta}) = 1 - \prod_{s=1}^{\tau} (1 - p_{is}^\dagger)$  be the probability that individual  $i$  is captured at least once in the course of the study. Then, if  $\boldsymbol{\theta}$  is known, the Horvitz–Thompson (HT; Horvitz and Thompson 1952) estimator

$$\widehat{N}(\boldsymbol{\theta}) = \sum_{i=1}^n \pi_i(\boldsymbol{\theta})^{-1} \quad (3)$$

is unbiased for the population size  $N$  and an associated estimate of the variance of  $\widehat{N}(\boldsymbol{\theta})$  is  $s^2(\boldsymbol{\theta}) = \sum_{i=1}^n \pi_i(\boldsymbol{\theta})^{-2} [1 - \pi_i(\boldsymbol{\theta})]$ . If  $\boldsymbol{\theta}$  is estimated by  $\widehat{\boldsymbol{\theta}}$  then one can use

$$\text{VAR}\left(\widehat{N}(\widehat{\boldsymbol{\theta}})\right) \approx s^2(\widehat{\boldsymbol{\theta}}) + \widehat{\mathcal{D}}^\top \widehat{\text{VAR}}(\widehat{\boldsymbol{\theta}}) \widehat{\mathcal{D}} \quad (4)$$

where, following from a Taylor series expansion of  $\widehat{N}(\widehat{\boldsymbol{\theta}})$  about  $\widehat{N}(\boldsymbol{\theta})$ ,

$$\begin{aligned} \mathcal{D} &= \frac{dN(\boldsymbol{\theta})}{d\boldsymbol{\theta}} = \sum_{i=1}^n \pi_i(\boldsymbol{\theta})^{-2} \frac{d\pi_i(\boldsymbol{\theta})}{d\boldsymbol{\theta}} \\ &= \sum_{i=1}^n \frac{-1}{\pi_i(\boldsymbol{\theta})^2} \sum_{s=1}^{\tau} \left[ \prod_{t=1, t \neq s}^{\tau} (1 - p_{it}^\dagger) \right] \frac{\partial p_{is}^\dagger}{\partial \boldsymbol{\theta}}. \end{aligned}$$

## 3. Vector generalized linear and additive models

To extend the above linear models, we use VGLMs and VGAMs which we briefly describe in this section. These models fit within a large statistical regression framework which will be described in Yee (2015). The details here are purposely terse; readers are directed to Yee

(2008, 2010) for accessible overviews and examples, and Yee and Wild (1996) and Yee and Hastie (2003) for technical details.

### 3.1. Basics

Consider observations on independent pairs  $(\mathbf{x}_i, \mathbf{y}_i)$ ,  $i = 1, \dots, n$ . We use “[−1]” to delete the first element, e.g.,  $\mathbf{x}_{i[-1]} = (x_{i2}, \dots, x_{id})^\top$ . For simplicity, we will occasionally drop the subscript  $i$  and simply write  $\mathbf{x} = (x_1, \dots, x_d)^\top$ . Consider a single observation where  $\mathbf{y}$  is a  $Q$ -dimensional vector. For the CR models of this paper,  $Q = \tau$  when the response is entered as a matrix of 0s and 1s. The only exception is for the  $\mathcal{M}_0/\mathcal{M}_h$  where the aggregated counts may be inputted, see Section 5.2. VGLMs are defined through the model for the conditional density

$$f(\mathbf{y}|\mathbf{x}; \mathbf{B}) = f(\mathbf{y}, \eta_1, \dots, \eta_M)$$

for some known function  $f(\cdot)$ , where  $\mathbf{B} = (\boldsymbol{\beta}_1 \boldsymbol{\beta}_2 \cdots \boldsymbol{\beta}_M)$  is a  $d \times M$  matrix of regression coefficients to be estimated. We may also write  $\mathbf{B}^\top = (\boldsymbol{\beta}_{(1)} \boldsymbol{\beta}_{(2)} \cdots \boldsymbol{\beta}_{(d)})$  so that  $\boldsymbol{\beta}_j$  is the  $j$ th column of  $\mathbf{B}$  and  $\boldsymbol{\beta}_{(k)}$  is the  $k$ th row.

The  $j$ th linear predictor is then

$$\eta_j = \boldsymbol{\beta}_j^\top \mathbf{x} = \sum_{k=1}^d \beta_{(j)k} x_k, j = 1, \dots, M, \quad (5)$$

where  $\beta_{(j)k}$  is the  $k$ th component of  $\boldsymbol{\beta}_j$ . In the CR context, we remind the reader that, as in Table 2, we have  $M = 2$  for  $\mathcal{M}_{bh}$ ,  $M = \tau$  for  $\mathcal{M}_{th}$  and  $M = 2\tau - 1$  for  $\mathcal{M}_{tbh}$ .

In GLMs the linear predictors are used to model the means. The  $\eta_j$  of VGLMs model the parameters of a model. In general, for a parameter  $\theta_j$  we take

$$\eta_j = g_j(\theta_j), j = 1, \dots, M$$

and we say  $g_j$  is a parameter link function. Write

$$\boldsymbol{\eta}_i = \begin{pmatrix} \eta_1(\mathbf{x}_i) \\ \vdots \\ \eta_M(\mathbf{x}_i) \end{pmatrix} = \mathbf{B}^\top \mathbf{x}_i = \begin{pmatrix} \boldsymbol{\beta}_1^\top \mathbf{x}_i \\ \vdots \\ \boldsymbol{\beta}_M^\top \mathbf{x}_i \end{pmatrix}. \quad (6)$$

In practice we may wish to constrain the effect of a covariate to be the same for some of the  $\eta_j$  and to have no effect for others. In our toy example, model  $\mathcal{M}_{th}$  with  $\tau = M = 2$ ,  $d = 3$ , we have

$$\begin{aligned} \eta_1(\mathbf{x}_i) &= \beta_{(1)1} + \beta_{(1)2} x_{i2} + \beta_{(1)3} x_{i3}, \\ \eta_2(\mathbf{x}_i) &= \beta_{(2)1} + \beta_{(2)2} x_{i2} + \beta_{(2)3} x_{i3}, \end{aligned}$$

which correspond to  $x_{i2}$  being the individual’s weight and  $x_{i3}$  an indicator of gender say, then we have the constraints  $\beta_{(1)2} \equiv \beta_{(2)2}$  and  $\beta_{(1)3} \equiv \beta_{(2)3}$ . Then, with “\*” denoting the parameters that are estimated,

$$\begin{aligned} \eta_1(\mathbf{x}_i) &= \beta_{(1)1}^* + \beta_{(1)2}^* x_{i2} + \beta_{(1)3}^* x_{i3}, \\ \eta_2(\mathbf{x}_i) &= \beta_{(2)1}^* + \beta_{(1)2}^* x_{i2} + \beta_{(1)3}^* x_{i3}, \end{aligned}$$

and we may write

$$\begin{aligned}
\boldsymbol{\eta}(\mathbf{x}_i) &= \begin{pmatrix} \eta_1(\mathbf{x}_i) \\ \eta_2(\mathbf{x}_i) \end{pmatrix} = \sum_{k=1}^3 \boldsymbol{\beta}_{(k)} x_{ik} \\
&= \begin{pmatrix} \beta_{(1)1} & \beta_{(1)2} & \beta_{(1)3} \\ \beta_{(2)1} & \beta_{(2)2} & \beta_{(2)3} \end{pmatrix} \begin{pmatrix} x_{i1} \\ x_{i2} \\ x_{i3} \end{pmatrix} \\
&= \begin{pmatrix} \beta_{(1)1}^* & \beta_{(1)2}^* & \beta_{(1)3}^* \\ \beta_{(2)1}^* & \beta_{(1)2}^* & \beta_{(1)3}^* \end{pmatrix} \begin{pmatrix} x_{i1} \\ x_{i2} \\ x_{i3} \end{pmatrix} \\
&= \begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix} \begin{pmatrix} \beta_{(1)1}^* \\ \beta_{(2)1}^* \end{pmatrix} x_{i1} + \begin{pmatrix} 1 \\ 1 \end{pmatrix} \beta_{(1)2}^* x_{i2} + \begin{pmatrix} 1 \\ 1 \end{pmatrix} \beta_{(1)3}^* x_{i3} \\
&= \sum_{k=1}^3 \mathbf{H}_k \boldsymbol{\beta}_{(k)}^* x_{ik}.
\end{aligned}$$

We can also write this as (noting that  $x_{i1} = 1$ )

$$\begin{aligned}
\boldsymbol{\eta}(\mathbf{x}_i) &= \begin{pmatrix} x_{i1} & 0 \\ 0 & x_{i1} \end{pmatrix} \begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix} \begin{pmatrix} \beta_{(1)1}^* \\ \beta_{(2)1}^* \end{pmatrix} + \begin{pmatrix} x_{i2} & 0 \\ 0 & x_{i2} \end{pmatrix} \begin{pmatrix} 1 \\ 1 \end{pmatrix} \beta_{(1)2}^* + \begin{pmatrix} x_{i3} & 0 \\ 0 & x_{i3} \end{pmatrix} \begin{pmatrix} 1 \\ 1 \end{pmatrix} \beta_{(1)3}^* \\
&= \sum_{k=1}^3 \text{diag}(x_{ik}, x_{ik}) \mathbf{H}_k \boldsymbol{\beta}_{(k)}^*.
\end{aligned}$$

