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singleRcapture: A Package for Single-Source Capture-Recapture Models

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Abstract

The estimation of population size represents a significant challenge within the domains of official statistics, social sciences, and natural sciences. In such situations capture-recapture methods can be applied, which can be classified according to the number of sources utilized, particularly whether a single or multiple sources are employed. This paper focuses on the first group of methods and introduces the package **singleRcapture**. The package implements state-of-the-art single-source capture-recapture models (e.g. zero-truncated one-inflated regression), new developments proposed by the authors, and provides a user-friendly application programming interface (API). The package is self-contained, providing point estimates and their variance, as well as implementing several bootstrap variance estimators or diagnostics to assess quality and conduct sensitivity analysis. It is intended for users interested in estimating the size of populations, particularly those that are difficult to reach or measure, for which information is available from only one source and dual/multiple system estimation is not applicable.

Keywords: population size estimation, hidden populations, truncated distributuons, count regression models, R.

1. Introduction

Population size estimation is a methodological approach employed across multiple scientific disciplines, serving as a basis for research, policy formulation, and decision-making processes (Böhning, Bunge, and Heijden 2018). In the field of statistics, particularly official statistics, precise population estimates are essential for developing robust economic models, optimizing resource allocation, and informing evidence-based policy formulation (cf. Baffour-Awuah 2009). Social scientists utilize advanced population estimation techniques to investigate *hard-to-reach* populations, such as homeless individuals or illicit drug users, thereby addressing the inherent limitations of conventional census methodologies. These techniques are crucial for obtaining accurate data on populations that are typically under-represented or difficult to access through traditional sampling methods (Vincent and Thompson 2022). In ecology and epidemiology, researchers focus on estimating the size of specific species or disease-affected populations within defined geographical regions, which is vital for conservation efforts, ecosystem management, and public health interventions.

Population size estimation can be approached through various methodologies, each with distinct advantages and limitations. Traditional approaches include full enumeration (e.g. census operations) and comprehensive sample surveys, which, while providing detailed data, are often resource-intensive and may result in delayed estimates, particularly for human populations. Alternative methods leverage existing data sources, such as administrative registers or carefully designed small-scale studies in wildlife research or census coverage surveys (Wolter 1986; Zhang 2019). Application of these sources often comes with statistical methods, known as *capture-recapture* or *multiple system estimation*, that utilizes data from multiple enumerations of the same population (cf. Dunne and Zhang 2024). This can be implemented using a single source with repeated observations, two, or multiple sources.

In this paper we focus methods that utilize a single data source with multiple enumerations of the same units (cf. van der Heijden, Bustami, Cruyff, Engbersen, and van Houwelingen 2003). In human population studies, such data might be derived from police records, health system databases, or border control logs, while for non-human populations, veterinary records or specialized field data serve as analogous sources. These methods are often applied for hard-to-reach or hidden population where standard sampling methods may be inappropriate because of the costs or problems with identification of members of these populations.

While methods for two or more sources are implemented in various open-source software, for instance **Rcapture** (Baillargeon and Rivest 2007), **marked** (Laake, Johnson, Conn, and Isaac 2013) or **VGAM** (Yee, Stoklosa, and Huggins 2015) the single-source capture-recapture (SSCR) methods are less available being only partially implemented in existing R packages. The goal of the paper is to introduce the **singleRcapture** and **singleRcaptureExtra** packages which by implementing *state-of-the-art* methods in SSCR and providing user friendly API which mimics existing R functions (e.g., `glm`) attempt to bridge this aforementioned gap. In the next subsection we describe the available R packages that could be used for estimating population size based on SSCR methods.

1.1. Software for capture-recapture for single and multiple sources

Majority of SSCR methods assume zero-truncated distributions or their extensions (e.g., inclusion of one-inflation). The **countreg** (Zeileis, Kleiber, and Jackman 2008), **VGAM** (Yee 2015) or **distributions3** (Hayes, Moller-Trane, Jordan, Northrop, Lang, and Zeileis 2024) implement some of those truncated distributions and the most general distributions such as Generally Altered, Inflated, Truncated and Deflated (GAITD) can be found in the **VGAM**. However, estimation of parameters of a given truncated (and possibly inflated) distribution is just a first step (similarly as in log-linear models in capture-recapture with two sources) and to best of our knowledge there is no open-source software that allows to estimate population size based on SSCR method, including variance estimator or diagnostics.

Therefore, the goal of the **singleRcapture** is R language is to bridge this gap to provide scientists and other practitioners a tool for estimation of population size based on SSCR methods.

The package implements state-of-the-art methods as recently described by Böhning *et al.* (2018) or Böhning and Friedl (2024) and its extensions (e.g., inclusion of covariates, different treatment of one-inflation) that we will cover in detail in Section 1. The package implements variance estimation based on various methods, allows for implementing custom models as well as diagnostics plots (e.g. rootograms) with parameters estimated using a modified IRLS algorithm implemented by us to for estimation stability. Furthermore, as many R users are familiar with **countreg** or **VGAM** we have implemented a lightweight extension **singleRcaptureExtra**, available through Github (`https://github.com/ncn-foreigners/singleRcaptureExtra`), that allows for integration of **singleRcapture** with those packages.

The remaining part of the paper is as follows. In Section 2 a brief description of the theoretical background is given and information on the fitting methods, the available methods and variance estimation is presented. In Section 3 the main functionalities of the package are introduced. Section 4 provides a case study along with assessment of results, diagnostics and estimation of specific sub-populations. Section 5 covers classes and `S3methods` implemented in the package. Section 6 covers integration with **countreg** and **VGAM** packages through **singleRcaptureExtra** package. The paper ends with conclusions and an appendix that shows how to a implement custom model and how one can use the `estimatePopsizeFit` which is faster than the main function but only estimates regression, which could be of interest to users interested in using any new bootstrap methods not programmed in the package (see Appendix A.1).

2. Theoretical background

2.1. How do we estimate population size with a single register?

Let Y_k represent the number of times k-th unit was observed in a register. Clearly, we only observe $k : Y_k > 0$ and we do not know how many units are missed (i.e. $Y_k = 0$) and to find the population size denoted by N we need to estimate it. In general, we assume that conditional distribution of Y_k given a vector of covariates $\boldsymbol{x}_k$ follows some version of zero-truncated count data distribution (and its extensions). Knowing the parameters of the distribution we may estimate the population size using Horowitz-Thompson type estimator given by:

$$\hat{N} = \sum_{k=1}^{N} \frac{I_k}{\mathbb{P}[Y_k > 0|\boldsymbol{X}_k]} = \sum_{k=1}^{N_{obs}} \frac{1}{\mathbb{P}[Y_k > 0|\boldsymbol{X}_k]}, \tag{1}$$

where $I_k := \mathcal{I}_{\mathbb{N}}(Y_k)$, and maximum likelihood estimate of N is obtained after substituting regression estimates for $\mathbb{P}[Y_k > 0|\boldsymbol{x}_k]$ into (1).

The basic SSCR assumes independence between counts which may be rather naive as the first capture may significantly influence the behaviour of a given unit or limit possibilities of further captures (e.g. due to incarceration). To solve these issues, Godwin and Böhning (2017a) and Godwin and Böhning (2017b) introduced one-inflated distributions that explicitly model probability of the singletons by giving additional mass ω for singletons denoted as $\mathcal{I}_{\{1\}}(y)$ (cf. Böhning and Friedl 2024)

$$\mathbb{P}^*[Y = y|Y > 0] = \omega\mathcal{I}_{\{1\}}(y) + (1 - \omega)\mathbb{P}[Y = y|Y > 0].$$

The analytic variance estimation is then done by computing two parts of the decomposition due to the law of total variance given by:

$$\mathrm{var}[\hat{N}] = \mathbb{E}\left[\mathrm{var}\left[\hat{N}|I_1,\ldots,I_n\right]\right] + \mathrm{var}\left[\mathbb{E}[\hat{N}|I_1,\ldots,I_n]\right], \tag{2}$$

where the first part can be estimated using the multivariate δ method given by:

$$\mathbb{E}\left[\mathrm{var}\left[\hat{N}|I_1,\ldots,I_n\right]\right] = \left(\frac{\partial(N|I_1,\ldots,I_N)}{\partial\boldsymbol{\beta}}\right)^\top \mathrm{cov}\left[\hat{\boldsymbol{\beta}}\right]\left(\frac{\partial(N|I_1,\ldots,I_N)}{\partial\boldsymbol{\beta}}\right)\Bigg|_{\boldsymbol{\beta}=\hat{\boldsymbol{\beta}}},$$

while the second part of the decomposition in (2) is under the assumption of independence of I_k's and after some omitted simplifications one sees that this is optimally estimated by:

$$\mathrm{var}\left(\mathbb{E}(\hat{N}|I_1,\ldots,I_n)\right) = \mathrm{var}\left(\sum_{k=1}^{N}\frac{I_k}{\mathbb{P}(Y_k>0)}\right) \approx \sum_{k=1}^{N_{obs}}\frac{1-\mathbb{P}(Y_k>0)}{\mathbb{P}(Y_k>0)^2},$$

which forms the basis for the interval estimation. Confidence intervals are usually constructed under the assumption of (asymptotic) normality of $\hat{N}$ or asymptotic normality of $\ln(\hat{N}-N)$ (or log normality of $\hat{N}$). The latter of which is an attempt to address a common criticism of student type confidence intervals in SSCR, that is a possibly skewed distribution of $\hat{N}$, and results in the $1-\alpha$ confidence interval given by:

$$\left(N_{obs}+\frac{\hat{N}-N_{obs}}{\xi}, N_{obs}+\left(\hat{N}-N_{obs}\right)\xi\right),$$

where:

$$\xi = \exp\left(z\left(1-\frac{\alpha}{2}\right)\sqrt{\ln\left(1+\frac{\widehat{\mathrm{Var}}(\hat{N})}{\left(\hat{N}-N_{obs}\right)^2}\right)}\right).$$

and where z is the quatile function of the standard normal distribution. The estimator $\hat{N}$ is best interpreted as being an estimator for the total number of observable units in the population since we have no means of estimating the number of units in the population for which the probability of being included in the data is 0 (cf. van der Heijden *et al.* 2003).

