

What is Zero-Inflated Poisson Regression and how can it be applied in R for data analysis?

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Zero-Inflated Poisson Regression is a statistical model that is used to analyze data with a large number of zeros. It is a combination of two models, the Poisson distribution and the zero-inflation model, which takes into account excess zeros in the data. This type of regression is typically used when the response variable follows a Poisson distribution but also has a high number of zeros, which cannot be explained by the Poisson model alone.

To apply Zero-Inflated Poisson Regression in R for data analysis, the "pscl" package can be used. This package provides functions for fitting and evaluating zero-inflated models, as well as predicting values and plotting results. The data must be prepared in a specific format, with the response variable being a count variable and the predictor variables being continuous or categorical. By using this model, the researcher can obtain insights on the relationship between the predictors and the response variable, while also accounting for the excess zeros in the data. Zero-Inflated Poisson Regression can be particularly useful in fields such as ecology, epidemiology, and social sciences where data often exhibit a high number of zeros.

Zero-Inflated Poisson Regression | R Data Analysis Examples

Zero-inflated Poisson regression is used to model count data that has an excess of zero counts.

Further, theory suggests that the excess zeros are generated by a separate process from the count values and that the excess zeros can be modeled independently. Thus, the zip model has two parts, a

Poisson count model and the logit model for predicting excess zeros. You may want to review these Data Analysis Example pages, Poisson Regression and Logit Regression.

This page uses the following packages. Make sure that you can load them before trying to run the examples on this page. If you do not have a package installed, run: `install.packages("packagename")`, or if you see the version is out of date, run: `update.packages()`.

`require(ggplot2)require(pscl)require(boot)`

Version info: Code for this page was tested in R version 3.4.1

Please Note: The purpose of this page is to show how to use various data analysis commands.

It does not cover all aspects of the research process which researchers are expected to do. In particular, it does not cover data cleaning and verification, verification of assumptions, model diagnostics and potential follow-up analyses.

Examples of Zero-Inflated Poisson regression

Example 1. School administrators study the attendance behavior of high school juniors at two schools. Predictors of the number of days of absence include gender of the student and standardized test scores in

math and language arts.

Example 2. The state wildlife biologists want to model how many fish are being caught by fishermen at a state park. Visitors are asked how long they stayed, how many people were in the group, were there children in the group and how many fish were caught. Some visitors do not fish, but there is no data on whether a person fished or not. Some visitors who did fish did not catch any fish so there are excess zeros in the data because of the people that did not fish.

Description of the data

Let's pursue Example 2 from above.

We have data on 250 groups that went to a park. Each group was questioned about how many fish they caught (`count`), how many children were in the group (`child`), how many people were in the group (`persons`),

and

whether or not they brought a camper to the park (`camper`).

In addition to predicting the number of fish caught, there is interest in

predicting the existence of excess zeros, i.e., the probability that a group

caught zero fish. We will use the variables `child`, `persons`, and

`camper` in our model. Let's look at the data.

```
zinb<-
```

```
read.csv("https://stats.idre.ucla.edu/stat/data/fish.csv")z
```

```
inb<-within(zinb, {nofish<-factor(nofish)livebait<-
```

```
factor(livebait)camper<-factor(camper)})summary(zinb)
```

```
## nofish livebait camper persons child xb
```

```
## 0:176 0: 34 0:103 Min. :1.00 Min. :0.000 Min. :-3.275
```

```
## 1: 74 1:216 1:147 1st Qu.:2.00 1st Qu.:0.000 1st Qu.: 0.008
```

```
## Median :2.00 Median :0.000 Median : 0.955
```

```
## Mean :2.53 Mean :0.684 Mean : 0.974
```

```
## 3rd Qu.:4.00 3rd Qu.:1.000 3rd Qu.: 1.964
```

```
## Max. :4.00 Max. :3.000 Max. : 5.353
```

```
## zg count
```

```
## Min. :-5.626 Min. : 0.0
```

```
## 1st Qu.:-1.253 1st Qu.: 0.0
```