In general, for VGLMs, we represent the models as

$$\begin{aligned}
\boldsymbol{\eta}(\mathbf{x}_i) &= \sum_{k=1}^d \boldsymbol{\beta}_{(k)} x_{ik} \\
&= \sum_{k=1}^d \mathbf{H}_k \boldsymbol{\beta}_{(k)}^* x_{ik} \\
&= \sum_{k=1}^d \text{diag}(x_{ik}, \dots, x_{ik}) \mathbf{H}_k \boldsymbol{\beta}_{(k)}^*
\end{aligned} \tag{7}$$

where  $\mathbf{H}_1, \mathbf{H}_2, \dots, \mathbf{H}_d$  are known constraint matrices of full column-rank (i.e.,  $\text{rank } \text{ncol}(\mathbf{H}_k)$ ),  $\boldsymbol{\beta}_{(k)}^*$  is a vector containing a possibly reduced set of regression coefficients. Then we may write

$$\mathbf{B}^\top = \left( \mathbf{H}_1 \boldsymbol{\beta}_{(1)}^* \quad \mathbf{H}_2 \boldsymbol{\beta}_{(2)}^* \quad \cdots \quad \mathbf{H}_d \boldsymbol{\beta}_{(d)}^* \right) \tag{8}$$

as an expression of (6) concentrating on columns rather than rows. Note that with no constraints at all, all  $\mathbf{H}_k = \mathbf{I}_M$  and  $\boldsymbol{\beta}_{(k)}^* = \boldsymbol{\beta}_{(k)}$ . We need both (6) and (8) since we focus on the  $\eta_j$  and at other times on the variables  $x_k$ . The constraint matrices for common models are pre-programmed in **VGAM** and can be set up by using arguments such as `parallel` and `zero` found in **VGAM** family functions. Alternatively, there is the argument `constraints` where they may be explicitly inputted. Using `constraints` is less convenient but provides the full generality of its power.



### 3.2. Handling time-varying covariates

Often, the covariates may be time-varying, e.g., when using temperature as a covariate, then a different value is observed and measured for each occasion  $j$  for  $j = 1, \dots, \tau$ . Again, using our toy example with  $M = 2$ ,  $d = 3$ , and  $\tau = 2$ , suppose we have time-dependent covariates  $\mathbf{x}_{ij}$ ,  $j = 1, 2$ . We may have the model

$$\begin{aligned}\eta_1(\mathbf{x}_{i1}) &= \beta_{(1)1}^* + \beta_{(1)2}^* x_{i21} + \beta_{(1)3}^* x_{i31}, \\ \eta_2(\mathbf{x}_{i2}) &= \beta_{(2)1}^* + \beta_{(1)2}^* x_{i22} + \beta_{(1)3}^* x_{i32},\end{aligned}$$

for the linear predictor on the two occasions. Here,  $x_{ikt}$  is for the  $i$ th animal,  $k$ th explanatory variable and  $t$ th time. We write this model as

$$\begin{aligned}\boldsymbol{\eta}(\mathbf{x}_{ij}) &= \begin{pmatrix} x_{i11} & 0 \\ 0 & x_{i12} \end{pmatrix} \begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix} \begin{pmatrix} \beta_{(1)1}^* \\ \beta_{(2)1}^* \end{pmatrix} + \begin{pmatrix} x_{i21} & 0 \\ 0 & x_{i22} \end{pmatrix} \begin{pmatrix} 1 \\ 1 \end{pmatrix} \beta_{(1)2}^* + \begin{pmatrix} x_{i31} & 0 \\ 0 & x_{i32} \end{pmatrix} \begin{pmatrix} 1 \\ 1 \end{pmatrix} \beta_{(1)3}^* \\ &= \sum_{k=1}^3 \text{diag}(x_{ik1}, x_{ik2}) \mathbf{H}_k \boldsymbol{\beta}_{(k)}^*.\end{aligned}$$

Thus to handle time-varying covariates one needs the `xij` facility of **VGAM** (e.g., see Section 6.3), which allows a covariate to have different values for different  $\eta_j$  through the general formula

$$\boldsymbol{\eta}(\mathbf{x}_{ij}) = \sum_{k=1}^d \text{diag}(x_{ik1}, \dots, x_{ikM}) \mathbf{H}_k \boldsymbol{\beta}_{(k)}^* = \sum_{k=1}^d \mathbf{X}_{(ik)}^\# \mathbf{H}_k \boldsymbol{\beta}_{(k)}^* \quad (9)$$

where  $x_{ikj}$  is the value of variable  $x_k$  for unit  $i$  for  $\eta_j$ . The derivation of (9), followed by some examples are given in Yee (2010). Implementing this model requires specification of the diagonal elements of the matrices  $\mathbf{X}_{(ik)}^\#$  and we see its use in Section 6.3. Clearly, a model may include a mix of time-dependent and time-independent covariates. The model is then specified through the constraint matrices  $\mathbf{H}_k$  and the covariate matrices  $\mathbf{X}_{(ik)}^\#$ . Typically in CR experiments, the time-varying covariates will be environmental effects. Fitting time-varying individual covariates requires some interpolation when an individual is not captured and is beyond the scope of the present work.

### 3.3. VGAMs

VGAMs replace the linear functions in (7) by smoothers such as splines. Hence, the central formula is

$$\boldsymbol{\eta}_i = \sum_{k=1}^d \mathbf{H}_k \mathbf{f}_k^*(x_{ik}) \quad (10)$$

where  $\mathbf{f}_k^*(x_k) = (f_{k(1)}^*(x_k), \dots, f_{k(M_k)}^*(x_k))^\top$  is a vector of  $M_k$  smooth functions of  $x_k$ , where  $M_k = \text{ncol}(\mathbf{H}_k)$  is the rank of the constraint matrix for  $x_k$ . Note that standard error bands are available upon plotting the estimated component functions (details at Yee and Wild (1996)), e.g., see Figure 1.

## 4. VGLMs and VGAMs applied to CR data

In this section we merge the results of Sections 2 and 3 to show how the eight models of *Otis et al.* (1978) can be fitted naturally within the VGLM/VGAM framework.

### 4.1. Linear predictors and constraint matrices

As in Section 3.1, we now write  $\mathbf{y}_i$  as the capture history vector for individual  $i$ . Written technically,  $\mathbf{y}_i \in (\{0, 1\})^\tau \setminus \{\mathbf{0}_\tau\}$  so that there is at least one 1 (capture). For simplicity let  $p_c$  and  $p_r$  be the capture and recapture probabilities. Recall that the value for  $M$  will depend on the CR model type and the number of capture occasions considered in the experiment, for example, consider model  $\mathcal{M}_b$  as in Table 2, then  $(\eta_1, \eta_2) = (g(p_c), g(p_r))$  for some link function  $g$ , thus  $M = 2$ . The upper half of Table 3 gives these for the eight *Otis et al.* (1978) models. The lower half of Table 3 gives the names of the **VGAM** family function that fits those models. They work very similarly to the `family` argument of `glm()`, e.g.,

```
R> vglm(cbind(y1, y2, y3, y4, y5, y6) ~ weight + sex + age,
+       family = posbernoulli.t, data = pdata)
```

is a simple call to fit a  $\mathcal{M}_{th}$  model. The response is a matrix containing 0 and 1 values only, and three individual covariates are used here. The argument name `family` was chosen for not necessitating `glm()` users learning a new argument name; and the concept of error distributions as for the GLM class does not carry over for VGLMs. Indeed, `family` denotes some full-likelihood specified statistical model worth fitting in its own right regardless of an ‘error distribution’ which may not make sense. Each family function has `logit()` as their default link, however, alternatives such as `probit()` and `cloglog()` are also permissible. Section 5 discusses the software side of **VGAM** in detail, and Section 6 gives more examples.

As noted above, constraint matrices are used to simplify complex models, e.g., model  $\mathcal{M}_{tth}$  into model  $\mathcal{M}_{th}$ . The default constraint matrices for the  $\mathcal{M}_{tth}(\tau)$  model are given in Table 4. These are easily constructed using the `drop.b`, `parallel.b` and `parallel.t` arguments in the family function. More generally, the  $\mathbf{H}_k$  may be inputted using the `constraints` argument—see Yee (2008) and Yee (2010) for examples. It can be seen that the building blocks of the  $\mathbf{H}_k$  are  $\mathbf{1}$ ,  $\mathbf{0}$ ,  $\mathbf{I}$  and  $\mathbf{O}$ . This is because one wishes to constrain the effect of  $x_k$  to be the same for capture and recapture probabilities. In general, we believe the  $\mathbf{H}_k$  in conjunction with (9) can accommodate all linear constraints between the estimated regression coefficients  $\hat{\beta}_{(j)k}$ .