2.2. Available models

The full list of implemented models in **singleRcapture** along with the expressions for probability density functions and point estimates can be found in the collective help file for all family functions:

```
R> ?ztpoisson
```

For the sake of simplicity we limit ourselves to just listing the family functions:

- Generalized Chao's (Chao 1987) and Zelterman's (Zelterman 1988) estimators via logistic regression on variable Z defined as $Z = 1$ if $Y = 2$ and $Z = 0$ if $Y = 1$ with $Z \sim b(p)$ where $b(\cdot)$ is the Bernoulli distribution and p can be modeled for each unit k by $\text{logit}(p_k) = \ln(\lambda_k/2)$ with Poisson parameter $\lambda_k = \boldsymbol{x}_k\boldsymbol{\beta}$ (for covariate extension see Böhning, Vidal-Diez, Lerdsuwansri, Viwatwongkasem, and Arnold (2013) and Böhning and van der Heijden (2009)):

$$\hat{N} = N_{obs} + \sum_{k=1}^{\boldsymbol{f}_1+\boldsymbol{f}_2} \left(2\exp\left(\boldsymbol{x}_k\hat{\boldsymbol{\beta}}\right) + 2\exp\left(2\boldsymbol{x}_k\hat{\boldsymbol{\beta}}\right)\right)^{-1}, \qquad \text{(Chao's estimator)}$$

$$\hat{N} = \sum_{k=1}^{N_{obs}} \left(1 - \exp\left(-2\exp\left(\boldsymbol{x}_k\hat{\boldsymbol{\beta}}\right)\right)\right)^{-1}. \qquad \text{(Zelterman's estimator)}$$

- Zero-truncated (`zt`*) and zero-one-truncated (`zot`*) Poisson (cf. Böhning and van der Heijden 2019), geometric, NB type II (NB2) regression where the non-truncated distribution is parameterized as:

$$\mathbb{P}[Y = y|\lambda, \alpha] = \frac{\Gamma\left(y + \alpha^{-1}\right)}{\Gamma\left(\alpha^{-1}\right) y!} \left(\frac{\alpha^{-1}}{\alpha^{-1} + \lambda}\right)^{\alpha^{-1}} \left(\frac{\lambda}{\lambda + \alpha^{-1}}\right)^{y}.$$

- Zero-truncated one-inflated (`ztoi`*) modifications distributions where the new probability $\mathbb{P}^*$ measure is defined in terms of count data measure $\mathbb{P}$ with support on $\mathbb{N} \cup \{0\}$ as:

$$\mathbb{P}^*[Y = y] = \begin{cases} \mathbb{P}[Y = 0] & y = 0, \\ \omega\left(1 - \mathbb{P}[Y = 0]\right) + (1 - \omega)\mathbb{P}[Y = 1] & y = 1, \\ (1 - \omega)\mathbb{P}[Y = y] & y > 1, \end{cases}$$
$$\mathbb{P}^*[Y = y|Y > 0] = \omega\mathcal{I}_{\{1\}}(y) + (1 - \omega)\mathbb{P}[Y = y|Y > 0].$$

- One-inflated zero-truncated (`oizt`*) modifications distributions where the new probability $\mathbb{P}^*$ measure is defined as:

$$\mathbb{P}^*[Y = y] = \omega\mathcal{I}_{\{1\}}(y) + (1 - \omega)\mathbb{P}[Y = y],$$

$$\mathbb{P}^*[Y = y|Y > 0] = \omega\frac{\mathcal{I}_{\{1\}}(y)}{1 - (1 - \omega)\mathbb{P}[Y = 0]} + (1 - \omega)\frac{\mathbb{P}[Y = y]}{1 - (1 - \omega)\mathbb{P}[Y = 0]}.$$

  Note that `ztoi`* and `oizt`* distributions are equivalent as shown by Böhning (2023) but population size estimators are different.

In addition, we have provided two new approaches that allow modelling singletons in a similar was as in Hurdle models. In particular we have proposed the following:

- Zero-truncated Hurdle model (`ztHurdle`*) for Poisson, geometric and NB2 is defined as:

$$\mathbb{P}^*[Y = y] = \begin{cases} \frac{\mathbb{P}[Y=0]}{1-\mathbb{P}[Y=1]} & y = 0, \\ \pi(1 - \mathbb{P}[Y = 1]) & y = 1, \\ (1 - \pi)\frac{\mathbb{P}[Y=y]}{1-\mathbb{P}[Y=1]} & y > 1, \end{cases}$$

$$\mathbb{P}^*[Y = y|Y > 0] = \pi\mathcal{I}_{\{1\}}(y) + (1 - \pi)\mathcal{I}_{\mathbb{N}\setminus\{1\}}(y)\frac{\mathbb{P}[Y = y]}{1 - \mathbb{P}[Y = 0] - \mathbb{P}[Y = 1]}.$$

- The Hurdle zero-truncated (`Hurdlezt`*) for Poisson, geometric and NB2 is defined as:

$$\mathbb{P}^*[Y=y]=\begin{cases}\pi & y=1,\\ (1-\pi)\frac{\mathbb{P}[Y=y]}{1-\mathbb{P}[Y=1]} & y\neq 1,\end{cases}$$

$$\mathbb{P}^*[Y=y|Y>0]=\begin{cases}\pi\frac{1-\mathbb{P}[Y=1]}{1-\mathbb{P}[Y=0]-\mathbb{P}[Y=1]} & y=1,\\ (1-\pi)\frac{\mathbb{P}[Y=y]}{1-\mathbb{P}[Y=0]-\mathbb{P}[Y=1]} & y>1.\end{cases}$$

The approaches presented above differ in terms of assumptions, computational complexity, or how they treat heterogeneity of captures and singletons. For instance, the dispersion parameter α in the NB2 type models is often interpreted as measuring the *severeness* of unobserved heterogeneity in the underlying poisson process (cf. Cruyff and van der Heijden 2008). When using any truncated NB model the hope is that due to the class of models considered the consistency is not lost despite the lack of information.

While not discussed in the literature yet the interpretation of heterogeneous α across the population (specified in `controlModel`) would be that the unobserved heterogeneity affects the accuracy of the prediction for the dependent variable Y more severely than others. The geometric model (NB with $\alpha=1$) is singled out in the package and often considered in the literature due to inherent computational issues with NB models which are exasperated by the fact that data in SSCR is usually of somewhat low quality. Sparseness of the data is in particular a common issue in SSCR and a big issue for all numerical methods for fitting the (zero-truncated) NB model.

The extra mass ω in the one-inflated models is an important extension to the researcher's toolbox for SSCR models. Since the inflation at $y=1$ is likely to occur in many types of applications. For example in estimating the number active people who committed criminal acts in a given time period being observed naturally induces a risk of no longer being able to be observed for all units with possibility of arrest. One constraint present in modelling via inflated models is that trying to include both the possibility of one inflation and one deflation leads to both numerical and theoretical problems since the parameter space (of (ω,λ) or (ω,λ,α)) is then a much more complicated set.

Hurdle models are another approach to modelling the one-inflation, they can also model deflation as well as both inflation and deflation simultaneously so they are more flexible and it seems that the Hurdle zero-truncated models are more numerically stable.

Although interpretation of regression parameters tends to be somewhat overlooked in the SSCR studies we should point out that interpretation of the ω inflation parameter (in `ztoi`* or `oizt`*) is more convenient that the interpretation of the π probability parameter (in Hurdle models). Additionally the interpretation of the λ parameter in (one) inflated models conforms to the intuition that given that unit k comes from the non-inflated part of the population then it follows a poisson distribution (respectively geometric or negative binomial) with the λ parameter (or λ,α), in hurdle models one loses that interpretation. It is somewhat interesting is that the estimates from Hurdle zero-truncated and one-inflated zero-truncated models are "usually" quite close to one another, this however require more studies.

2.3. Fitting method

As previously noted the **singleRcapture** package supports modelling (linear) dependence on covariates of all parameters. To that end a modified IRLS algorithm is employed, full details are available in Yee (2015). In order to employ the algorithm a modified model matrix is created $\boldsymbol{X}_{\text{vlm}}$ at call to `estimatePopsize`. In the context of the models implemented in **singleRcapture** this matrix can be written as:

$$\boldsymbol{X}_{vlm} = \begin{pmatrix} \boldsymbol{X}_1 & \boldsymbol{0} & \dots & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{X}_2 & \dots & \boldsymbol{0} \\ \vdots & \vdots & \ddots & \vdots \\ \boldsymbol{0} & \boldsymbol{0} & \dots & \boldsymbol{X}_p \end{pmatrix} \tag{3}$$

where each $\boldsymbol{X}_i$ corresponds to a model matrix associated with user specified formula.

In the context of multi-parameter families we have a matrix of linear predictors $\boldsymbol{\eta}$ instead of a vector, with the number of columns matching the number of parameters in the distribution. “Weights” are then modified to be information matrices $\mathbb{E}\left[-\frac{\partial^2 \ell}{\partial \boldsymbol{\eta}_{(k)}^{\top} \partial \boldsymbol{\eta}_{(k)}}\right]$ where $\boldsymbol{\eta}_{(k)}$ is the k’th row of $\boldsymbol{\eta}$, while in the usual IRLS they are scalars $\mathbb{E}\left[-\frac{\partial^2 \ell}{\partial \eta_k^2}\right]$ which is often just $-\frac{\partial^2 \ell}{\partial \eta^2}$.

Algorithm 1: A modified IRLS algorithm used in the **singleRcapture** package

```
1 Initialize with iter← 1, $\boldsymbol{\eta}$ ←start , $\boldsymbol{W} \leftarrow I, \ell \leftarrow \ell(\boldsymbol{\beta})$.
2 Store values from the previous step: $\ell_{-} \leftarrow \ell, \boldsymbol{W}_{-} \leftarrow \boldsymbol{W}, \boldsymbol{\beta}_{-} \leftarrow \boldsymbol{\beta}$ (the last assignment is omitted
    during the first iteration), and assign values in current iteration
    $\boldsymbol{\eta} \leftarrow \boldsymbol{X}_{\text{vlm}}\boldsymbol{\beta} + \boldsymbol{o}, \boldsymbol{W}_{(k)} \leftarrow \mathbb{E}\left[-\frac{\partial^2 \ell}{\partial \boldsymbol{\eta}_{(k)}^{\top} \partial \boldsymbol{\eta}_{(k)}}\right], Z \leftarrow \boldsymbol{\eta}_{(k)} + \frac{\partial \ell}{\partial \boldsymbol{\eta}_{(k)}} \boldsymbol{W}_{(k)}^{-1} - \boldsymbol{o}_{(k)}$.
3 Assign current coefficient value: $\boldsymbol{\beta} \leftarrow (\boldsymbol{X}_{\text{vlm}} \boldsymbol{W} \boldsymbol{X}_{\text{vlm}})^{-1} \boldsymbol{X}_{\text{vlm}} \boldsymbol{W} \boldsymbol{Z}$.
4 If $\ell(\boldsymbol{\beta}) < \ell(\boldsymbol{\beta}_{-})$ try selecting the smallest value $h$ such that for $\boldsymbol{\beta}_h \leftarrow 2^{-h}\left(\boldsymbol{\beta} + \boldsymbol{\beta}_{-}\right)$ the
    inequality $\ell(\boldsymbol{\beta}_h) > \ell(\boldsymbol{\beta}_{-})$ holds if this is successful $\boldsymbol{\beta} \leftarrow \boldsymbol{\beta}_h$ else stop the algorithm.
5 If convergence is achieved or iter is higher than maxiter end algorithm, else iter← 1+iter
    and return to step 2.
```

2.4. Bootstrap variance estimators

We have implemented three types of bootstrap algorithms: parametric, semi-parametric and nonparametric with the nonparametric being bootstrap being the usual bootstrap algorithm which as argued in Norris and Pollock (1996) and Zwane and Van der Heijden (2003).