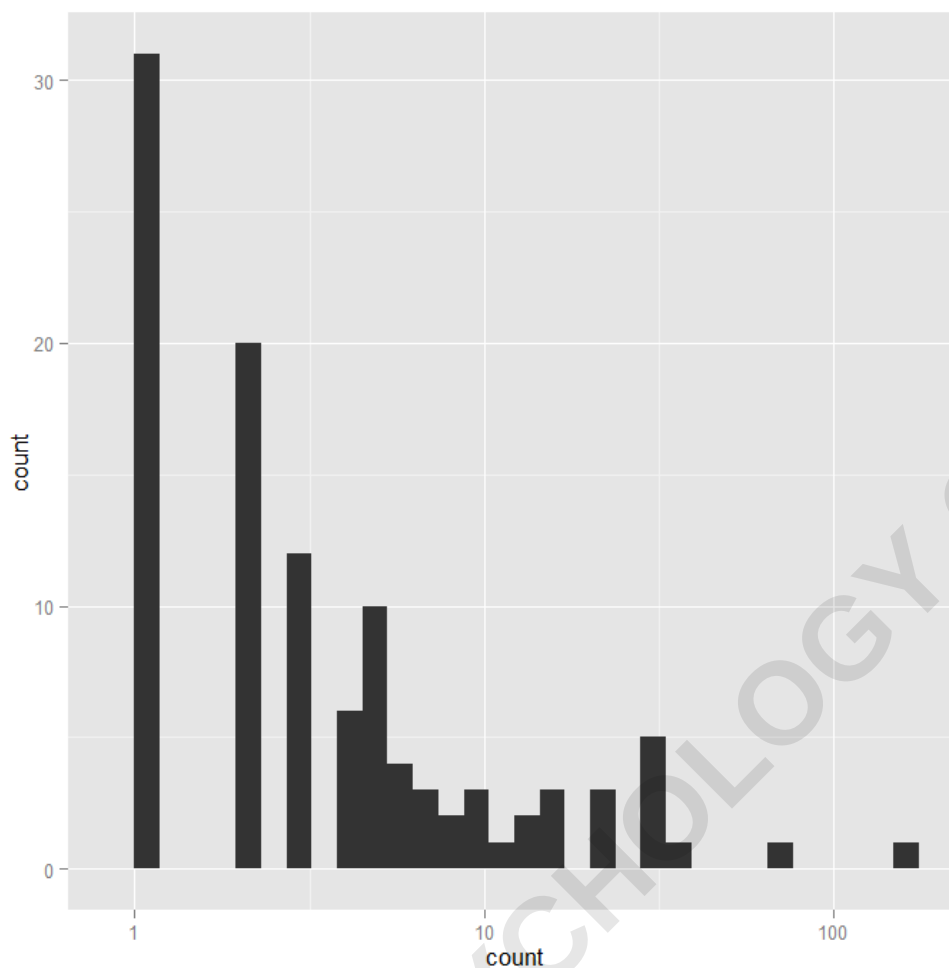
```
## Median : 0.605 Median : 0.0
```

```
## Mean : 0.252 Mean : 3.3
```

```
## 3rd Qu.: 1.993 3rd Qu.: 2.0
```

```
## Max. : 4.263 Max. :149.0
```

```
## histogram with x axis in log10  
scaleggplot(zinb,aes(count))+geom_histogram()+scale_  
x_log10()
```



Analysis methods you might consider

Below is a list of some analysis methods you may have encountered.

Some of the methods listed are quite reasonable while others have either fallen out of favor or have limitations.

Zero-inflated Poisson regression

Though we can run a Poisson regression in R using the

`glm` function in

one of the core packages, we need another package to run

the zero-inflated Poisson model. We use the `pscl` package.

```
summary(m1<-  
zeroinfl(count~child+camper|persons,data= zinb))
```

```
## Call:
```

```
## zeroinfl(formula = count ~ child + camper | persons,  
data = zinb)
```

```
##
```

```
## Pearson residuals:
```

```
## Min 1Q Median 3Q Max
```

```
## -1.2369 -0.7540 -0.6080 -0.1921 24.0847
```

```
##
```

```
## Count model coefficients (poisson with log link):
```

```
## Estimate Std. Error z value Pr(>|z|)
```

```
## (Intercept) 1.59789 0.08554 18.680 <2e-16 ***
```

```
## child -1.04284 0.09999 -10.430 <2e-16 ***
```

```
## camper1 0.83402 0.09363 8.908 <2e-16 ***
```

```
##
```

```
## Zero-inflation model coefficients (binomial with logit
```


link):

```
## Estimate Std. Error z value Pr(>|z|)
## (Intercept) 1.2974 0.3739 3.470 0.000520 ***
## persons -0.5643 0.1630 -3.463 0.000534 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Number of iterations in BFGS optimization: 12
## Log-likelihood: -1032 on 5 Df
```

The output looks very much like the output from two OLS regressions in R.

Below the model call, you will find a block of output containing Poisson regression coefficients for each of the variables along with standard errors, z-scores, and p-values for the coefficients. A second block follows that

corresponds to the inflation model. This includes logit coefficients for predicting excess zeros along with their standard errors, z-scores, and p-values.

