

# 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 to fit various single-source capture-recapture (SSCR) models. In genera, SSCR approaches assume that capture history follows certain distribution (e.g. negative binomial, poisson, one-inflated poisson) but the observational data consist only positive counts i.e. we observe zero truncated distributions.

## 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](#)

## 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

## countreg

countreg package includes function zero trunc

## VGAM

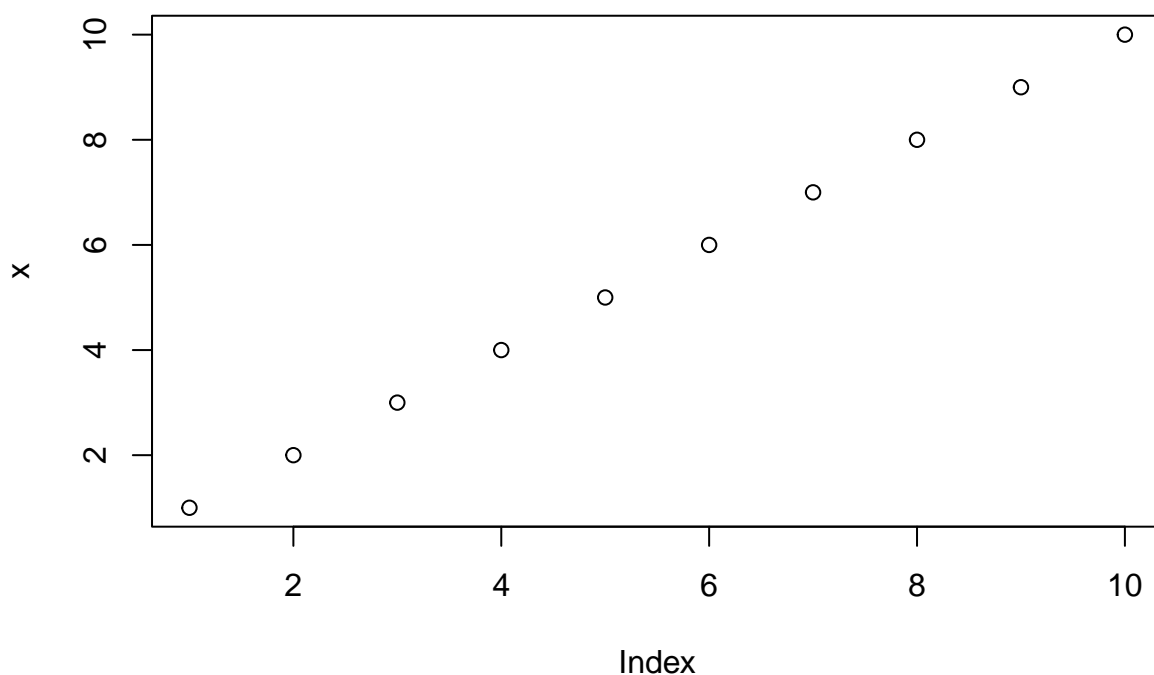
The most advanced

## stan and brms

## Case studies

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

```
x <- 1:10  
plot(x)
```



### 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). doi: <https://doi.org/10.1002/bimj.202100343>. URL <https://onlinelibrary.wiley.com/doi/abs/10.1002/bimj.202100343>. [p1]

R Core Team. *R: A Language and Environment for Statistical Computing*. R Foundation for Statistical Computing, Vienna, Austria, 2012. URL <http://www.R-project.org/>. ISBN 3-900051-07-0. [p1]

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