For time-varying covariates models, the  $M$  diagonal elements  $x_{ikj}$  in (9) correspond to the value of covariate  $x_k$  at time  $j$  for individual  $i$ . These are inputted successively in order using the `xij` argument, e.g., as in Section 6.3.

Model	$\boldsymbol{\eta}^\top$
$\mathcal{M}_0/\mathcal{M}_h$	$g(p)$
$\mathcal{M}_b/\mathcal{M}_{bh}$	$(g(p_c), g(p_r))$
$\mathcal{M}_t/\mathcal{M}_{th}$	$(g(p_1), \dots, g(p_\tau))$
$\mathcal{M}_{tb}/\mathcal{M}_{tbh}$	$(g(p_{c1}), \dots, g(p_{c\tau}), g(p_{r2}), \dots, g(p_{r\tau}))$
Model	family =
$\mathcal{M}_0/\mathcal{M}_h$	posbinomial(omit.constant = TRUE) posbernoulli.b(drop.b = FALSE ~ 0) posbernoulli.t(parallel.t = FALSE ~ 0) posbernoulli.tb(drop.b = FALSE ~ 0, parallel.t = FALSE ~ 0)
$\mathcal{M}_b/\mathcal{M}_{bh}$	posbernoulli.b() posbernoulli.tb(drop.b = FALSE ~ 1, parallel.t = FALSE ~ 0)
$\mathcal{M}_t/\mathcal{M}_{th}$	posbernoulli.t() posbernoulli.tb(drop.b = FALSE ~ 0, parallel.t = FALSE ~ 1)
$\mathcal{M}_{tb}/\mathcal{M}_{tbh}$	posbernoulli.tb()

Table 3: Upper table gives the  $\boldsymbol{\eta}$  for the eight [Otis \*et al.\* \(1978\)](#) models. Lower table gives the relationships between the eight models and function calls. See [Table 2](#) for definitions. The  $g = \text{logit link}$  is default for all.

## 4.2. Penalized likelihood and smoothing parameters

For each covariate  $x_k$ , the smoothness of each component function  $f_{(j)k}^*$  in (10) can be controlled by the non-negative smoothing parameters  $\lambda_{(j)k}$ . [Yee and Wild \(1994\)](#) show that, when vector splines are used as the smoother, the penalized conditional log-likelihood

$$\ell_p \equiv \log L_p = \ell_c - \frac{1}{2} \sum_{k=1}^d \sum_{j=1}^{\text{ncol}(\mathbf{H}_k)} \lambda_{(j)k} \int_{a_k}^{b_k} \left\{ f_{(j)k}^{*''}(t) \right\}^2 dt \quad (11)$$

is maximized. Here,  $\ell_c$  is the logarithm of the conditional likelihood function (2). The penalized conditional likelihood (11) is a natural extension of the penalty approach described in [Green and Silverman \(1994\)](#) to models with multiple  $\eta_j$ .

An important practical issue is to control for overfitting and smoothness in the model. The `s()` function used within `vgam()` signifies the smooth functions  $f_{(j)k}^*$  estimated by vector splines, and there is an argument `spar` for the smoothing parameters, and a relatively small (positive) value will mean much flexibility and wiggleness. As `spar` increases the solution converges to the least squares estimate. More commonly, the argument `df` is used, and this is known as the equivalent degrees of freedom (EDF). A value of unity means a linear fit, and the default is the value 4 which affords a reasonable amount of flexibility.

	parallel.t	!parallel.t
parallel.b	$\begin{pmatrix} \mathbf{0}_\tau & \mathbf{1}_\tau \\ \mathbf{1}_{\tau-1} & \mathbf{1}_{\tau-1} \end{pmatrix}, \begin{pmatrix} \mathbf{1}_\tau \\ \mathbf{1}_{\tau-1} \end{pmatrix}$	$\begin{pmatrix} \mathbf{0}_\tau & \mathbf{I}_\tau \\ \mathbf{1}_{\tau-1} & \mathbf{I}_{\tau[-1,]} \end{pmatrix}, \begin{pmatrix} \mathbf{I}_\tau \\ \mathbf{I}_{\tau[-1,]} \end{pmatrix}$
!parallel.b	$\begin{pmatrix} \mathbf{O}_{\tau \times (\tau-1)} & \mathbf{1}_\tau \\ \mathbf{I}_{\tau-1} & \mathbf{1}_{\tau-1} \end{pmatrix}, \begin{pmatrix} \mathbf{1}_\tau \\ \mathbf{1}_{\tau-1} \end{pmatrix}$	$\begin{pmatrix} \mathbf{O}_{\tau \times (\tau-1)} & \mathbf{I}_\tau \\ \mathbf{I}_{\tau-1} & \mathbf{I}_{\tau[-1,]} \end{pmatrix}, \begin{pmatrix} \mathbf{I}_\tau \\ \mathbf{I}_{\tau[-1,]} \end{pmatrix}$

Table 4: For the general  $\mathcal{M}_{tbh}(\tau)$  family `posbernoulli.tb()`, the constraint matrices corresponding to the arguments `parallel.t`, `parallel.b` and `drop.b`. In each cell the LHS matrix is  $\mathbf{H}_k$  when `drop.b` is `FALSE` for  $x_k$ . The RHS matrix is when `drop.b` is `TRUE` for  $x_k$ ; it simply deletes the left submatrix of  $\mathbf{H}_k$ . These  $\mathbf{H}_k$  should be seen in light of Table 3. Notes: (i) the default for `posbernoulli.tb()` is  $\mathbf{H}_1 =$  the LHS matrix of the top-right cell and  $\mathbf{H}_k =$  the RHS matrix of the top-left cell; and (ii)  $\mathbf{I}_{\tau[-1,]} = (\mathbf{0}_{\tau-1} | \mathbf{I}_{\tau-1})$ .

## 5. Software details for CR models in VGAM

Having presented the conditional likelihood (2) and VGLMs/VGAMs for CR models, we further discuss the fitting in **VGAM**. It is assumed that users are somewhat familiar with modelling in R and using `glm()` class objects. **VGAM**, authored by TWY, uses S4 classes. In order to present the new family functions developed for `vglm()` and `vgam()`, some additional preliminaries for **VGAM** are given below. Version 0.9-4 or later is assumed, and the latest prerelease version is available at <http://www.stat.auckland.ac.nz/yee/VGAM/prerelease>.

In `vglm()/vgam()`, both  $\mathcal{M}_0$  and  $\mathcal{M}_h$  are serviced by `family = posbinomial()`, i.e., the positive-binomial family. For models  $\mathcal{M}_b$ ,  $\mathcal{M}_t$  and  $\mathcal{M}_{tb}$ , each of these are serviced by their corresponding `family = posbernoulli.-type` functions as in Table 3. Formulas of the form  $\sim 1$  correspond to  $\mathcal{M}_0$ ,  $\mathcal{M}_b$ ,  $\mathcal{M}_t$  and  $\mathcal{M}_{tb}$ ; otherwise they are  $\mathcal{M}_h$ ,  $\mathcal{M}_{bh}$ ,  $\mathcal{M}_{th}$  and  $\mathcal{M}_{tbh}$ .

Below we describe each of the eight models with their **VGAM** representation and their default values, we also give additional remarks. All eight models can be fit using `posbernoulli.tb()`, it is generally not recommended as it is less efficient in terms of memory requirements and speed.

### 5.1. Basic software details

All family functions except `posbinomial()` should have a  $n \times \tau$  capture history matrix as the response, preferably with column names. Indicators of the past capture of individual  $i$ , defined as  $z_{ij}$ , are stored on **VGAM** objects as the `cap.hist1` component in the `extra` slot. Also, there is a component called `cap1` which indicates on which sampling occasion the first capture occurred.

As will be illustrated in Section 6.3, a fitted CR object stores the point estimate for the population size estimator (3), in the `extra` slot with component name `N.hat`. Likewise, its standard error (4) has component name `SE.N.hat`. By default all the family functions return fitted values corresponding to the probabilities in the conditional likelihood function (2), however, Appendix B describes an alternative type of fitted value; the choice is made by the argument `type.fitted`, and the fitted values are returned by the `fitted()` methods

function.

Notice that in Table 3, the **VGAM** family functions have arguments such as `parallel.b` which may be assigned a logical or else a formula with a logical as the response. If it is a single logical then the function may or may not apply that constraint to the intercept. The formula is the most general and some care must be taken with the intercept term. Here are some examples of the syntax:

- `parallel.b = TRUE ~ x2` means a parallelism assumption is applied to variables  $x_2$  and the intercept, since formulas include the intercept by default.
- `parallel.b = TRUE ~ x2-1` means a parallelism assumption is applied to variable  $x_2$  only.
- `parallel.b = FALSE ~ 0` means a parallelism assumption is applied to every variable including the intercept.

## 5.2. Models $\mathcal{M}_0/\mathcal{M}_h$

For  $\mathcal{M}_0/\mathcal{M}_h$ , the defaults are given as

```
R> args(posbinomial)
```

```
function (link = "logitlink", multiple.responses = FALSE, parallel = FALSE,
  omit.constant = FALSE, p.small = 1e-04, no.warning = FALSE,
  zero = NULL)
NULL
```

Both models can alternatively be fitted using `posbernoulli.t()`, `posbernoulli.b()` and `posbernoulli.tb()` by setting the appropriate constrains/arguments (Table 3). For example, setting `posbernoulli.t(parallel.t = FALSE ~ 0)` constrains all the  $p_j$  to be equal.