All of the predictors in both the count and inflation portions of the

model are statistically significant. This model fits the data significantly better than the null model, i.e., the intercept-only model. To show that this is the case, we can compare with the current model to a null model without predictors using chi-squared test on the difference of log likelihoods.

```
mnull<-update(m1, .~1)pchisq(2*(logLik(m1)-logLik(mnull)),df=3,lower.tail=FALSE)
```

```
## 'log Lik.' 4.041e-41 (df=5)
```

Since we have three predictor variables in the full model, the degrees of freedom for the chi-squared test is 3. This yields a high significant p-value; thus, our overall model is statistically significant.

We can get confidence intervals for the parameters and the exponentiated parameters using bootstrapping. For the

Poisson model, these would be incident risk ratios, for the zero inflation model, odds ratios. We use the `boot` package. First, we get the coefficients from our original model to use as start values for the model to speed up the time it takes to estimate. Then we write a short function that takes data and indices as input and returns the parameters we are interested in. Finally, we pass that to the `boot` function and do 1200 replicates, using `snow` to distribute across four cores. Note that you should adjust the number of cores to whatever your machine has. Also, for final results, one may wish to increase the number of replications to help ensure stable results.

```
dput(coef(m1,"count"))
```

```
## structure(c(1.59788828690411, -1.04283909332231,  
0.834023618148891  
## ), .Names = c("(Intercept)", "child", "camper1"))
```

```
dput(coef(m1,"zero"))
```

```
## structure(c(1.29744027908309, -0.564347365357873),  
.Names = c("(Intercept)",  
## "persons"))
```

```
f<-function(data,i) {require(pscl)m<-  
zeroinfl(count~child+camper|persons,data=  
data,start=list(count=c(1.598,-1.0428,0.834),zero=c(1.297  
,-0.564)))as.vector(t(do.call(rbind,coef(summary(m)))))}s  
et.seed(10)res<-boot(zinb,  
f,R=1200,parallel="snow",ncpus=4)## print resultsres
```

```
##
```

```
## ORDINARY NONPARAMETRIC BOOTSTRAP
```

```
##
```

```
##
```

```
## Call:
```

```
## boot(data = zinb, statistic = f, R = 1200, parallel =  
"snow",
```

```
## ncpus = 4)
```

```
##
```

```
##
```

```
## Bootstrap Statistics :
```

```
## original bias std. error
## t1* 1.59789 -0.056661 0.30307
## t2* 0.08554 0.004257 0.01670
## t3* -1.04284 -0.002510 0.40557
## t4* 0.09999 0.004395 0.01539
## t5* 0.83402 0.017178 0.40465
## t6* 0.09363 0.004581 0.01536
## t7* 1.29744 0.020810 0.48058
## t8* 0.37385 0.008224 0.03662
## t9* -0.56435 -0.030103 0.26673
## t10* 0.16296 0.005272 0.02981
```

The results are alternating parameter estimates and standard errors. That is, the first row has the first parameter estimate from our model. The second has the standard error for the first parameter. The third column contains the bootstrapped standard errors, which are considerably larger than those estimated by `zeroinfl.`

Now we can get the confidence intervals for all the parameters.

We start on the original scale with percentile and bias adjusted CIs.

We also compare these results with the regular confidence intervals based on the standard errors.

```
## basic parameter estimates with percentile and bias
adjusted  CIs
parms<-t(sapply(c(1,3,5,7,9),function(i)
{out<-boot.ci(res,index=c(i,
i+1),type=c("perc","bca"))with(out,c(Est=  t0,pLL=
percent,pUL=  percent,bcaLL=  bca,bcaLL=  bca))}))##
add row names
row.names(parms)<-names(coef(m1))##
print results
parms
```

```
## Est pLL pUL bcaLL bcaLL
```

```
## count_(Intercept) 1.5979 0.8793 2.07810 1.087354
2.22614
```

```
## count_child -1.0428 -1.7509 -0.17531 -1.618509
-0.02203
```

```
## count_camper1 0.8340 0.0596 1.62653 0.001571
1.59995
```

```
## zero_(Intercept) 1.2974 0.3503 2.21984 0.293577
```

2.12070

```
## zero_persons -0.5643 -1.1087 -0.07847 -1.008526
0.00633
```

```
##      compare      with      normal      based
approximationconfint(m1)
```

```
## 2.5 % 97.5 %
```

```
## count_(Intercept) 1.4302 1.7655
```

```
## count_child -1.2388 -0.8469
```

```
## count_camper1 0.6505 1.0175
```

```
## zero_(Intercept) 0.5647 2.0302
```

```
## zero_persons -0.8838 -0.2449
```

The bootstrapped confidence intervals are considerably wider than the normal based approximation. The bootstrapped CIs are more consistent with the CIs from Stata when using robust standard errors.