The idea of semi-parametric bootstrap is to modify the usual bootstrap to include the additional uncertainty due to the sample size being a random variable. This type of bootstrap can be in short described as in the Algorithm 2.

Algorithm 2: Semi-parametric bootstrap

```
1 Draw the sample size $N'_{obs} \sim \text{Be}\left(N', \frac{N_{obs}}{N'}\right)$, where $N' = \lfloor \hat{N} \rfloor + b\left(\lfloor \hat{N} \rfloor - \hat{N}\right)$.
2 Draw $N'_{obs}$ units from the data uniformly without replacement.
3 Obtain new population size estimate $N_b$ using bootstrap data.
4 Repeat $1 - 3$ $B$ times.
```

In other words, we first draw the sample size and then the sample conditional on the sample size. Note that in using semi-parametric bootstrap one implicitly assumes that the population size estimate $\hat{N}$ is accurate. The last implemented bootstrap type is the parametric algorithm which in short first draws the finite population of size $\approx \hat{N}$ from the superpopulation model and then samples from this population according to the selected model as described in Algorithm 3.

Algorithm 3: Parametric bootstrap

```
1 Draw the number of covariates equal to $\lfloor\hat{N}\rfloor + b\left(\lfloor\hat{N}\rfloor - \hat{N}\right)$ proportional to the estimated
   contribution $(\mathbb{P}\left[Y_k > 0|\boldsymbol{x}_k\right])^{-1}$ with replacement.
2 Using the fitted model and regression coefficients $\hat{\boldsymbol{\beta}}$ draw for each covariate the $Y$ value from the
   corresponding probability measure on $\mathbb{N}\cup\{0\}$.
3 Truncate units with drawn $Y$ value equal to 0.
4 Obtain population size estimate $N_b$ based on the truncated data.
5 Repeat $1-3$ $B$ times.
```

Note that for this type of algorithm to result in consistent standard error estimates it is imperative that the estimated model for the entire superpopulation probability space is consistent which may be much less realistic than semi-parametric bootstrap. The parametric bootstrap algorithm is the default in **singleRcapture**.

3. The main function

3.1. The `estimatePopsize` function

The main function that **singleRcapture** is built around is `estimatePopsize`. The leading design principle was to make using `estimatePopsize` as close to standard `stats::glm()` as possible or packages for fitting zero-truncated regression models as **countreg** (e.g. `countreg::ztpoisson()` function). This function is used to first fit an appropriate (vector) generalized linear model and then estimates the population size along with its variance. It is assumed that the response vector (i.e. the dependent variable) corresponds to the number of times a given unit was observed in the source. The most important arguments are given in Table 1 with the `formula, data, model` being the three arguments which must be provided in the `estimatePopsize` syntax.

The most important part of the `estimatePopsize` is to specify the `model` parameter. This is a crucial part as it allows to select appropriate model to estimate the *unobserved* part of the population. For instance, to fit Chao's or Zelterman's model one should select `chao` or `zelterman` and if a researcher assumes that the one-inflation is present may select one of the zero-truncated one-inflated (`ztoi`*) or one-inflated zero-truncated (`oizt`*) such as `oiztpoisson` for Poisson or `ztoinegbin` for NB2.

If researcher assumes that heterogeneity is observed for NB2 models one may specify formula in the `controlModel` argument with the `controlModel` function and the `alphaFormula` argument. This allows to provide a formula for dispersion parameter in the NB2 models. If heterogeneity is assumed for `ztoi`* or `oizt`* one may specify the `omegaFormula` argument which corresponds to ω parameter in these models. Finally, if covariates are assumed for the hurdle models (ztHurdle* or Hurdlezt*) then piFormula can be specified as it provides a formula for probability parameter in these models.

Argument	Description
formula	The main formula (i.e for the Poisson λ parameter)
data	the data.frame (or data.frame coercible) object
model	either a function a string or a family class object specifying which model should be used possible values are listed in documentation. The supplied argument should have the form model = "ztpoisson", model = ztpoisson or if link function should be specified then model = ztpoisson(lambdaLink = "log") can be used
method	numerical method used to fit regression IRLS or optim
popVar	a method for estimating variance of $\hat{N}$ and confidence interval creation (either bootstrap, analytic or skipping the estimation entirely)
controlMethod, controlModel or controlPopVar	control parameters for numerical fitting, specifying additional formulas (inflation, dispersion) and population size estimation respectively
offset	a matrix of offset values with number of columns matching the number of distribution parameters providing offset values to each of linear predictors
...	additional optional arguments passed to other methods eg. estimatePopsizeFit

Table 1: estimatePopsize() arguments description

3.2. Controlling the variance estimation with the controlPopVar

The estimatePopsize function allows to specify the variance estimation method via the popVar (e.g. analytic or variance bootstrap) as well as controlling the estimation process by specifying controlPopVar. In the control function controlPopVar user may specify the bootType argument which has three possible values "parametric", "semi-parametric" and "nonparametric". Additional arguments accepted by the contorlPopVar function which are relevant to bootstrap are:

- alpha, B – significance level and number of bootstrap samples to be performed respectively with 0.05 and 500 being the default options.
- cores – number of process cores to use in bootstrap (1 by default) parallel computing is done via **doParallel** (Microsoft and Weston 2022a), **foreach** (Microsoft and Weston 2022b) or **parallel** packages (R Core Team 2023).
- keepbootStat – logical value indicating whether to keep a vector of statistics produced by bootstrap.
- traceBootstrapSize, bootstrapVisualTrace – logical values indicating whether sample and population size should be tracked (FALSE by default) these work only when cores = 1.

- `fittingMethod`, `bootstrapFitcontrol` – fitting method (by default the same as used in the original call) and control parameters (`controlMethod`) for model fitting in bootstrap.

In addition, user may specify the type of confidence interval using `confType` and the type of covariance matrix by `covType` for analytical variance estimator (observed or Fisher information matrix).

In the next sections we provide a case study on the usage of a simple zero-truncated Poisson regression and a more advanced model: one-inflated zero-truncated geometric regression with `cloglog` link function. First, we describe example dataset, then we present how to estimate the population size and assess the quality and diagnostics measures. Finally, we show how to estimate population size in a user-specified sub-populations.

4. Data analysis example

The package can be installed in a standard way using:

```
R> install.packages("singleRcapture")
```

Then, we need to load the package using the following code

```
R> library(singleRcapture)
```

4.1. Dataset

We will use dataset from van der Heijden *et al.* (2003) that contains information about immigrants in four cities (Amsterdam, Rotterdam, The Hague and Utrecht) in Netherlands that have been staying in the country without a legal permit in 1995 and have appeared in police records that year. This dataset is included in the package under the name `netherlandsimmigrant`:

```
R> data(netherlandsimmigrant)
R> head(netherlandsimmigrant)
```

```
  capture gender    age       reason       nation
1       1   male <40yrs Other reason North Africa
2       1   male <40yrs Other reason North Africa
3       1   male <40yrs Other reason North Africa
4       1   male <40yrs Other reason         Asia
5       1   male <40yrs Other reason         Asia
6       2   male <40yrs Other reason North Africa
```

The number of times each individual appeared in the records is included in the `capture` variable with the available covariates being `gender, age, reason, nation` being respectively the persons gender and age, reason for being captured and region of the world from which each person comes:

```
R> summary(netherlandsimmigrant)

    capture          gender         age                reason
 Min.   :1.000   female: 398   <40yrs:1769   Illegal stay: 259
 1st Qu.:1.000   male  :1482   >40yrs: 111   Other reason:1621
 Median :1.000
 Mean   :1.162
 3rd Qu.:1.000
 Max.   :6.000
                      nation
 American and Australia: 173
 Asia                  : 284
 North Africa          :1023
 Rest of Africa        : 243
 Surinam               :  64
 Turkey                :  93
```

One point which we should make while analysing this data set is that there is a disproportionate number of individuals who were observed only once (i.e. 1645).

```
R> table(netherlandsimmigrant$capture)


   1    2    3    4    5    6
1645  183   37   13    1    1
```

The basic syntax is vary similar to that of `glm` with the output of the summary method being also quite similar except for the additional results of the population size estimates (denoted as `Population size estimation results`).

```
R> basicModel <- estimatePopsize(
+   formula = capture ~ gender + age + nation,
+   model   = ztpoisson(),
+   data    = netherlandsimmigrant
+ )

Warning in singleRcaptureinternalIRLSmultipar(dependent = y, covariates = X, :
Convergence at halfstepsize

R> summary(basicModel)


Call:
estimatePopsize.default(formula = capture ~ gender + age + nation,
    data = netherlandsimmigrant, model = ztpoisson())
```

```
Pearson Residuals:
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
-0.486442 -0.486442 -0.298080  0.002093 -0.209444 13.910844

Coefficients:
-----------------------
For linear predictors associated with: lambda
                     Estimate Std. Error z value  P(>|z|)
(Intercept)           -1.3411     0.2149  -6.241 4.35e-10 ***
gendermale             0.3972     0.1630   2.436 0.014832 *
age>40yrs             -0.9746     0.4082  -2.387 0.016972 *
nationAsia            -1.0926     0.3016  -3.622 0.000292 ***
nationNorth Africa     0.1900     0.1940   0.979 0.327398
nationRest of Africa  -0.9106     0.3008  -3.027 0.002468 **
nationSurinam         -2.3364     1.0136  -2.305 0.021159 *
nationTurkey          -1.6754     0.6028  -2.779 0.005445 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

AIC: 1712.901
BIC: 1757.213
Residual deviance: 1128.553

Log-likelihood: -848.4504 on 1872 Degrees of freedom
Number of iterations: 8
-----------------------
Population size estimation results:
Point estimate 12690.35
Observed proportion: 14.8% (N obs = 1880)
Std. Error 2808.165
95% CI for the population size:
          lowerBound upperBound
normal      7186.449   18194.25
logNormal   8431.277   19718.31
95% CI for the share of observed population:
          lowerBound upperBound
normal     10.332933   26.16035
logNormal   9.534288   22.29793
```

The output on the population size contains information on the point estimate, observed proportion (based on the input dataset), standard error and two confidence intervals: one with reference to the point estimated, the second to the observed proportion.

According to this simple model the population size is about 12.5k with about 15% of units observed in the register. The 95% CI under normality indicate that the true population size may be between 7k-18k with about 10% to 26% observed in the register.