If comparing all eight models using `AIC()` or `BIC()` then setting `omit.constant = TRUE` will allow for comparisons to be made with the positive-Bernoulli functions given below. The reason is that this omits the log-normalizing constant  $\log\left(\frac{\tau}{\tau y_i^*}\right)$  from its conditional log-likelihood so that it is comparable with the logarithm of (2).

An extreme case for  $\mathcal{M}_h$  is where  $p_{ij} = p_i$  with  $p_i$  being parameters in their own right (Otis *et al.* 1978). While this could possibly be fitted by creating a covariate of the form `factor(1:n)` there would be far too many parameters for comfort. Such an extreme case is not recommended to avoid over-parameterization.

## 5.3. Models $\mathcal{M}_t/\mathcal{M}_{th}$

```
R> args(posbernoulli.t)
```

```
function (link = "logitlink", parallel.t = FALSE ~ 1, iprob = NULL,
  p.small = 1e-04, no.warning = FALSE, type.fitted = c("probs",
  "onempall0"))
NULL
```

Note that for  $\mathcal{M}_t$ , capture probabilities are the same for each individual but may vary with time, i.e.,  $H_0 : p_{ij} = p_j$ . One might wish to constrain the probabilities of a subset of sampling occasions to be equal by forming the appropriate constraint matrices.

Argument `iprob` is for an optional initial value for the probability, however all **VGAM** family functions are self-starting and usually do not need such input.

#### 5.4. Models $\mathcal{M}_b/\mathcal{M}_{bh}$

```
R> args(posbernoulli.b)
```

```
function (link = "logitlink", drop.b = FALSE ~ 1, type.fitted = c("likelihood.cond",
  "mean.uncond"), I2 = FALSE, ipcapture = NULL, iprecapture = NULL,
  p.small = 1e-04, no.warning = FALSE)
NULL
```

Setting `drop.b = FALSE ~ 0` assumes there is no behavioural effect and this reduces to  $\mathcal{M}_0/\mathcal{M}_h$ . The default constraint matrices are

$$\mathbf{H}_1 = \begin{pmatrix} 0 & 1 \\ 1 & 1 \end{pmatrix}, \quad \mathbf{H}_2 = \cdots = \mathbf{H}_d = \begin{pmatrix} 1 \\ 1 \end{pmatrix}$$

so that the first coefficient  $\beta_{(1)1}^*$  corresponds to the behavioural effect. Section 6.4 illustrates how the VGLM/VGAM framework can handle short-term and long-term behavioural effects.

#### 5.5. Models $\mathcal{M}_{tb}/\mathcal{M}_{tbh}$

There are three arguments which determine whether there are behavioural effects and/or time effects: `parallel.b`, `parallel.t` and `drop.b`. The last two are as above. The defaults are

```
R> args(posbernoulli.tb)
```

```
function (link = "logitlink", parallel.t = FALSE ~ 1, parallel.b = FALSE ~
  0, drop.b = FALSE ~ 1, type.fitted = c("likelihood.cond",
  "mean.uncond"), imethod = 1, iprob = NULL, p.small = 1e-04,
  no.warning = FALSE, ridge.constant = 1e-04, ridge.power = -4)
NULL
```

One would usually want to keep the behavioural effect to be equal over different sampling occasions, therefore `parallel.b` should be normally left to its default. Allowing it to be `FALSE` for a covariate  $x_k$  means an additional  $\tau - 1$  parameters, something that is not warranted unless the data set is very large and/or the behavioural effect varies greatly over time.

Arguments `ridge.constant` and `ridge.power` concern the working weight matrices and are explained in Appendix A.

Finally, we note that using

```
R> vglm(..., family = posbernoulli.tb(parallel.b = TRUE ~ 0, parallel.t = TRUE ~ 0,
+                                     drop.b = TRUE ~ 0))
```

fits the most general model. Its formula is effectively (5) for  $M = 2\tau - 1$ , hence there are  $(2\tau - 1)d$  regression coefficients in total—far too many for most data sets.

## 6. Examples

We present several examples using **VGAM** on both real-life and simulated CR data.

### 6.1. Deer mice

Our first example uses a well-known data set analyzed in both [Huggins \(1991\)](#) and [Amstrup \*et al.\* \(2005\)](#). The CR data was collected on the deer mouse (*Peromyscus maniculatus*), a small rodent native to North America, and about 8 to 10 cm long, not counting the length of the tail. There were  $n = 38$  individual mice caught over  $\tau = 6$  trapping occasions. Individual body weight, sex and age (young or adult) were also recorded, which we used as covariates to model heterogeneity. The data are given in the following data frame `deermice`:

```
R> head(deermice, 4)

  y1 y2 y3 y4 y5 y6 sex age weight
1  1  1  1  1  1  1  0  y     12
2  1  0  0  1  1  1  1  y     15
3  1  1  0  0  1  1  0  y     15
4  1  1  0  1  1  1  0  y     15
```

Each row represents the capture history followed by the corresponding covariate values for each observed individual. We compared our results with those given in [Huggins \(1991\)](#), who reported an analysis which involved fitting all eight model variations. Prior to this we relabelled the age and sex covariates to match those given in [Huggins \(1991\)](#).

```
R> deermice <- within(deermice, {
+   age <- 2 - as.numeric(age)
+   sex <- 1 - as.numeric(sex)
+ })
```

Below we demonstrate model fitting for each model in **VGAM**:

```
R> M.0 <- vglm(cbind(y1, y2, y3, y4, y5, y6) ~ 1,
+             posbernoulli.t(parallel = TRUE ~ 1), data = deermice)
R> M.b <- vglm(cbind(y1, y2, y3, y4, y5, y6) ~ 1,
+             posbernoulli.b, data = deermice)
R> M.t <- vglm(cbind(y1, y2, y3, y4, y5, y6) ~ 1,
+             posbernoulli.t, data = deermice)
R> M.h <- vglm(cbind(y1, y2, y3, y4, y5, y6) ~ weight + sex + age,
+             posbernoulli.t(parallel = TRUE ~ weight + sex + age), data = deermice)
R> M.th <- vglm(cbind(y1, y2, y3, y4, y5, y6) ~ weight + sex + age,
+             posbernoulli.t, data = deermice)
R> M.tb <- vglm(cbind(y1, y2, y3, y4, y5, y6) ~ 1,
+             posbernoulli.tb, data = deermice)
R> M.bh <- vglm(cbind(y1, y2, y3, y4, y5, y6) ~ weight + sex + age,
+             posbernoulli.b, data = deermice)
R> M.tbh <- vglm(cbind(y1, y2, y3, y4, y5, y6) ~ weight + sex + age,
+             posbernoulli.tb, data = deermice)
```

Notice that `parallel = TRUE` was used for models  $\mathcal{M}_0/\mathcal{M}_h$ . Population size estimates with standard errors (SE), log-likelihood and AIC values, can all be easily obtained using the following, for example, consider model  $\mathcal{M}_{bh}$ :

```
R> c(M.bh@extra$N.hat, M.bh@extra$SE.N.hat)
```

```
[1] 47.144  7.322
```

```
R> c(logLik(M.bh), AIC(M.bh))
```

```
[1] -139.5  289.1
```

We did this for each model, and obtained the following:

```
R> Table
```

	M.tbh	M.bh	M.tb	M.th	M.h	M.b	M.t	M.0
N.hat	47.13	47.14	46.48	39.66	39.85	42.26	38.40	38.47
SE	9.70	7.32	12.64	1.61	1.72	3.75	0.66	0.72
-2ln(L)	274.66	279.08	296.36	279.10	289.74	300.86	304.84	314.54
AIC	294.66	289.09	310.36	297.10	297.75	304.87	316.84	316.54

Based on the AIC, it was concluded that  $\mathcal{M}_{bh}$  was superior (although other criteria can also be considered), yielding the following coefficients (as well as their SEs):

```
R> round(coef(M.bh), 2)
```

```
(Intercept):1 (Intercept):2      weight      sex      age
           1.18           -2.91           0.16           0.92           -1.88
```

```
R> round(sqrt(diag(vcov(M.bh))), 2)
```

```
(Intercept):1 (Intercept):2      weight      sex      age
           0.41           0.90           0.06           0.35           0.63
```

which, along with the estimates for the population size, agree with the results of [Huggins \(1991\)](#). The first coefficient, 1.18, is positive and hence implies a trap-happy effect.