Now we can estimate the incident risk ratio (IRR) for the Poisson model and odds ratio (OR) for the logistic (zero inflation) model. This is done using

almost identical code as before, but passing a transformation function to the `h` argument of `boot.ci`, in this case, `exp` to exponentiate.

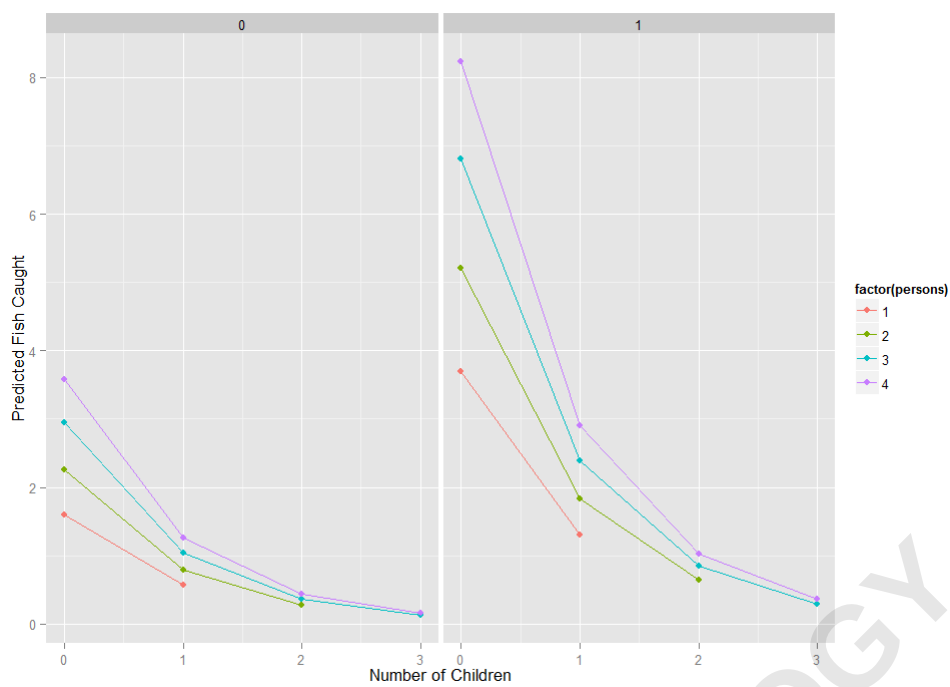
```
## exponentiated parameter estimates with percentile
and bias adjusted CIsexpparms<-
t(sapply(c(1,3,5,7,9),function(i) {out<-
boot.ci(res,index=c(i, i+1),type=c("perc","bca"),h=
exp)with(out,c(Est= t0,pLL= percent,pUL=
percent,bcaLL= bca,bcaLL= bca))}))## add row
namesrow.names(expparms)<-names(coef(m1))## print
resultsexpparms
```

```
## Est pLL pUL bcaLL bcaLL
## count_(Intercept) 4.9426 2.4091 7.9892 2.9664 9.2641
## count_child 0.3525 0.1736 0.8392 0.1982 0.9782
## count_camper1 2.3026 1.0614 5.0862 1.0016 4.9528
## zero_(Intercept) 3.6599 1.4195 9.2058 1.3412 8.3370
## zero_persons 0.5687 0.3300 0.9245 0.3648 1.0063
```

To better understand our model, we can compute the expected number of fish caught for different combinations of our predictors. In fact, since we are

working with essentially categorical predictors, we can compute the expected values for all combinations using the `expand.grid` function to create all combinations and then the `predict` function to do it. We also remove any rows where the number of children exceeds the number of persons, which does not make sense logically, using the `subset` function. Finally we create a graph.

```
newdata1<-  
expand.grid(0:3,factor(0:1),1:4)colnames(newdata1)<-  
c("child","camper","persons")newdata1<-  
subset(newdata1,subset=(child<=persons))newdata1$p  
hat<-predict(m1, newdata1)ggplot(newdata1,aes(x=  
child,y=  
phat,colour=factor(persons)))+geom_point()+geom_line  
( )+facet_wrap(~camper)+labs(x="Number of  
Children",y="Predicted Fish Caught")
```



Things to consider

See Also

References