Since there is a reasonable suspicion that the act of observing a unit in the dataset may led to undesirable consequences from the point of view of the subject of the observation (here possible deportation, detainment or similar). For those reason researcher may consider one-inflated models such as `oiztgeom` and presented below.

```
R> set.seed(123456)
R> modelInflated <- estimatePopsize(
+     formula = capture ~ nation,
+     model   = oiztgeom(omegaLink = "cloglog"),
+     data    = netherlandsimmigrant,
+     controlModel = controlModel(
+         omegaFormula = ~ gender + age
+     ),
+     popVar = "bootstrap",
+     controlPopVar = controlPopVar(bootType = "semiparametric")
+ )
R> summary(modelInflated)
```

```
Call:
estimatePopsize.default(formula = capture ~ nation, data = netherlandsimmigrant,
    model = oiztgeom(omegaLink = "cloglog"), popVar = "bootstrap",
    controlModel = controlModel(omegaFormula = ~gender + age),
    controlPopVar = controlPopVar(bootType = "semiparametric"))

Pearson Residuals:
    Min.  1st Qu.   Median     Mean  3rd Qu.     Max.
-0.41643 -0.41643 -0.30127  0.00314 -0.18323 13.88376

Coefficients:
-----------------------
For linear predictors associated with: lambda
                     Estimate Std. Error z value  P(>|z|)
(Intercept)           -1.2552     0.2149  -5.840 5.22e-09 ***
nationAsia            -0.8193     0.2544  -3.220  0.00128 **
nationNorth Africa     0.2057     0.1838   1.119  0.26309
nationRest of Africa  -0.6692     0.2548  -2.627  0.00862 **
nationSurinam         -1.5205     0.6271  -2.425  0.01532 *
nationTurkey          -1.1888     0.4343  -2.737  0.00619 **
-----------------------
For linear predictors associated with: omega
            Estimate Std. Error z value  P(>|z|)
(Intercept)  -1.4577     0.3884  -3.753 0.000175 ***
gendermale   -0.8738     0.3602  -2.426 0.015267 *
age>40yrs     1.1745     0.5423   2.166 0.030326 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
AIC: 1677.125
BIC: 1726.976
Residual deviance: 941.5416

Log-likelihood: -829.5625 on 3751 Degrees of freedom
Number of iterations: 10
-----------------------
Population size estimation results:
Point estimate 6699.953
Observed proportion: 28.1% (N obs = 1880)
Boostrap sample skewness: 1.621389
0 skewness is expected for normally distributed variable
---
Bootstrap Std. Error 1719.353
95% CI for the population size:
lowerBound upperBound
  5001.409  11415.969
95% CI for the share of observed population:
lowerBound upperBound
  16.46816   37.58941
```

This approach suggest that the population size is about 7k which is about 5k less than the naive Poisson approach. Comparison of AIC and BIC suggest that the one-inflation model fits the data better with BIC for `oiztgeom` 1727 and 1757 for `ztpoisson`.

We can access the results of population size estimation using the following code which returns list with numerical results.

```
R> basicModel$populationSize

Point estimate: 12690.35
Variance: 7885790
95% confidence intervals:
          lowerBound upperBound
normal      7186.449   18194.25
logNormal   8431.277   19718.31

R> modelInflated$populationSize

Point estimate: 6699.953
Variance: 2956175
95% confidence intervals:
lowerBound upperBound
  5001.409  11415.969
```

Decision whether to use zero-truncated Poisson or one-inflated zero-truncated geometric should be on the assessment of the model and the assumptions on the data generation process.

In the next sections we provide details how to assess the results using statistical tests and diagnostics.

4.2. Testing marginal frequencies

A popular method of testing the model fit in single source capture-recapture studies is comparing the fitted marginal frequencies $\sum_{j=1}^{N_{obs}} \hat{\mathbb{P}}\left[Y_j = k|\boldsymbol{x}_j, Y_j > 0\right]$ with the observed marginal frequencies $\sum_{j=1}^{N} \mathcal{I}_{\{k\}}(Y_k) = \sum_{j=1}^{N_{obs}} \mathcal{I}_{\{k\}}(Y_k)$ for $k \geq 1$. If a fitted model bears sufficient resemblance to the real data collection process these quantities should be quite close and both G and χ^2 tests may be employed in order to test the statistical significance of the discrepancy with the following **singleRcapture** syntax for the Poisson model (rather poor fit):

```
R> margFreq <- marginalFreq(basicModel)
R> summary(margFreq, df = 1, dropl5 = "group")

Test for Goodness of fit of a regression model:

                 Test statistics df P(>X^2)
Chi-squared test           50.06  1 1.5e-12
G-test                     34.31  1 4.7e-09

--------------------------------------------------------------
Cells with fitted frequencies of < 5 have been grouped
Names of cells used in calculating test(s) statistic: 1 2 3
```

and for the one-inflated model (better fit):

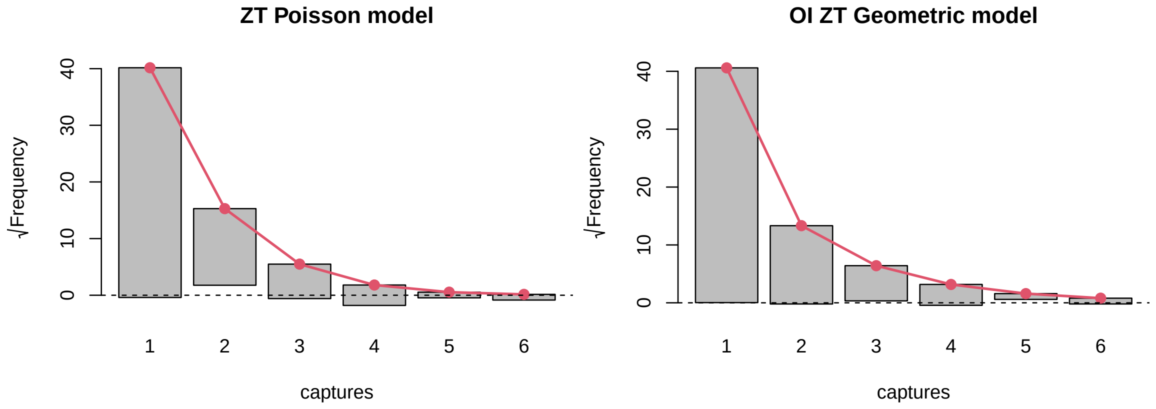
```
R> margFreq_inf <- marginalFreq(modelInflated)
R> summary(margFreq_inf, df = 1, dropl5 = "group")

Test for Goodness of fit of a regression model:

                 Test statistics df P(>X^2)
Chi-squared test            1.88  1    0.17
G-test                      2.32  1    0.13

--------------------------------------------------------------
Cells with fitted frequencies of < 5 have been grouped
Names of cells used in calculating test(s) statistic: 1 2 3 4
```

where the `dropl5` argument is used to indicate how to handle the cells with less than 5 fitted observations, note however that currently there is no continuity correction.

4.3. Diagnostics

The `singleRStaticCountData` class has a `plot` method implementing several types of quick demonstrative plots such as the rootogram (cf. Kleiber and Zeileis 2016) for comparing the fitted and marginal frequencies which we can get with the syntax:

```
R> plot(    basicModel, plotType = "rootogram", main = "ZT Poisson model")
R> plot(modelInflated, plotType = "rootogram", main = "OI ZT Geometric model")
```



Plots suggest that the `otztgeom` model fits the data better. Furthermore, important issue in population size estimation is the diagnostics of the models in order to verify whether influential observations are present in the data. For this purpose leave-one-out (LOO) diagnostic implemented in the `dfbeta` from the **stats** package was adapted and demonstrated below:

```
R> dfb <- dfbeta(basicModel)
R> round(t(apply(dfb, 2, quantile)*100), 4)

                          0%     25%     50%    75%    100%
(Intercept)          -0.9909 -0.1533  0.0191 0.0521  8.6619
gendermale           -9.0535 -0.0777 -0.0283 0.1017  2.2135
age>40yrs            -2.0010  0.0179  0.0379 0.0691 16.0061
nationAsia           -9.5559 -0.0529  0.0066 0.0120 17.9914
nationNorth Africa   -9.6605 -0.0842 -0.0177 0.0087  3.1260
nationRest of Africa -9.4497 -0.0244  0.0030 0.0083 10.9787
nationSurinam        -9.3138 -0.0065  0.0021 0.0037 99.3383
nationTurkey         -9.6198 -0.0220  0.0079 0.0143 32.0980
```

```
R> dfi <- dfbeta(modelInflated)
R> round(t(apply(dfi, 2, quantile)*100), 4)

                           0%     25%     50%     75%    100%
(Intercept)           -1.4640  0.0050  0.0184  0.0557  9.0600
nationAsia            -6.6331 -0.0346  0.0157  0.0347 12.2406
nationNorth Africa    -7.2770 -0.0768 -0.0170  0.0085  1.9415
nationRest of Africa  -6.6568 -0.0230  0.0081  0.0262  7.1710
nationSurinam         -6.2308 -0.0124  0.0162  0.0421 62.2045
```

```
nationTurkey          -6.4795 -0.0273  0.0204  0.0462 21.1338
(Intercept):omega     -6.8668 -0.0193  0.0476  0.0476  9.3389
gendermale:omega      -2.2733 -0.2227  0.1313  0.2482 11.1234
age>40yrs:omega      -30.2130 -0.2247 -0.1312 -0.0663  2.0393
```

Furthermore, result of the `dfbeta` can be further used in the function `dfpopsize` which allows for quantification of LOO on the population size.

```
R> dfb_pop <- dfpopsize(basicModel, dfbeta = dfb)
R> dfi_pop <- dfpopsize(modelInflated, dfbeta = dfi)
```

```
Warning in dfpopsize.singleRStaticCountData(modelInflated, dfbeta = dfi):
dfpopsize may (in some cases) not work correctly when bootstrap was chosen as
population variance estimate.
```

```
R> summary(dfb_pop)
```

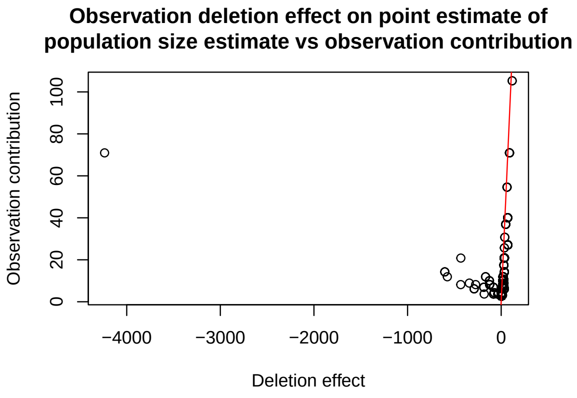
```
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
-4236.407     2.660     2.660     5.445    17.281   117.445
```

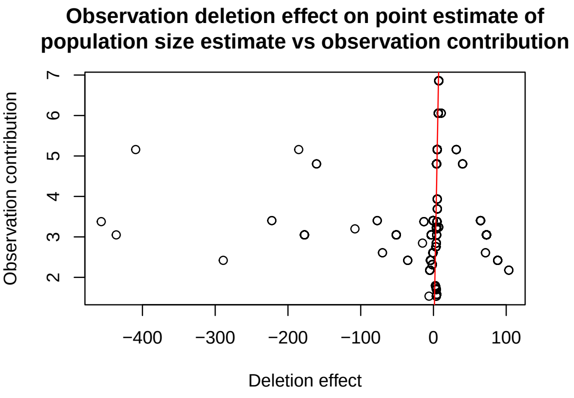
```
R> summary(dfi_pop)
```

```
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
-456.6443   -3.1121   -0.7243    3.4333    5.1535  103.5949
```

The comparison of deletion effect on population size estimate and inverse probability weights, which refer to the contribution of a given observation to the population size estimation, is presented in the Figure bellow:

```
R> plot(basicModel, plotType = "dfpopContr", dfpop = dfb_pop)
R> plot(modelInflated, plotType = "dfpopContr", dfpop = dfi_pop)
```





These plot informs on the change of the population size if a given observation will be removed. For instance if we remove observation 542 from the data then population size will rise by about

4236 for the `ztpoisson` model. While for the `oiztgeom` the largest change is 457 for the 900 observation.