Now to illustrate the utility of fitting VGAMs, we performed some model checking on  $\mathcal{M}_{bh}$  by confirming that the component function of `weight` is indeed linear. To do this, we smoothed this covariate but did not allow it to be too flexible due to the size of the data set.

```
R> fit.bh <- vgam(cbind(y1, y2, y3, y4, y5, y6) ~ s(weight, df = 3) + sex + age,
+               posbernoulli.b, data = deermice)
R> plot(fit.bh, se = TRUE, las = 1, lcol = "blue", scol = "orange",
+       rcol = "purple", scale = 5)
```



Notice that the `s()` function was used to smooth over the weight covariate with the equivalent degrees of freedom set to 3. Plots of the estimated component functions against each covariate are given in Figure 1. In general, `weight` does seem to have a (positive) linear effect on the logit scale. Young deer mice appear more easily caught compared to adults, and gender seems to have a smaller effect than weight. A more formal test of linearity is

```
R> summary(fit.bh)
```

Call:

```
vgam(formula = cbind(y1, y2, y3, y4, y5, y6) ~ s(weight, df = 3) +
      sex + age, family = posbernoulli.b, data = deermice)
```

Names of additive predictors: logitlink(pcapture),  
logitlink(precapture)

Dispersion Parameter for posbernoulli.b family: 1

Log-likelihood: -137.9 on 69.04 degrees of freedom

Number of Fisher scoring iterations: 12

DF for Terms and Approximate Chi-squares for Nonparametric Effects

	Df	Npar	Df	Npar	Chisq	P(Chi)
(Intercept):1	1					
(Intercept):2	1					
s(weight, df = 3)	1		2		3.2	0.194
sex	1					
age	1					

and not surprisingly, this suggests there is no significant nonlinearity. This is in agreement with Section 6.1 of [Hwang and Huggins \(2011\)](#) who used kernel smoothing.

Section 6.4 reports a further analysis of the `deermice` data using a behavioural effect comprising of long-term and short-term memory.

## 6.2. Yellow-bellied Prinia

Our second example also uses a well-known and well-studied data set collected on the Yellow-bellied Prinia (*Prinia flaviventris*), a common bird species located in Southeast Asia. A CR experiment was conducted at the Mai Po Nature Reserve in Hong Kong during 1991, where captured individuals had their wing lengths measured and fat index recorded. A total of  $\tau = 19$  weekly capture occasions were considered, where  $n = 151$  distinct birds were captured. In previous studies, models  $\mathcal{M}_h$  and  $\mathcal{M}_{th}$  have both been fitted to these data, where both wing length and fat index were used as covariates. We focus our attention on the former model, and considered the `posbinomial()` function, with some further emphasis on demonstrating smoothing on covariates. The `prinia` data consists of four columns and rows corresponding to each observed individual:

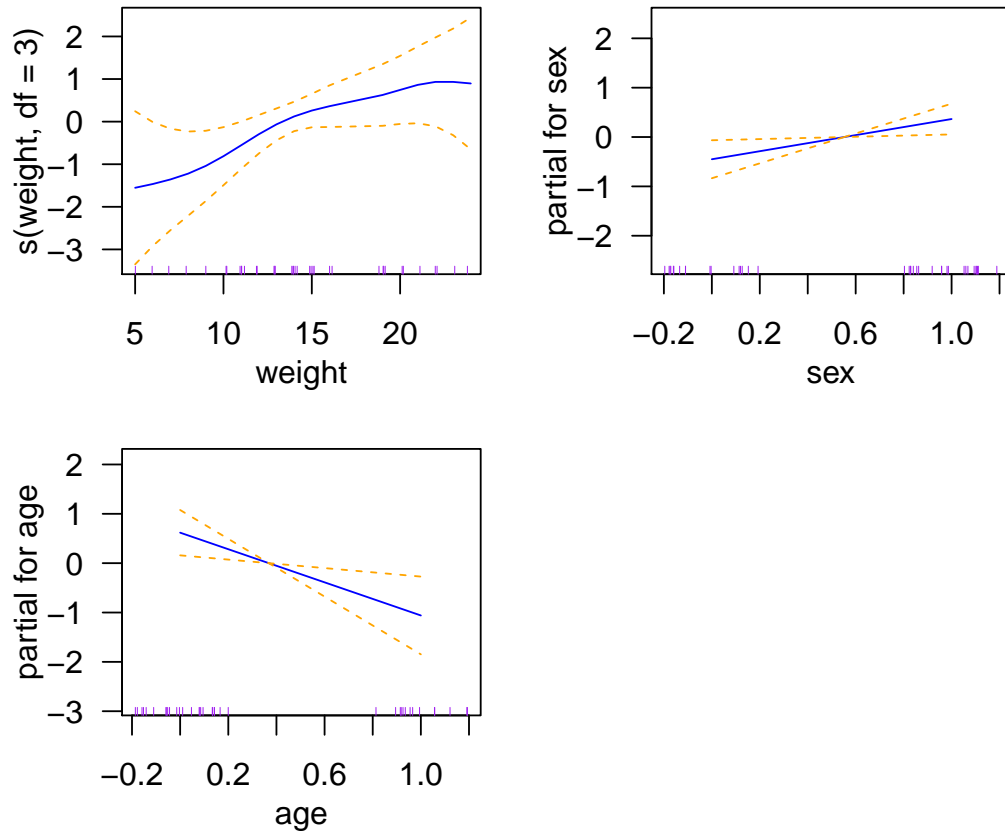


Figure 1: Estimated component functions with approximate  $\pm 2$  pointwise SE bands fitting a  $\mathcal{M}_{bh}$ -VGAM, using the `deermice` data. The rugplot gives jittered values of each covariate value  $x_{ik}$ .

```
R> head(prinia, 4)[, 1:4]
```

	length	fat	cap	noncap
1	1.00650	1	5	14
2	1.26463	1	3	16
3	-0.02598	1	6	13
4	3.07148	0	1	18

The first two columns give the observed covariate values for each individual, followed by the number of times each individual was captured/not captured respectively (columns 3–4). Notice that the wing length (`length`) was standardized here. We considered smoothing over the wing length, and now plotted the fitted capture probabilities with and without fat content against wing length present, see Figure 2.

```
R> M.h.GAM <-  
+ vgam(cbind(cap, noncap) ~ s(length, df = 3) + fat,
```

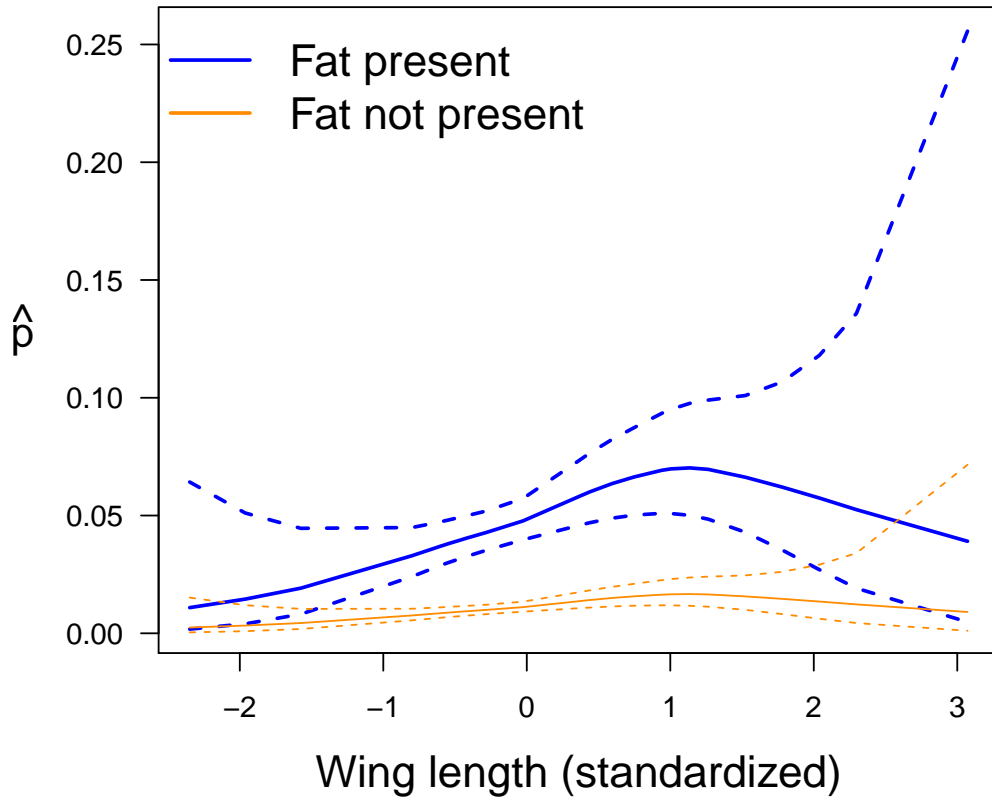


Figure 2: Capture probability estimates with approximate  $\pm 2$  pointwise SEs, versus wing length with (blue) and without (orange) fat content present fitting a  $\mathcal{M}_h$ -VGAM, using the `prinia` data. Notice that the standard errors are wider at the boundaries.

```
+      posbinomial(omit.constant = TRUE, parallel = TRUE ~ s(length, df = 3) + fat),
+      data = prinia)
R> M.h.GAM@extra$N.hat
```

```
[1] 447.6
```

```
R> M.h.GAM@extra$SE.N.hat
```

```
[1] 108.9
```

Both the estimates for the population size and shape of the fitted capture probabilities with smoothing (Figure 2) matched those in previous studies, e.g., see Figure 1 of [Hwang and Huggins \(2007\)](#). Notice that capture probabilities are larger for individuals with fat content

present, also the approximate  $\pm 2$  pointwise SEs become wider at the boundaries—this feature is commonly seen in smooths.

