An overview of R packages for single-source capture-recapture models

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Abstract In this paper we provide an overview of R packages that allow fitting various single-source capture-recapture (SSCR) models. In general, SSCR approaches assume that capture history follows certain discrete distribution (e.g. negative binomial, poisson, one-inflated poisson) but the observational data consist of only positive counts i.e. we observe zero truncated distributions. In this paper we cover both frequentist and bayesian approach, provide functions for population size estimation as well as analytical and bootstrap estimators. The paper focus on extraDistr, countreg, VGAM and brms packages that are suited for the SSCR models.

Introduction

Introductory section which may include references in parentheses (R Core Team, 2012), or cite a reference such as R Core Team (2012) in the text.

Single-source capture-recapture models

Böhning (2022)

R package for single-source capture-recapture model

This section may contain a figure such as Figure 1.



Figure 1: The logo of R.

Truncated discrete distributions

In order to use truncated distributions we may use default functions truncaed at 0 Loading required packages

```
library(extraDistr)
library(countreg)

#> Loading required package: MASS

#> Warning: package 'MASS' was built under R version 4.1.2
library(VGAM)

#> Warning: package 'VGAM' was built under R version 4.1.2

#> Loading required package: stats4

#> Loading required package: splines

#>
#> Attaching package: 'VGAM'
```

```
#> The following objects are masked from 'package:countreg':
#>
       dzipois, pzipois, qzipois, rzipois
#>
#> The following objects are masked from 'package:extraDistr':
#>
       dfrechet, dgev, dgompertz, dgpd, dgumbel, dhuber, dkumar, dlaplace,
#>
#>
       dlomax, dpareto, drayleigh, dskellam, dslash, pfrechet, pgev,
#>
       pgompertz, pgpd, pgumbel, phuber, pkumar, plaplace, plomax,
#>
       ppareto, prayleigh, pslash, qfrechet, qgev, qgompertz, qgpd,
#>
       qgumbel, qhuber, qkumar, qlaplace, qlomax, qpareto, qrayleigh,
       rfrechet, rgev, rgompertz, rgpd, rgumbel, rhuber, rkumar, rlaplace,
#>
       rlomax, rpareto, rrayleigh, rskellam, rslash
library(brms)
#> Warning: package 'brms' was built under R version 4.1.2
#> Loading required package: Rcpp
#> Warning: package 'Rcpp' was built under R version 4.1.2
#> Loading 'brms' package (version 2.17.0). Useful instructions
\#> can be found by typing help('brms'). A more detailed introduction
#> to the package is available through vignette('brms_overview').
#>
#> Attaching package: 'brms'
#> The following objects are masked from 'package:VGAM':
#>
#>
       acat, cratio, cumulative, dfrechet, dirichlet, exponential,
#>
       frechet, geometric, lognormal, multinomial, negbinomial, pfrechet,
       qfrechet, rfrechet, s, sratio
#> The following objects are masked from 'package:extraDistr':
#>
       ddirichlet, dfrechet, pfrechet, qfrechet, rdirichlet, rfrechet
#>
#> The following object is masked from 'package:stats':
#>
#>
       ar
library(numDeriv)
extraDistr
library(extraDistr)
set.seed(123)
```

countreg

countreg package includes function zerotrunc

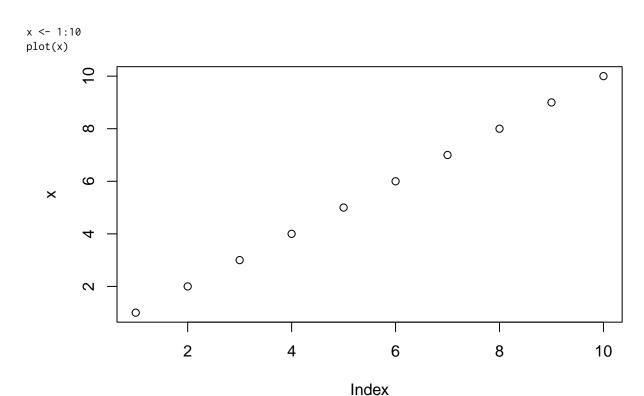
VGAM

The most advanced

stan and brms

Case studies

There will likely be several sections, perhaps including code snippets, such as:



Summary

This file is only a basic article template. For full details of *The R Journal* style and information on how to prepare your article for submission, see the Instructions for Authors.

Bibliography

D. Böhning. On the equivalence of one-inflated zero-truncated and zero-truncated one-inflated count data likelihoods. *Biometrical Journal*, n/a(n/a), 2022. doi: https://doi.org/10.1002/bimj.202100343. URL https://onlinelibrary.wiley.com/doi/abs/10.1002/bimj.202100343. [p1]

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