The full list of plot types along with the list of optional arguments which may be passed from the call to the `plot` method down to base R and **graphics** functions is listed in the help file of the `plot` method.

```
R> ?plot.singleRStaticCountData
```

4.4. The `stratifyPopsize` function

Researchers may be interested on only in the total population size but also in specific sub-populations (e.g. males, females, group pages). For that reason we have created the `stratifyPopsize` function which allows to estimate the size by stratas defined by the coefficients in the model (the default option). In the output below we present results based on the `ztpoisson` and `oiztgeom` models.

```
R> popSizeStratas <- stratifyPopsize(basicModel)
R> cols <- c("name", "Observed", "Estimated", "logNormalLowerBound",
+           "logNormalUpperBound")
R> popSizeStratas_report <- popSizeStratas[, cols]
R> cols_custom <- c("Name", "Obs", "Estimated", "LowerBound", "UpperBound")
R> names(popSizeStratas_report) <- cols_custom
R> popSizeStratas_report

                             Name  Obs  Estimated LowerBound UpperBound
1                  gender==female  398  3811.0911  2189.0443   6902.133
2                    gender==male 1482  8879.2594  6090.7762  13354.880
3                     age==<40yrs 1769 10506.8971  7359.4155  15426.455
4                     age==>40yrs  111  2183.4535   872.0130   5754.876
5  nation==American and Australia  173   708.3688   504.6086   1037.331
6                    nation==Asia  284  2742.3147  1755.2548   4391.590
7            nation==North Africa 1023  3055.2033  2697.4900   3489.333
8          nation==Rest of Africa  243  2058.1533  1318.7466   3305.786
9                 nation==Surinam   64  2386.4513   505.2457  12287.983
10                 nation==Turkey   93  1739.8592   638.0497   5068.959

R> popSizeStratas_inflated <- stratifyPopsize(modelInflated)
R> popSizeStratas_inflated_report <- popSizeStratas_inflated[, cols]
R> names(popSizeStratas_inflated_report) <- cols_custom
R> popSizeStratas_inflated_report

                             Name  Obs Estimated LowerBound UpperBound
1  nation==American and Australia  173  516.2432   370.8463   768.4919
2                    nation==Asia  284 1323.5377   831.1601  2258.9954
3            nation==North Africa 1023 2975.8801  2254.7071  4119.3050
4          nation==Rest of Africa  243 1033.9753   667.6106  1716.4484
```

```
5                nation==Surinam   64  354.2236   193.8891   712.4739
6                 nation==Turkey   93  496.0934   283.1444   947.5309
7                 gender==female  398 1109.7768   778.7197  1728.7066
8                   gender==male 1482 5590.1764  3838.4550  8644.0776
9                    age==<40yrs 1769 6437.8154  4462.3472  9862.2147
10                   age==>40yrs  111  262.1379   170.9490   492.0347
```

The function `stratifyPopsize`, that is prepared for the objects of the `singleRStaticCountData` class, accepts three optional parameters `stratas, alpha, cov` which correspond to specification of sub-populations, the significance levels and the covariance matrix that will be used to compute standard errors. An example of the full call is presented below.

```
R> library(sandwich)
R> popSizeStratasCustom <- stratifyPopsize(
+   object  = basicModel,
+   stratas = ~ gender + age,
+   alpha   = rep(c(0.1, 0.05), each=2),
+   cov     = vcovHC(basicModel, type = "HC4")
+ )
R>
R> popSizeStratasCustom_report <- popSizeStratasCustom[, c(cols, "confLevel")]
R> names(popSizeStratasCustom_report) <- c(cols_custom, "alpha")
R> popSizeStratasCustom_report
```

```
            Name  Obs Estimated LowerBound UpperBound alpha
1 gender==female  398  3811.091  2275.6416   6602.161  0.10
2   gender==male 1482  8879.259  6261.5125  12930.751  0.10
3    age==<40yrs 1769 10506.897  7297.2081  15580.138  0.05
4    age==>40yrs  111  2183.453   787.0676   6464.009  0.05
```

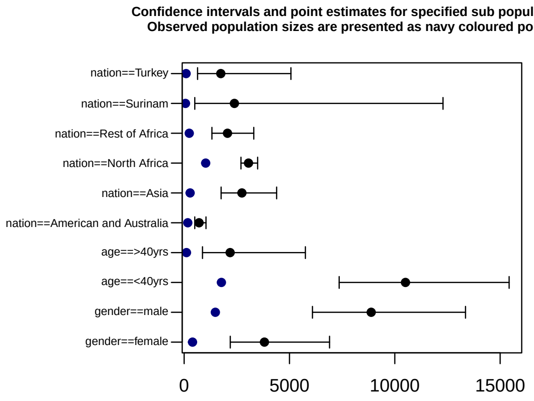
We provide integration with the **sandwich** (Zeileis, Köll, and Graham 2020) package to correct variance-covariance matrix in the δ method. In the code we have used the `vcovHC` method for `singleRStaticCountData` class from the **sandwich** package, different significance levels for confidence intervals in each strata and a formula to specify that we wanted estimates for both males and females subdivided by `nation` and `age`. The `stratas` parameter may be specified either as:

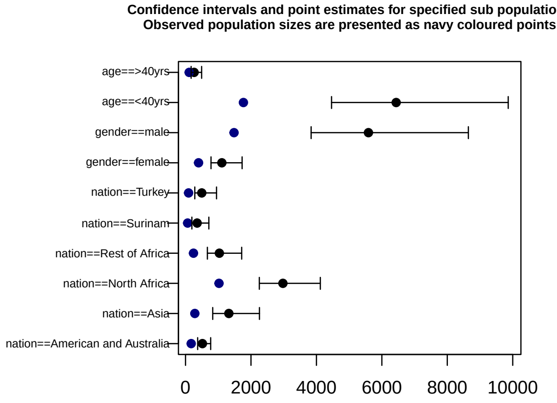
- a formula with empty left hand side which we have seen here (e.g. `~ gender * age`),
- a logical vector with number of entries equal to number of rows in the dataset in which case only one strata will be created (e.g. `netherlandsimmigrant$gender == "male"`),
- a (named) list where each element is a logical vector, names of the list will be used to specify names variable in returned object (e.g. `list("Strata 1" = netherlandsimmigrant$gender == "male" & netherlandsimmigrant$nation == "Suriname", "Strata 2" = netherlandsimmigr == "female" & netherlandsimmigrant$nation == "North Africa")`),

- a vector of names of explanatory variables which will result in every level of explanatory variable having its own sub population for each variable specified (e.g. `c("gender", "age")`),
- or not supplied at all in which case stratas will correspond to levels of each factor in the data without any interactions (string vectors will be converted to factors for the convenience of the user).

One may also specify `plotType = "strata"` in the `plot` function which results in a plot with point and CI estimates of the population size.

```
R> par(mar = c(2.5, 8.5, 4.1, 2.5), cex.main = .7, cex.lab = .6)
R> plot(basicModel, plotType = "strata")
R> plot(modelInflated, plotType = "strata")
```





For plotting only the `logNormal` type of confidence interval is used since the studentized confidence intervals often result in negative lower bounds.

5. Classes and methods

For the purpose of the package we have created classes `singleRStaticCountData`, `singleR` (for now the two former classes are the same, the distinction is made for future development), `singleRfamily`, `popSizeEstResults`, `summarysingleRStaticCountData` and `summarysingleRmargin` which allows for extracting relevant information regarding the population size.

For instance, function `popSizeEst` allows to extract information on the estimated size of the population as given below:

```
R> (popEst <- popSizeEst(basicModel))

Point estimate: 12690.35
Variance: 7885790
95% confidence intervals:
          lowerBound upperBound
normal      7186.449   18194.25
logNormal   8431.277   19718.31
```

and the resulting object `popEst` is of the `popSizeEstResults` class contains the following fields:

- `pointEstimate`, `variance` – numerics containing point estimate and variance of this estimate.
- `confidenceInterval` – a `data.frame` with confidence intervals.
- `boot` – If bootstrap was performed a numeric vector containing the $\hat{N}$ values from the bootstrap, a character vector with value `"No bootstrap performed"` otherwise.
- `control` – a `controlPopVar` object with controls used to obtained the object.

The only explicitly defined method for `popSizeEstResults`, `summarysingleRmargin` and `summarysingleRStaticCountData` classes is the `print` method, but the former one also accepts R primitives like `coef`:

```
R> coef(summary(basicModel))
```

```
                        Estimate Std. Error    z value      P(>|z|)
(Intercept)           -1.3410661  0.2148870 -6.2407965 4.353484e-10
gendermale             0.3971793  0.1630155  2.4364504 1.483220e-02
age>40yrs             -0.9746058  0.4082420 -2.3873235 1.697155e-02
nationAsia            -1.0925990  0.3016259 -3.6223642 2.919228e-04
nationNorth Africa     0.1899980  0.1940007  0.9793677 3.273983e-01
nationRest of Africa -0.9106361  0.3008092 -3.0272880 2.467587e-03
nationSurinam         -2.3363949  1.0135639 -2.3051284 2.115938e-02
nationTurkey          -1.6753917  0.6027744 -2.7794674 5.444812e-03
```

analogously to `glm` from **stats**. The `singleRfamily` inherits the `family` class from **stats** and has explicitly defined `print` and `simulate` methods defined. Example usage is presented below

```
R> set.seed(1234567890)
R> N <- 10000
R> gender <- rbinom(N, 1, 0.2)
R> eta <- -1 + 0.5*gender
R> counts <- simulate(ztpoisson(), eta = cbind(eta), seed = 1)
R> summary(data.frame(gender, eta, counts))
```

```
     gender            eta               counts
 Min.   :0.0000   Min.   :-1.0000   Min.   :0.0000
 1st Qu.:0.0000   1st Qu.:-1.0000   1st Qu.:0.0000
 Median :0.0000   Median :-1.0000   Median :0.0000
 Mean   :0.2036   Mean   :-0.8982   Mean   :0.4196
 3rd Qu.:0.0000   3rd Qu.:-1.0000   3rd Qu.:1.0000
 Max.   :1.0000   Max.   :-0.5000   Max.   :5.0000
```

Function	Description
`fitted`	Which work almost exactly like `glm` counterparts but return more information, namely on fitted values for the truncated and non-truncated probability distribution.
`logLik`	which compared to `glm` method has the possibility of returning not just the value of the fitted log-likelihood but also the entire function (argument `type = "function"`) along with two first derivatives (argument `deriv = 0:2`)
`model.matrix`	which has the possibility of returning the X_{vlm} matrix defined in 3
`simulate`	which calls `simulate` method for the chosen model and fitted $\boldsymbol{\eta}$
`predict`	which has the possibility of returning either of fitted ditribution parameters for each unit (`type = "response"`), just linear predictors (`type = "link"`), means of the fitted distributnios of Y and $Y \mid Y > 0$ (`type = "mean"`) and the inverse probability weights (`type = "contr"`). There us also the `se.fit` argument which can be set to `TRUE` to obtain standard errors for each of those by using the δ method. Also it is possible to use a custom covariance matrix for standard error computation (argument `cov`).
`redoPopEstimation`	A function that applies all post-hoc procedures that were taken (such as heteroscedastic consistent covariance matrix estimation or bias reduction) to population size estimation and standard error estimation.
`residuals`	for obtaining residuals of several types, we refer interested readers to the manual `?singleRcapture:::residuals.singleRStaticCountData`.
`stratifyPopsize`, `summary`	which were already discussed. Compared to `glm` class summary has the possibility of adding confidence interval to the coefficient matrix (argument `confint = TRUE`) and using custom covariance matrix (argument `cov = someMatrix`)
`plot`	which was already discussed
`popSizeEst`	an extractor showcased above.
`cooks.distance`	which works only for single predictor models
`dfbeta, dfpopsize`	Multithreading in `dfbeta` is available and `dfpopsize` calls `dfbeta` if no `dfbeta` object was provided at call.
`bread, estfun, vcovHC`	for (almost) full **sandwich** compatibility.
`AIC, BIC, extractAIC, family, confint, df.residual, model.frame, hatvalues, nobs, print`	Which work exactly like `glm` counterparts.