### 6.3. A time-varying covariate example

To illustrate time-varying covariates in the  $\mathcal{M}_{th}$  and  $\mathcal{M}_{tth}$  model via the `xij` argument, we mimicked the results of [Huggins \(1989\)](#) who fitted the  $\mathcal{M}_{tth}$  model to a small simulated data set of  $n = 18$  observed individuals and  $\tau = 10$  trapping occasions. To help illustrate the procedure we also fitted model  $\mathcal{M}_{th}$ . The true population was  $N = 20$ . For the  $i$ th individual, model  $\mathcal{M}_{th}$  will be written as ( $i = 1, \dots, 18, j = 1, \dots, 10$ )

$$\text{logit } p_{ij} = \beta_{(1)1}^* + \beta_{(1)2}^* \cdot \mathbf{x2}_i + \beta_{(1)3}^* \cdot \mathbf{x3}_j, \quad (12)$$

and model  $\mathcal{M}_{tth}$  will be written as ( $i = 1, \dots, 18, j = 1, \dots, 10$ )

$$\text{logit } p_{ij} = \beta_{(1)1}^* z_{ij} + \beta_{(2)1}^* + \beta_{(1)2}^* \cdot \mathbf{x2}_i + \beta_{(1)3}^* \cdot \mathbf{x3}_j, \quad (13)$$

where  $\beta_{(1)1}^*$  in (13) is the behavioural effect, and  $z_{ij}$  is defined in Table 1. Variable `x2` is an ordinary individual covariate such as weight, as in the previous examples. The variable `x3` is a time-varying or occasion-specific covariate such as temperature or daily rainfall that is handled using the `xij` argument described in Section 3.2. Note that the environmental covariates are involved in the  $\eta_j$  for individuals that have not been and have been previously captured so that if behavioural response is included in the model (e.g.,  $\mathcal{M}_{tth}$ ) these must be repeated to construct the overall model matrix. Also, note that there can be no recaptures on the first occasion so that the environmental variable for this occasion need not be repeated. We first examined the data

```
R> head(Huggins89table1, 4)
```

```

  x2 y01 y02 y03 y04 y05 y06 y07 y08 y09 y10 t01 t02 t03 t04 t05 t06
1 6.3  0   1   0   1   1   0   0   1   0   0 5.8 2.9 3.7 2.2 3.5 3.6
2 4.0  0   1   1   1   1   0   0   1   0   0 5.8 2.9 3.7 2.2 3.5 3.6
3 4.7  0   1   0   0   1   1   1   1   0   0 5.8 2.9 3.7 2.2 3.5 3.6
4 4.8  0   0   1   1   1   0   1   1   0   0 5.8 2.9 3.7 2.2 3.5 3.6
  t07 t08 t09 t10
1 1.9   3 4.8 4.7
2 1.9   3 4.8 4.7
3 1.9   3 4.8 4.7
4 1.9   3 4.8 4.7
```

The time-varying/occasion-specific covariate variable `x3` is represented by variables `t01`–`t10`. As noted above, we need to construct the `T02`–`T10` to model the recapture probabilities through  $\eta_j$  for  $j = 11, \dots, 19$

```
R> Hdata <- transform(Huggins89table1, x3.tij = t01,
+                       T02 = t02, T03 = t03, T04 = t04, T05 = t05, T06 = t06,
+                       T07 = t07, T08 = t08, T09 = t09, T10 = t10)
R> Hdata <- subset(Hdata,
+                 y01 + y02 + y03 + y04 + y05 + y06 + y07 + y08 + y09 + y10 > 0)
```

The last step deletes the two observations which were never caught, such that  $n = 18$ . Thus model (12) can be fitted by

```
R> fit.th <-
+ vglm(cbind(y01, y02, y03, y04, y05, y06, y07, y08, y09, y10) ~ x2 + x3.tij,
+       xij = list(x3.tij ~ t01 + t02 + t03 + t04 + t05 + t06 + t07 + t08 +
+                 t09 + t10 - 1),
+       posbernoulli.t(parallel.t = TRUE ~ x2 + x3.tij),
+       data = Hdata, trace = FALSE,
+       form2 = ~ x2 + x3.tij + t01 + t02 + t03 + t04 + t05 + t06 + t07 + t08 +
+                 t09 + t10)
```

The `form2` argument is required if `xij` is used and it needs to include all the variables in the model. It is from this formula that a very large model matrix is constructed, from which the relevant columns are extracted to construct the diagonal matrix in (9) in the specified order of diagonal elements given by `xij`. Their names need to be uniquely specified. To check the constraint matrices we can use

```
R> constraints(fit.th, matrix = TRUE)
```

	(Intercept)	x2	x3.tij
logitlink(E[y01])	1	1	1
logitlink(E[y02])	1	1	1
logitlink(E[y03])	1	1	1
logitlink(E[y04])	1	1	1
logitlink(E[y05])	1	1	1
logitlink(E[y06])	1	1	1
logitlink(E[y07])	1	1	1
logitlink(E[y08])	1	1	1
logitlink(E[y09])	1	1	1
logitlink(E[y10])	1	1	1

Model (13) can be fitted by

```
R> fit.tbh <-
+ vglm(cbind(y01, y02, y03, y04, y05, y06, y07, y08, y09, y10) ~ x2 + x3.tij,
+       xij = list(x3.tij ~ t01 + t02 + t03 + t04 + t05 + t06 +
+                 t07 + t08 + t09 + t10 +
+                 T02 + T03 + T04 + T05 + T06 +
+                 T07 + T08 + T09 + T10 - 1),
+       posbernoulli.tb(parallel.t = TRUE ~ x2 + x3.tij),
+       data = Hdata, trace = FALSE,
+       form2 = ~ x2 + x3.tij +
+                 t01 + t02 + t03 + t04 + t05 + t06 + t07 + t08 + t09 + t10 +
+                 T02 + T03 + T04 + T05 + T06 + T07 + T08 + T09 + T10)
```

To compare with model (12) we have

```
R> c(logLik(fit.th), AIC(fit.th))
```

```
[1] -97.08 200.16
```

```
R> c(logLik(fit.tbh), AIC(fit.tbh))
```

```
[1] -94.15 196.30
```

so that the behavioural response model does indeed give a better fit. To check, the constraint matrices are (cf., Table 4)

```
R> head(constraints(fit.tbh, matrix = TRUE), 4)
```

```

                (Intercept):1 (Intercept):2 x2 x3.tij
logitlink(pcapture.1)         0             1  1     1
logitlink(pcapture.2)         0             1  1     1
logitlink(pcapture.3)         0             1  1     1
logitlink(pcapture.4)         0             1  1     1

```

```
R> tail(constraints(fit.tbh, matrix = TRUE), 4)
```

```

                (Intercept):1 (Intercept):2 x2 x3.tij
logitlink(precapture.7)       1             1  1     1
logitlink(precapture.8)       1             1  1     1
logitlink(precapture.9)       1             1  1     1
logitlink(precapture.10)      1             1  1     1

```

The coefficients  $\hat{\beta}_{(j)k}^*$  and their standard errors are

```
R> coef(fit.tbh)
```

```

(Intercept):1 (Intercept):2          x2          x3.tij
      1.0938      -0.6306      0.3845      -0.8369

```

```
R> sqrt(diag(vcov(fit.tbh)))
```

```

(Intercept):1 (Intercept):2          x2          x3.tij
      0.5365      1.3608      0.2229      0.1857

```

The first coefficient, 1.09, is positive and hence implies a trap-happy effect. The Wald statistic for the behavioural effect, being 2.04, suggests the effect is real.

Estimates of the population size can be obtained from

```
R> fit.tbh@extra$N.hat
```

```
[1] 20.94
```

```
R> fit.tbh@extra$SE.N.hat
```

```
[1] 3.456
```

This compares with  $\hat{N} = 20.86$  with a standard error of 4.51 (Huggins 1989).

In closing, we refit model `fit.tbh` using `Select()` to illustrate the avoidance of manual specification of cumbersome formulas and response matrices with many columns. For example, suppose `pdata` is a data frame with columns `y01`, `y02`, ..., `y30`. Then `Select(pdata, "y")` will return the matrix `cbind(y01, y02, ..., y30)` if there are no other variables beginning with "y".

Starting with `Huggins89table1`, the following code works quite generally provided the original variables are labelled as `y01`, `y02`, ..., and `t01`, `t02`, .... The code makes a copy of `cbind(t01, ..., t10)` for the capture probabilities and calls the variables `cbind(T01, ..., T10)` for the recapture probabilities. Also, `Form2` contains more variables than what is needed.

```
R> Hdata <- subset(Huggins89table1, rowSums(Select(Huggins89table1, "y")) > 0)
R> Hdata.T <- Select(Hdata, "t")
R> colnames(Hdata.T) <- gsub("t", "T", colnames(Hdata.T))
R> Hdata <- data.frame(Hdata, Hdata.T)
R> Hdata <- transform(Hdata, x3.tij = y01)
R> Form2 <- Select(Hdata, prefix = TRUE, as.formula = TRUE)
R> Xij <- Select(Hdata, c("t", "T"), as.formula = TRUE,
+               sort = FALSE, rhs = "0", lhs = "x3.tij", exclude = "T01")
R> fit.tbh <- vglm(Select(Hdata, "y") ~ x2 + x3.tij,
+               form2 = Form2, xij = list(Xij),
+               posbernoulli.tb(parallel.t = TRUE ~ x2 + x3.tij),
+               data = Hdata, trace = FALSE)
R> coef(fit.tbh)
```

```
(Intercept):1 (Intercept):2          x2          x3.tij
      1.0938      -0.6306      0.3845      -0.8369
```

Note that this illustrates the ability to enter a matrix response without an explicit `cbind()`, e.g., `Y <- Select(Hdata, "y")` and the invocation `vglm(Y ~ ...)` would work as well. However, the utility of `cbind()` encourages the use of column names, which is good style and avoids potential coding errors.

#### 6.4. Ephemeral and enduring memory

Yang and Chao (2005) consider modelling the behavioural effect with both enduring (long-term) and ephemeral (short-term) memory components. For example, the short-term component depends on whether or not the animal was caught on the most recent sampling occasion. We call this a lag-1 effect. In the example of this section, which combines aspects of Sections 6.1 and 6.3, we illustrate how this may be easily achieved within the VGLM framework; it is another case of using the `xij` argument. We retain the enduring component as with the  $\mathcal{M}_{tbh}$ :  $\mathbf{H}_1$  contains a column that applies to all the recapture probabilities. For simplicity, we first consider a lag-1 effect only (as in Yang and Chao (2005)) for the short-term component.

In the following, we fit a  $\mathcal{M}_{tbh}$  model to `deermice` with both long-term and short-term effects:

$$\begin{aligned}\text{logit } p_{cs} &= \beta_{(2)1}^* + \beta_{(1)2}^* \text{sex} + \beta_{(1)3}^* \text{weight}, \\ \text{logit } p_{rt} &= \beta_{(1)1}^* + \beta_{(2)1}^* + \beta_{(1)2}^* \text{sex} + \beta_{(1)3}^* \text{weight} + \beta_{(1)4}^* y_{t-1},\end{aligned}$$

where  $s = 2, \dots, \tau$ ,  $t = 1, \dots, \tau$  and  $\tau = 6$ .

```
R> deermice <- transform(deermice, Lag1 = y1)
R> M.tbh.lag1 <-
+ vglm(cbind(y1, y2, y3, y4, y5, y6) ~ sex + weight + Lag1,
+       posbernoulli.tb(parallel.t = FALSE ~ 0,
+                       parallel.b = FALSE ~ 0,
+                       drop.b = FALSE ~ 1),
+       xij = list(Lag1 ~ fill(y1) + fill(y2) + fill(y3) + fill(y4) +
+                 fill(y5) + fill(y6) +
+                 y1 + y2 + y3 + y4 + y5),
+       form2 = ~ sex + weight + Lag1 +
+               fill(y1) + fill(y2) + fill(y3) + fill(y4) +
+               fill(y5) + fill(y6) +
+               y1 + y2 + y3 + y4 + y5 + y6,
+       data = deermice)
R> coef(M.tbh.lag1)
```

```
(Intercept):1 (Intercept):2          sex          weight          Lag1
      1.277694      -1.578218      1.151380      0.005837      0.023057
```

The coefficient of `Lag1`, 0.0231, is the estimated ephemeral effect  $\hat{\beta}_{(1)4}^*$ . The estimated enduring effect  $\hat{\beta}_{(1)1}^*$  has value 1.2777. Note that the `fill()` function is used to create 6 variables having 0 values, i.e.,  $\mathbf{0}_n$ .

There is an alternative method to fit the above model; here we set  $\mathbf{H}_{\text{Lag1}} = (\mathbf{0}_\tau^\top, \mathbf{1}_{\tau-1}^\top)^\top$  and the variables `fill(y1), ..., fill(y6)` can be replaced by variables that do not need to be 0. Importantly, the two methods have  $\mathbf{X}_{(ik)}^\# \mathbf{H}_k$  in (9) being the same regardless. The second alternative method requires constraint matrices to be inputted using the `constraints` argument. For example,

```
R> deermice <- transform(deermice, Lag1 = y1)
R> deermice <- transform(deermice, f1 = y1, f2 = y1, f3 = y1, f4 = y1,
+                       f5 = y1, f6 = y1)
R> tau <- 6
R> H2 <- H3 <- cbind(rep(1, 2*tau-1))
R> H4 <- cbind(c(rep(0, tau), rep(1, tau-1)))
R> M.tbh.lag1.method2 <-
+ vglm(cbind(y1, y2, y3, y4, y5, y6) ~ sex + weight + Lag1,
+       posbernoulli.tb(parallel.b = TRUE ~ 0, parallel.t = TRUE ~ 0),
+       constraints = list("(Intercept)" = cbind(H4, 1), sex = H2, weight = H3,
+                 Lag1 = H4),
```



```

+     xij = list(Lag1 ~ f1 + f2 + f3 + f4 + f5 + f6 +
+               y1 + y2 + y3 + y4 + y5),
+     form2 = Select(deermice, prefix = TRUE, as.formula = TRUE),
+     data = deermice)
R> coef(M.tbh.lag1.method2)

```

(Intercept):1	(Intercept):2	sex	weight	Lag1
1.277694	-1.578218	1.151380	0.005837	0.023057

is identical. In closing, it can be noted that more complicated models can be handled. For example, the use of `pmax()` to handle lag-2 effects as follows.

```

R> deermice <- transform(deermice, Lag2 = y1)
R> M.bh.lag2 <-
+ vglm(cbind(y1, y2, y3, y4, y5, y6) ~ sex + weight + Lag2,
+      posbernoulli.tb(parallel.t = FALSE ~ 0,
+                      parallel.b = FALSE ~ 0,
+                      drop.b = FALSE ~ 1),
+      xij = list(Lag2 ~ fill(y1) + fill(y2) + fill(y3) + fill(y4) +
+                fill(y5) + fill(y6) +
+                y1 + pmax(y1, y2) + pmax(y2, y3) + pmax(y3, y4) +
+                pmax(y4, y5)),
+      form2 = ~ sex + weight + Lag2 +
+              fill(y1) + fill(y2) + fill(y3) + fill(y4) +
+              fill(y5) + fill(y6) +
+              y1 + pmax(y1, y2) + pmax(y2, y3) + pmax(y3, y4) +
+              pmax(y4, y5) + y6,
+      data = deermice)
R> coef(M.bh.lag2)

```

(Intercept):1	(Intercept):2	sex	weight	Lag2
1.967699	-1.658977	1.217247	0.007467	-0.722267

Models with separate lag-1 and lag-2 effects may also be similarly estimated as above.

## 7. Discussion

We have presented how the VGLM/VGAM framework naturally handles the conditional-likelihood and closed population CR models in a GLM-like manner. Recently, [Stoklosa \*et al.\* \(2011\)](#) proposed a partial likelihood approach for heterogeneous models with covariates. There, the recaptures of the observed individuals were modelled, which yielded a binomial distribution, and hence a GLM/GAM framework in R is also possible. However, some efficiency is lost, as any individuals captured only once on the last occasion are excluded. The advantage of partial likelihood is that the full range of GLM based techniques, which includes more than GAMs, are readily applicable. [Huggins and Hwang \(2007\)](#); [Hwang and Huggins \(2011\)](#) and [Stoklosa and Huggins \(2012\)](#) implemented smoothing on covariates for more general models,

however these methods required implementing sophisticated coding for estimating the model parameters. Zwane and van der Heijden (2004) also used the **VGAM** package for smoothing and CR data, but considered multinomial logit models as an alternative to the conditional likelihood. We believe the methods here, based on spline smoothing and classical GAM, are a significant improvement in terms of ease of use, capability and efficiency.

When using any statistical software, the user must take a careful approach when analyzing and interpreting their output data. In our case, one must be careful when estimating the population via the HT estimator. Notice that (3) is a sum of the reciprocal of the estimated capture probabilities seen at least once,  $\hat{\pi}_i(\boldsymbol{\theta})$ . Hence, for very small  $\hat{\pi}_i(\boldsymbol{\theta})$ , the population size estimate may give a large and unrealistic value (this is also apparent when using the **mra** package and **Rcapture** which gives the warning message: **The abundance estimation for this model can be unstable**). To avoid this, Stoklosa and Huggins (2012) proposed a robust HT estimator which places a lower bound on  $\hat{\pi}_i(\boldsymbol{\theta})$  to prevent it from giving unrealistically large values. In **VGAM**, a warning similar to **Rcapture** is also implemented, and there are arguments to control how close to 0 “very small” is and to suppress the warning entirely.