Table 2: `S3Methods` implemented in the **singleRcapture**

The full list of explicitly defined methods for `singleRStaticCountData` methods is

6. Integration with the VGAM, countreg packages

As noted at the beginning we provide an integration with the **VGAM** and **countreg** packages via the **singleRcaptureExtra** package available through Github at `https://github.com/ncn-foreigners/singleRcaptureExtra`.

```
R> install.packages("pak")
```

```
R> pak::pak("ncn-foreigners/singleRcaptureExtra")
```

The **singleRcaptureExtra** allows for converting objects created by `vglm, vgam, countreg` functions from packages **VGAM, countreg** to a `singleRStaticCountData` via the respective `estimatePopsize` methods for their classes. The help files for all the methods and all the control functions are accessed by

```
R> ?estimatePopsize.vgam
R> ?controlEstPopVgam
```

Using the fitted `zerotrunc, vglm, vgam` class objects in population size estimation such as the one additive models with smooth terms for dataset from Böhning *et al.* (2013). Note that we use a different dataset than the one presented in the case study as our goal is to show usage of additive models and how it handled in the **singleRcapture** package.

```
R> library(VGAM)
R> library(singleRcaptureExtra)
R> modelVgam <- vgam(
+   TOTAL_SUB ~ (s(log_size, df  = 3) + s(log_distance, df  = 2)) / C_TYPE,
+   data = farmsubmission,
+   # Using different link since
+   # VGAM uses parametrisation with 1/alpha
+   family = posnegbinomial(
+     lsize = negloglink
+   )
+ )
```

Estimation of the population size can be accomplished with the following syntax simple syntax.

```
R> modelVgamPop <- estimatePopsize(modelVgam)
```

The resulting object is of class `singleRforeign` to underline that the parameters were estimated outside the **singleRcapture**. Resulting object consist of the following elements

```
R> str(modelVgamPop,1)
```

```
List of 5
 $ foreignObject :Formal class 'vgam' [package "VGAM"] with 43 slots
 $ call          : language estimatePopsize.vgam(formula = modelVgam)
 $ sizeObserved  : int 12036
 $ populationSize:List of 5
  ..- attr(*, "class")= chr "popSizeEstResults"
 $ derivFunc     :function (eta)
 - attr(*, "class")= chr [1:4] "singleRadditive" "singleRforeign" "singleRStaticCountData"
```

Compare with a similar linear model from base **singleRcapture**:

```
R> modelBase <- estimatePopsize(
+   TOTAL_SUB ~ (log_size + log_distance) * C_TYPE,
+   data = farmsubmission,
+   model = ztnegbin()
+ )
R> summary(modelBase)
```

```
Call:
estimatePopsize.default(formula = TOTAL_SUB ~ (log_size + log_distance) *
    C_TYPE, data = farmsubmission, model = ztnegbin())

Pearson Residuals:
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
-0.729357 -0.317558 -0.152482  0.000609  0.148985  6.604269

Coefficients:
-----------------------
For linear predictors associated with: lambda
                         Estimate Std. Error z value  P(>|z|)
(Intercept)              -1.77609    0.45894  -3.870 0.000109 ***
log_size                  0.49391    0.02521  19.594  < 2e-16 ***
log_distance             -0.14106    0.04098  -3.442 0.000578 ***
C_TYPEDairy              -1.68591    0.55327  -3.047 0.002310 **
log_size:C_TYPEDairy      0.26504    0.03495   7.583 3.37e-14 ***
log_distance:C_TYPEDairy  0.08568    0.04874   1.758 0.078762 .
-----------------------
For linear predictors associated with: alpha
            Estimate Std. Error z value  P(>|z|)
(Intercept)  0.57673    0.07267   7.936 2.09e-15 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

AIC: 34481.99
BIC: 34533.76
Residual deviance: 17611.16

Log-likelihood: -17233.99 on 24065 Degrees of freedom
Number of iterations: 9
-----------------------
Population size estimation results:
Point estimate 38877
Observed proportion: 31% (N obs = 12036)
Std. Error 1749.448
95% CI for the population size:
          lowerBound upperBound
normal      35448.14   42305.85
logNormal   35661.32   42530.37
95% CI for the share of observed population:
          lowerBound upperBound
normal      28.44996   33.95382
logNormal   28.29978   33.75085
```

```
R> summary(modelVgamPop)
```

```
Call:
estimatePopsize.vgam(formula = modelVgam)

-----------------------
Population size estimation results:
Point estimate 37760.01
Observed proportion: 31.9% (N obs = 12036)
Std. Error 1630.429
95% CI for the population size:
          lowerBound upperBound
normal      34564.42   40955.59
logNormal   34757.77   41158.93
95% CI for the share of observed population:
          lowerBound upperBound
normal      29.38793   34.82193
logNormal   29.24274   34.62823

-------------------------------
-- Summary of foreign object --
-------------------------------

Call:
vgam(formula = TOTAL_SUB ~ (s(log_size, df = 3) + s(log_distance,
    df = 2))/C_TYPE, family = posnegbinomial(lsize = negloglink),
    data = farmsubmission)

Names of additive predictors: loglink(munb), negloglink(size)

Dispersion Parameter for posnegbinomial family:   1

Log-likelihood: -17214.62 on 24063.17 degrees of freedom

Number of Fisher scoring iterations:  11

DF for Terms and Approximate Chi-squares for Nonparametric Effects

                                                   Df Npar Df Npar Chisq
(Intercept):1                                       1
(Intercept):2                                       1
s(log_size, df = 3)                                 1     1.8     51.949
s(log_distance, df = 2)                             1     1.0      3.503
s(log_size, df = 3):s(log_distance, df = 2):C_TYPE  2
                                                     P(Chi)
(Intercept):1
(Intercept):2
s(log_size, df = 3)                                0.000000
s(log_distance, df = 2)                            0.063835
s(log_size, df = 3):s(log_distance, df = 2):C_TYPE
```

7. Concluding remarks

In this paper we have introduced two packages for single source capture-recapture models, namely **singleRcapture** and **singleRcaptureExtra**. The packages implement state of the art methods for estimating population size based on a single data set with multiple counts. The package allows for different methods to account for heterogeneity in capture probabilities, modelled using covariates, as well as behavioural change, modelled using one-inflation. We have build the package in a such way that it is easy to implement new models using `family` objects which is demonstrated in the Appendix A.2.

In future work we plan to consider Bayesian estimation using Stan (e.g. via the **brms** package; Carpenter, Gelman, Hoffman, Lee, Goodrich, Betancourt, Brubaker, Guo, Li, and Riddell (2017); Bürkner (2017)) and for one-inflation models we may use the recent approach proposed by Tuoto, Di Cecco, and Tancredi (2022) and implement our own families using the **brms** package.

8. Acknowledgements

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A. Detailed information

A.1. The `estimatePopsizeFit` function

In this section we provide step-by-step description how to prepare data to use the `sec-estimatePopsizeFit` function that may be useful for instance for estimation of variance.

1. We create data matrix $\boldsymbol{X}_{vlm}$

```
R> X <- matrix(data = 0, nrow = 2 * NROW(farmsubmission), ncol = 7)
```

2. We fill the first n rows with `model.matrix` according to the specified formula and specify the attribute `attr(X, "hwm")` that informs the function which elements of the design matrix correspond to which linear predictor (covariates for counts and covariates for one-inflation)

```
R> X[1:NROW(farmsubmission), 1:4] <- model.matrix(
+   ~ 1 + log_size + log_distance + C_TYPE,
+   farmsubmission
+ )
R>
R> X[-(1:NROW(farmsubmission)), 5:7] <- model.matrix(
+   ~ 1 + log_distance + C_TYPE,
+   farmsubmission
+ )
R>
R> attr(X, "hwm") <- c(4, 3)
```

3. We obtain starting $\boldsymbol{\beta}$ parameters using `glm.fit` function.

```
R> start <- glm.fit(# get starting points
+   y = farmsubmission$TOTAL_SUB,
+   x = X[1:NROW(farmsubmission), 1:4],
+   family = poisson()
+ )$coefficients
R>
R> start

[1] -0.82583943  0.33254499 -0.03277732  0.32746933
```

4. We use `estimatePopsizeFit` function to fit the model assuming zero-truncated one-inflated geometric distribution as specified in the `family` argument.

```
R> res <- estimatePopsizeFit(
+   y            = farmsubmission$TOTAL_SUB,
+   X            = X,
+   method       = "IRLS",
+   priorWeights = 1,
+   family       = ztoigeom(),
+   control      = controlMethod(silent = TRUE),
+   coefStart    = c(start, 0, 0, 0),
+   etaStart     = matrix(X %*% c(start, 0, 0, 0), ncol = 2),
+   offset       = cbind(rep(0, NROW(farmsubmission)),
+                        rep(0, NROW(farmsubmission)))
+ )
```

5. We compare our results with those that can be obtained from `stats::optim` function.

```
R> ll <- ztoigeom()$makeMinusLogLike(y = farmsubmission$TOTAL_SUB, X = X)

R> res2 <- estimatePopsizeFit(
+   y = farmsubmission$TOTAL_SUB,
+   X = X,
+   method = "optim",
+   priorWeights = 1,
+   family = ztoigeom(),
+   coefStart = c(start, 0, 0, 0),
+   control = controlMethod(silent = TRUE),
+   offset = cbind(rep(0, NROW(farmsubmission)), rep(0, NROW(farmsubmission)))
+ )
```

```
R> data.frame(singleRcapture = round(c(res$beta, -ll(res$beta), res$iter), 4),
+             optim = round(c(res2$beta, -ll(res2$beta), res2$iter[1]), 4))
```

```
  singleRcapture       optim
1        -2.7845     -2.6408
2         0.6170      0.6258
3        -0.0646     -0.0829
4         0.5346      0.5325
5        -3.1745     -0.1244
6         0.1281     -0.1630
7        -1.0865     -1.1055
8    -17278.7613 -17280.3414
9        15.0000   1002.0000
```

A.2. Structure of a family function

- `makeMinusLogLike` – A factory function for creating the:

  $$\ell(\boldsymbol{\beta}), \frac{\partial \ell}{\partial \boldsymbol{\beta}}, \frac{\partial^2 \ell}{\partial \boldsymbol{\beta}^\top \partial \boldsymbol{\beta}}$$

  functions from $\boldsymbol{y}$ vector and $\boldsymbol{X}_{vlm}$ the argument `deriv` with possible values in `c(0, 1, 2)` provides which derivative to return with the default `0` being just the minus log-likelihood.