There are limitations for  $\mathcal{M}_h$ -type models, in that they rely on the very strong assumption that all the heterogeneity is explained by the unit-level covariates. This assumption is often not true, see, e.g., Rivest and Baillargeon (2014). To this end, a proposal is to add random-effects to the VGLM class. This would result in the VGLMM class (“M” for mixed) which would be potentially very useful if developed successfully. Of course, VGLMMs would contain GLMMs (McCulloch *et al.* 2008) as a special case. Further future implementations also include: automatic smoothing parameter selection (via, say, generalized cross validation or AIC); including a bootstrap procedure as an alternative for standard errors.

GAMs are now a standard statistical tool in the modern data analyst’s toolbox. With the exception of the above references, CR analysis has since been largely confined to a few regression coefficients (at most), and devoid of any data-driven exploratory analyses involving graphics. This work has sought to rectify this need by introducing GAM-like analyses using a unified statistical framework. Furthermore, the functions are easy to use and often can be invoked by a single line of code. Finally, we believe this work is a substantial improvement over other existing software for closed population estimation, and we have shown **VGAM**’s favourable speed and reliability over other closed population CR R-packages.

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## Appendix A: Derivatives

We give the first and (expected) second derivatives of the models. Let  $z_{ij} = 1$  if individual  $i$  has been captured before occasion  $j$ , else  $= 0$ . Also, let  $p_{cj}$  and  $p_{rj}$  be the probability that an individual is captured/recaptured at sampling occasion  $j$ , and  $Q_{s:t} = \prod_{j=s}^t (1 - p_{cj})$ . Occasionally, subscripts  $i$  are omitted for clarity. Huggins (1989) gives a general form for the derivatives of the conditional likelihood (2).

For the  $\mathcal{M}_{tbh}$ , the score vector is

$$\begin{aligned}\frac{\partial \ell_i}{\partial p_{cj}} &= (1 - z_{ij}) \left[ \frac{y_{ij}}{p_{cj}} - \frac{1 - y_{ij}}{1 - p_{cj}} \right] - \frac{Q_{1:\tau}/(1 - p_{cj})}{1 - Q_{1:\tau}}, \quad j = 1, \dots, \tau, \\ \frac{\partial \ell_i}{\partial p_{rj}} &= z_{ij} \left[ \frac{y_{ij}}{p_{rj}} - \frac{1 - y_{ij}}{1 - p_{rj}} \right], \quad j = 2, \dots, \tau,\end{aligned}$$

and the non-zero elements of the expected information matrix (EIM) can be written

$$\begin{aligned}-\mathbb{E} \left( \frac{\partial^2 \ell}{\partial p_{cj}^2} \right) &= \frac{Q_{1:(j-1)}}{1 - Q_{1:\tau}} \left\{ \frac{1}{p_{cj}} + \frac{1 - Q_{(j+1):\tau}}{1 - p_{cj}} \right\} - \left( \frac{\partial Q_{1:\tau}/\partial p_{cj}}{1 - Q_{1:\tau}} \right)^2 \\ &= \frac{1}{(1 - p_{cj})^2 (1 - Q_{1:\tau})} \left\{ \frac{Q_{1:j}}{p_{cj}} - \frac{Q_{1:\tau}}{1 - Q_{1:\tau}} \right\}, \\ -\mathbb{E} \left( \frac{\partial^2 \ell}{\partial p_{rj}^2} \right) &= \frac{1 - Q_{1:j}/(1 - p_{cj})}{p_{rj}(1 - p_{rj})(1 - Q_{1:\tau})}, \\ -\mathbb{E} \left( \frac{\partial^2 \ell}{\partial p_{cj} \partial p_{ck}} \right) &= \frac{\frac{\partial Q_{1:\tau}}{\partial p_{cj}} \frac{\partial Q_{1:\tau}}{\partial p_{ck}}}{(1 - Q_{1:\tau})^2} - \frac{\frac{\partial^2 Q_{1:\tau}}{\partial p_{cj} \partial p_{ck}}}{(1 - Q_{1:\tau})}, \quad j \neq k,\end{aligned}$$

where  $\partial Q_{1:\tau}/\partial p_{cj} = -Q_{1:\tau}/(1 - p_{cj})$  and  $\partial^2 Q_{1:\tau}/(\partial p_{cj} \partial p_{ck}) = Q_{1:\tau}/\{(1 - p_{cj})(1 - p_{ck})\}$ .

Arguments `ridge.constant` and `ridge.power` in `posbernoulli.tb()` add a ridge parameter to the first  $\tau$  EIM diagonal elements, i.e., those for  $p_{cj}$ . This ensures that the working weight matrices are positive-definite, and is needed particularly in the first few iteratively reweighted least squares iterations. Specifically, at iteration  $a$  a positive value  $\omega K \times a^p$  is added, where  $K$  and  $p$  correspond to the two arguments, and  $\omega$  is the mean of elements of such working weight matrices. The ridge factor decays to zero as iterations proceed and plays a negligible role upon convergence.

For individual  $i$ , let  $y_{0i}$  be the number of noncaptures before the first capture,  $y_{r0i}$  be the number of noncaptures after the first capture, and  $y_{r1i}$  be the number of recaptures after the first capture. For the  $\mathcal{M}_{bh}$ , the score vector is

$$\begin{aligned}\frac{\partial \ell_i}{\partial p_c} &= \frac{1}{p_c} - \frac{y_{0i}}{1 - p_c} - \frac{\tau(1 - p_{ij})^{\tau-1}}{1 - Q_{1:\tau}}, \\ \frac{\partial \ell_i}{\partial p_r} &= \frac{y_{r1i}}{p_r} - \frac{y_{r0i}}{1 - p_c}.\end{aligned}$$

The non-zero elements of the EIM can be written

$$\begin{aligned}
-\mathbb{E}\left(\frac{\partial^2 \ell}{\partial p_c^2}\right) &= \frac{p_c}{1 - Q_{1:\tau}} \sum_{j=1}^{\tau} (1 - p_c)^{j-1} \left( \frac{j-1}{(1-p_c)^2} + \frac{1}{p_c^2} \right) - \frac{\partial}{\partial p_c} \left( \frac{\partial Q_{1:\tau} / \partial p_c}{1 - Q_{1:\tau}} \right) \\
&= \frac{1 - Q_{1:\tau} - p_c[1 + (\tau-1)Q_{1:\tau}]}{p_c(1-p_c)^2(1-Q_{1:\tau})} + \frac{1}{p_c^2} - \\
&\quad \tau(\tau-1) \frac{(1-p_c)^{\tau-2}}{1-Q_{1:\tau}} + \tau^2 \frac{(1-p_c)^{\tau-2}}{(1-Q_{1:\tau})^2}, \\
-\mathbb{E}\left(\frac{\partial^2 \ell}{\partial p_r^2}\right) &= \frac{1}{p_r(1-p_r)(1-Q_{1:\tau})} \sum_{j=1}^{\tau} \{1 - (1-p_c)^{j-1}\} \\
&= \frac{\tau - (1 - Q_{1:\tau})/p_c}{p_r(1-p_r)(1-Q_{1:\tau})}.
\end{aligned}$$

For the  $\mathcal{M}_{th}$ , the score vector is

$$\frac{\partial \ell_i}{\partial p_j} = \frac{y_{ij}}{p_{ij}} - \frac{1 - y_{ij}}{1 - p_{ij}} - \frac{Q_{1:\tau}/(1 - p_{ij})}{1 - Q_{1:\tau}}, \quad j = 1, \dots, \tau,$$

and the EIM elements are

$$\begin{aligned}
-\mathbb{E}\left(\frac{\partial^2 \ell}{\partial p_j^2}\right) &= \frac{1 - p_j - Q_{1:\tau}}{p_j(1-p_j)^2(1-Q_{1:\tau})^2}, \\
-\mathbb{E}\left(\frac{\partial^2 \ell}{\partial p_j \partial p_k}\right) &= \frac{p_j p_k Q_{1:\tau}(1 - Q_{1:\tau}) + Q_{1:\tau}^2}{(1 - Q_{1:\tau})^2(1 - p_j)(1 - p_k)}, \quad j \neq k.
\end{aligned}$$

## Appendix B: Fitted values

By default all the family functions have fitted values corresponding to the probabilities in the conditional likelihood function (2), viz.

$$\hat{p}_{ij}^{y_{ij}} (1 - \hat{p}_{ij})^{1-y_{ij}} \cdot \left[ 1 - \prod_{s=1}^{\tau} (1 - \hat{p}_{i,cs}) \right]^{-1}.$$

Alternatively, the unconditional means of the  $Y_j$  can be returned as the fitted values upon selecting `type.fitted = "mean"` argument. They are  $\mu_1 = E(Y_1) = p_{c1}/(1 - Q_{1:\tau})$ ,  $\mu_2 = [(1 - p_{c1})p_{c2} + p_{c1}p_{r2}]/(1 - Q_{1:\tau})$ , and for  $j = 3, 4, \dots, \tau$ ,

$$\mu_j = (1 - Q_{1:\tau})^{-1} \left\{ p_{cj} Q_{1:(j-1)} + p_{rj} \left[ p_{c1} + \sum_{s=2}^{j-1} p_{cs} Q_{1:(s-1)} \right] \right\}.$$

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