- `links` – List with link functions.

- `mu.eta, variance` – Functions of linear predictors that return expected value and variance. There is a ‘type‘ argument with 2 possible values `"trunc"` and `"nontrunc"` that specifies whether to return $\mathbb{E}[Y|Y > 0], \mathrm{var}[Y|Y > 0]$ or $\mathbb{E}[Y], \mathrm{var}[Y]$ respectively, also the `deriv` argument with values in `c(0, 1, 2)` is used for indicating the derivative with respect to the linear predictors with is used for providing standard error in `predict` method.

- `family` – Character that specifies name of the model.

- `valideta, validmu` – For now only returns true. In near future will be used to check whether applied linear predictors are valid (i.e. are transformed into some elements of parameter space the subjected to inverse link function).

- `funcZ, Wfun` – Functions that create pseudo residuals and working weights used in IRLS algorithm.

- `devResids` – Function that given the linear predictors prior weights vector and response vector returns deviance residuals.

- `pointEst, popVar` – Functions that given prior weights linear predictors and in the later case also estimation of $\mathrm{cov}(\hat{\boldsymbol{\beta}})$ and $\boldsymbol{X}_{\boldsymbol{vlm}}$ matrix return point estimate for population size and analytic estimation of its variance.There is a additional boolean parameter `contr` in the former function that if set to true returns contribution of each unit.

- `etaNames` – Names of linear predictors.
- `densityFunction` – A function that given linear predictors returns value of PMF at values `x`. Additional argument `type` specifies whether to return $\mathbb{P}[Y|Y>0]$ or $\mathbb{P}[Y]$.
- `simulate` – A function that generates values of dependent vector given linear predictors.
- `getStart` – Expression for generating starting points.

B. Implementing custom singleRcapture family function

Suppose we want to implement a very specific zero truncated family function in the **singleRcapture** which corresponds to the following "untruncated" distribution:

$$\mathbb{P}[Y=y|\lambda,\pi]=\begin{cases}1-\frac{1}{2}\lambda-\frac{1}{2}\pi & \text{when: } y=0\\ \frac{1}{2}\pi & \text{when: } y=1\\ \frac{1}{2}\lambda & \text{when: } y=2,\end{cases} \tag{4}$$

with $\lambda,\pi\in(0,1)$ being dependent on covariates. The following would be one way of implementing it, with `lambda, pi` in the code meaning $\frac{1}{2}\lambda$, $\frac{1}{2}\pi$ in the equation above:

```
R> myFamilyFunction <- function(lambdaLink = c("logit", "cloglog", "probit"),
+                               piLink     = c("logit", "cloglog", "probit"),
+                               ...) {
+   if (missing(lambdaLink)) lambdaLink <- "logit"
+   if (missing(piLink))         piLink <- "logit"
+
+   links <- list()
+   attr(links, "linkNames") <- c(lambdaLink, piLink)
+
+   lambdaLink <- switch(lambdaLink,
+     "logit"   = singleRcapture:::singleRinternallogitLink,
+     "cloglog" = singleRcapture:::singleRinternalcloglogLink,
+     "probit"  = singleRcapture:::singleRinternalprobitLink
+   )
+
+   piLink <- switch(piLink,
+     "logit"   = singleRcapture:::singleRinternallogitLink,
+     "cloglog" = singleRcapture:::singleRinternalcloglogLink,
+     "probit"  = singleRcapture:::singleRinternalprobitLink
+   )
+
+   links[1:2] <- c(lambdaLink, piLink)
+
+   mu.eta <- function(eta, type = "trunc", deriv = FALSE, ...) {
+     pi     <-     piLink(eta[, 2], inverse = TRUE) / 2
+     lambda <- lambdaLink(eta[, 1], inverse = TRUE) / 2
+
+     if (!deriv) {
+       switch (type,
+         "nontrunc" = pi + 2 * lambda,
+         "trunc" = 1 + lambda / (pi + lambda)
+       )
+     } else {
```

```
+       # Only necessary if one wishes to use standard errors in predict method
+       switch (type,
+         "nontrunc" = {
+           matrix(c(2, 1) * c(
+             lambdaLink(eta[, 1], inverse = TRUE, deriv = 1) / 2,
+                 piLink(eta[, 2], inverse = TRUE, deriv = 1) / 2
+           ), ncol = 2)
+         },
+         "trunc" = {
+           matrix(c(
+             pi / (pi + lambda) ^ 2,
+             -lambda / (pi + lambda) ^ 2
+           ) * c(
+             lambdaLink(eta[, 1], inverse = TRUE, deriv = 1) / 2,
+                 piLink(eta[, 2], inverse = TRUE, deriv = 1) / 2
+           ), ncol = 2)
+         }
+       )
+     }
+   }
+
+   variance <- function(eta, type = "nontrunc", ...) {
+     pi     <-     piLink(eta[, 2], inverse = TRUE) / 2
+     lambda <- lambdaLink(eta[, 1], inverse = TRUE) / 2
+
+     switch (type,
+     "nontrunc" = pi * (1 - pi) + 4 * lambda * (1 - lambda - pi),
+     "trunc" = lambda * (1 - lambda) / (pi + lambda)
+     )
+   }
+
+   Wfun <- function(prior, y, eta, ...) {
+     pi     <-     piLink(eta[, 2], inverse = TRUE) / 2
+     lambda <- lambdaLink(eta[, 1], inverse = TRUE) / 2
+
+     G01 <- ((lambda + pi) ^ (-2)) * piLink(eta[, 2], inverse = TRUE, deriv = 1) *
+       lambdaLink(eta[, 1], inverse = TRUE, deriv = 1) * prior / 4
+
+     G00 <- ((lambda + pi) ^ (-2)) - (pi ^ (-2)) - lambda / ((lambda + pi) * (pi ^ 2))
+     G00 <- G00 * prior * (piLink(eta[, 2], inverse = TRUE, deriv = 1) ^ 2) / 4
+
+     G11 <- ((lambda + pi) ^ (-2)) - (((lambda + pi) * lambda) ^ -1)
+     G11 <- G11 * prior * (lambdaLink(eta[, 1], inverse = TRUE, deriv = 1) ^ 2) / 4
+
+     matrix(
+       -c(G11, # lambda
+          G01, # mixed
+          G01, # mixed
+          G00  # pi
+       ),
+       dimnames = list(rownames(eta), c("lambda", "mixed", "mixed", "pi")),
+       ncol = 4
+     )
+   }
+
+   funcZ <- function(eta, weight, y, prior, ...) {
+     pi     <-     piLink(eta[, 2], inverse = TRUE) / 2
+     lambda <- lambdaLink(eta[, 1], inverse = TRUE) / 2
+
+     weight <- weight / prior
+
+     G0 <- (2 - y) / pi     - ((lambda + pi) ^ -1)
+     G1 <- (y - 1) / lambda - ((lambda + pi) ^ -1)
+
+     G1 <- G1 * lambdaLink(eta[, 1], inverse = TRUE, deriv = 1) / 2
+     G0 <- G0 *     piLink(eta[, 2], inverse = TRUE, deriv = 1) / 2
+
+     uMatrix <- matrix(c(G1, G0), ncol = 2)
+
+     weight <- lapply(X = 1:nrow(weight), FUN = function (x) {
+       matrix(as.numeric(weight[x, ]), ncol = 2)
+     })
+
+     pseudoResid <- sapply(X = 1:length(weight), FUN = function (x) {
+       #xx <- chol2inv(chol(weight[[x]])) # less computationally demanding
+       xx <- solve(weight[[x]]) # more stable
+       xx %*% uMatrix[x, ]
+     })
+     pseudoResid <- t(pseudoResid)
+     dimnames(pseudoResid) <- dimnames(eta)
+     pseudoResid
+   }
+
+   minusLogLike <- function(y, X, offset,
+                            weight    = 1,
+                            NbyK      = FALSE,
+                            vectorDer = FALSE,
+                            deriv     = 0,
+                            ...) {
+     y <- as.numeric(y)
+     if (is.null(weight)) {
+       weight <- 1
+     }
+     if (missing(offset)) {
+       offset <- cbind(rep(0, NROW(X) / 2), rep(0, NROW(X) / 2))
+     }
+
+     if (!(deriv %in% c(0, 1, 2))) stop("Only score function and derivatives up to 2 are supported.")
+     deriv <- deriv + 1 # to make it conform to how switch in R works, i.e. indexing begins with 1
+
+     switch (deriv,
+       function(beta) {
+         eta <- matrix(as.matrix(X) %*% beta, ncol = 2) + offset
+         pi     <-     piLink(eta[, 2], inverse = TRUE) / 2
+         lambda <- lambdaLink(eta[, 1], inverse = TRUE) / 2
+         -sum(weight * ((2 - y) * log(pi) + (y - 1) * log(lambda) - log(pi + lambda)))
+       },
+       function(beta) {
+         eta <- matrix(as.matrix(X) %*% beta, ncol = 2) + offset
+         pi     <-     piLink(eta[, 2], inverse = TRUE) / 2
+         lambda <- lambdaLink(eta[, 1], inverse = TRUE) / 2
+
+         G0 <- (2 - y) / pi     - ((lambda + pi) ^ -1)
+         G1 <- (y - 1) / lambda - ((lambda + pi) ^ -1)
+
+         G1 <- G1 * weight * lambdaLink(eta[, 1], inverse = TRUE, deriv = 1) / 2
+         G0 <- G0 * weight *     piLink(eta[, 2], inverse = TRUE, deriv = 1) / 2
+
+         if (NbyK) {
+           XX <- 1:(attr(X, "hwm")[1])
+           return(cbind(as.data.frame(X[1:nrow(eta), XX]) * G1, as.data.frame(X[-(1:nrow(eta)), -XX]) *
+         }
+         if (vectorDer) {
+           return(cbind(G1, G0))
+         }
+
+         as.numeric(c(G1, G0) %*% X)
+       },
+       function (beta) {
+         lambdaPredNumber <- attr(X, "hwm")[1]
+         eta <- matrix(as.matrix(X) %*% beta, ncol = 2) + offset
+         pi     <-     piLink(eta[, 2], inverse = TRUE) / 2
+         lambda <- lambdaLink(eta[, 1], inverse = TRUE) / 2
+
+         res <- matrix(nrow = length(beta), ncol = length(beta),
+                       dimnames = list(names(beta), names(beta)))
+
+         # pi^2 derivative
+         dpi <- (2 - y) / pi - (lambda + pi) ^ -1
+         G00 <- ((lambda + pi) ^ (-2)) - (2 - y) / (pi ^ 2)
+
+         G00 <- t(as.data.frame(X[-(1:(nrow(X) / 2)), -(1:lambdaPredNumber)] *
+         (G00 * ((piLink(eta[, 2], inverse = TRUE, deriv = 1) / 2) ^ 2) +
+         dpi * piLink(eta[, 2], inverse = TRUE, deriv = 2) / 2) * weight)) %*%
+         as.matrix(X[-(1:(nrow(X) / 2)), -(1:lambdaPredNumber)])
+         # mixed derivative
+         G01 <- (lambda + pi) ^ (-2)
+
+         G01 <- t(as.data.frame(X[1:(nrow(X) / 2), 1:lambdaPredNumber]) *
+         G01 * (lambdaLink(eta[, 1], inverse = TRUE, deriv = 1) / 2) *
+         (piLink(eta[, 2], inverse = TRUE, deriv = 1) / 2) * weight) %*%
+         as.matrix(X[-(1:(nrow(X) / 2)), -(1:lambdaPredNumber)])
+         # lambda^2 derivative
+         G11 <- ((lambda + pi) ^ (-2)) - (y - 1) / (lambda ^ 2)
+         dlambda <- (y - 1) / lambda - ((lambda + pi) ^ -1)
+
+         G11 <- t(as.data.frame(X[1:(nrow(X) / 2), 1:lambdaPredNumber] *
+         (G11 * ((lambdaLink(eta[, 1], inverse = TRUE, deriv = 1) / 2) ^ 2) +
+         dlambda * lambdaLink(eta[, 1], inverse = TRUE, deriv = 2) / 2) * weight)) %*%
+         X[1:(nrow(X) / 2), 1:lambdaPredNumber]
+
+         res[-(1:lambdaPredNumber), -(1:lambdaPredNumber)] <- G00
+         res[1:lambdaPredNumber, 1:lambdaPredNumber] <- G11
+         res[1:lambdaPredNumber, -(1:lambdaPredNumber)] <- t(G01)
+         res[-(1:lambdaPredNumber), 1:lambdaPredNumber] <- G01
+
+         res
+       }
+     )
+   }
+
+   validmu <- function(mu) {
+     (sum(!is.finite(mu)) == 0) && all(0 < mu) && all(2 > mu)
+   }
+
+   # this is optional
+   devResids <- function(y, eta, wt, ...) {
+     0
+   }
+
+   pointEst <- function (pw, eta, contr = FALSE, ...) {
+     pi     <-     piLink(eta[, 2], inverse = TRUE) / 2
+     lambda <- lambdaLink(eta[, 1], inverse = TRUE) / 2
+     N <- pw / (lambda + pi)
+     if(!contr) {
+       N <- sum(N)
+     }
+     N
+   }
+
+   popVar <- function (pw, eta, cov, Xvlm, ...) {
+     pi     <-     piLink(eta[, 2], inverse = TRUE) / 2
+     lambda <- lambdaLink(eta[, 1], inverse = TRUE) / 2
+
+     bigTheta1 <- -pw / (pi + lambda) ^ 2 # w.r to pi
+     bigTheta1 <- bigTheta1 * piLink(eta[, 2], inverse = TRUE, deriv = 1) / 2
+     bigTheta2 <- -pw / (pi + lambda) ^ 2 # w.r to lambda
+     bigTheta2 <- bigTheta2 * lambdaLink(eta[, 1], inverse = TRUE, deriv = 1) / 2# w.r to lambda
+
+     bigTheta <- t(c(bigTheta2, bigTheta1) %*% Xvlm)
+
+     f1 <- t(bigTheta) %*% as.matrix(cov) %*% bigTheta
+
+     f2 <- sum(pw * (1 - pi - lambda) / ((pi + lambda) ^ 2))
+
+     f1 + f2
+   }
+
+   dFun <- function (x, eta, type = c("trunc", "nontrunc")) {
+     if (missing(type)) type <- "trunc"
+     pi     <-     piLink(eta[, 2], inverse = TRUE) / 2
+     lambda <- lambdaLink(eta[, 1], inverse = TRUE) / 2
+
+     switch (type,
+       "trunc" = {
+         (pi * as.numeric(x == 1) + lambda * as.numeric(x == 2)) / (pi + lambda)
+       },
+       "nontrunc" = {
+         (1 - pi - lambda) * as.numeric(x == 0) +
+         pi * as.numeric(x == 1) + lambda * as.numeric(x == 2)
+       }
+     )
+   }
+
+   simulate <- function(n, eta, lower = 0, upper = Inf) {
+     pi     <-     piLink(eta[, 2], inverse = TRUE) / 2
+     lambda <- lambdaLink(eta[, 1], inverse = TRUE) / 2
+     CDF <- function(x) {
```

```
+       ifelse(x == Inf, 1,
+       ifelse(x < 0, 0,
+       ifelse(x < 1, 1 - pi - lambda,
+       ifelse(x < 2, 1 - lambda, 1))))
+     }
+     lb <- CDF(lower)
+     ub <- CDF(upper)
+     p_u <- stats::runif(n, lb, ub)
+     sims <- rep(0, n)
+     cond <- CDF(sims) <= p_u
+     while (any(cond)) {
+       sims[cond] <- sims[cond] + 1
+       cond <- CDF(sims) <= p_u
+     }
+     sims
+   }
+
+   getStart <- expression(
+     if (method == "IRLS") {
+       etaStart <- cbind(
+         family$links[[1]](mean(observed == 2) * (1 + 0 * (observed == 2))), # lambda
+         family$links[[2]](mean(observed == 1) * (1 + 0 * (observed == 1)))  # pi
+       ) + offset
+     } else if (method == "optim") {
+       init <- c(
+         family$links[[1]](weighted.mean(observed == 2, priorWeights) * 1 + .0001),
+         family$links[[2]](weighted.mean(observed == 1, priorWeights) * 1 + .0001)
+       )
+       if (attr(terms, "intercept")) {
+         coefStart <- c(init[1], rep(0, attr(Xvlm, "hwm")[1] - 1))
+       } else {
+         coefStart <- rep(init[1] / attr(Xvlm, "hwm")[1], attr(Xvlm, "hwm")[1])
+       }
+       if ("(Intercept):pi" %in% colnames(Xvlm)) {
+         coefStart <- c(coefStart, init[2], rep(0, attr(Xvlm, "hwm")[2] - 1))
+       } else {
+         coefStart <- c(coefStart, rep(init[2] / attr(Xvlm, "hwm")[2], attr(Xvlm, "hwm")[2]))
+       }
+     }
+   )
+
+   structure(
+     list(
+       makeMinusLogLike = minusLogLike,
+       densityFunction  = dFun,
+       links     = links,
+       mu.eta    = mu.eta,
+       valideta  = function (eta) {TRUE},
+       variance  = variance,
+       Wfun      = Wfun,
+       funcZ     = funcZ,
+       devResids = devResids,
+       validmu   = validmu,
+       pointEst  = pointEst,
+       popVar    = popVar,
+       family    = "myFamilyFunction",
+       etaNames  = c("lambda", "pi"),
+       simulate  = simulate,
+       getStart  = getStart,
+       extraInfo = c(
+         mean       = "pi / 2 + lambda",
+         variance   = paste0("(pi / 2) * (1 - pi / 2) + 2 * lambda * (1 - lambda / 2 - pi / 2)"),
+         popSizeEst = "(1 - (pi + lambda) / 2) ^ -1",
+         meanTr     = "1 + lambda / (pi + lambda)",
+         varianceTr = paste0("lambda * (1 - lambda / 2) / (pi + lambda)")
+       )
+     ),
+     class = c("singleRfamily", "family")
+   )
+ }
```

A quick tests shows us that this implementation in fact works:

```
R> set.seed(123)
R> Y <- simulate(
+     myFamilyFunction(lambdaLink = "logit", piLink = "logit"),
+     nsim = 1000, eta = matrix(0, nrow = 1000, ncol = 2),
+     truncated = FALSE
+ )
R> mm <- estimatePopsize(
+     formula = Y ~ 1,
+     data = data.frame(Y = Y[Y > 0]),
+     model = myFamilyFunction(lambdaLink = "logit",
+                              piLink = "logit"),
+     # the usual observed information matrix
+     # is ill-suited for this distribution
+     controlPopVar = controlPopVar(covType = "Fisher")
+ )
R> summary(mm)


Call:
estimatePopsize.default(formula = Y ~ 1, data = data.frame(Y = Y[Y >
    0]), model = myFamilyFunction(lambdaLink = "logit", piLink = "logit"),
    controlPopVar = controlPopVar(covType = "Fisher"))

Pearson Residuals:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
-0.8198 -0.8198  0.8099  0.0000  0.8099  0.8099

Coefficients:
-----------------------
For linear predictors associated with: lambda
            Estimate Std. Error z value P(>|z|)
(Intercept)  0.01217    0.20253    0.06   0.952
-----------------------
For linear predictors associated with: pi
```

```
            Estimate Std. Error z value P(>|z|)
(Intercept) -0.01217    0.08926  -0.136   0.892

AIC: 687.4249
BIC: 695.8259
Residual deviance: 0

Log-likelihood: -341.7124 on 984 Degrees of freedom
Number of iterations: 2
-----------------------
Population size estimation results:
Point estimate 986
Observed proportion: 50% (N obs = 493)
Std. Error 70.30092
95% CI for the population size:
          lowerBound upperBound
normal      848.2127   1123.787
logNormal   866.3167   1144.053
95% CI for the share of observed population:
          lowerBound upperBound
normal      43.86951   58.12221
logNormal   43.09241   56.90759
```

Where the link functions such as `singleRcapture:::singleRinternalcloglogLink` are just internal functions in **singleRcapture** that compute link functions their inverses and derivatives of both links and inverse link up to third order:

```
R> singleRcapture:::singleRinternalcloglogLink

function (x, inverse = FALSE, deriv = 0)
{
    deriv <- deriv + 1
    if (isFALSE(inverse)) {
        res <- switch(deriv, log(-log(1 - x)), -1/((1 - x) *
            log(1 - x)), -(1 + log(1 - x))/((x - 1)^2 * log(1 -
            x)^2), (2 * log(1 - x)^2 + 3 * log(1 - x) + 2)/(log(1 -
            x)^3 * (x - 1)^3))
    }
    else {
        res <- switch(deriv, 1 - exp(-exp(x)), exp(x - exp(x)),
            (1 - exp(x)) * exp(x - exp(x)), (exp(2 * x) - 3 *
                exp(x) + 1) * exp(x - exp(x)))
    }
    res
}
<bytecode: 0x1284589f8>
<environment: namespace:singleRcapture>
```

one might of course include code for computing them manually.

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