What are some examples of data analysis using the Zero-Truncated Negative Binomial model in SAS?

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The Zero-Truncated Negative Binomial (ZTNB) model is a statistical technique used for analyzing count data that is limited to non-zero values. This model is commonly used in SAS for handling data with excess zeros, such as in medical studies or insurance claims data. Some examples of data analysis using the ZTNB model in SAS include assessing the effectiveness of a new medication by analyzing the number of hospital visits for patients, predicting the number of car accidents based on various risk factors, and estimating the number of insurance claims based on policyholder characteristics. Additionally, the ZTNB model can also be used for analyzing environmental data, such as the number of bacteria in a water sample, or for evaluating the success of marketing campaigns by examining the number of customer purchases. The ZTNB model in SAS provides a flexible and powerful tool for analyzing count data with excess zeros and can be applied in a wide range of fields and industries.

Zero-Truncated Negative Binomial | SAS Data Analysis Examples

Version info: Code for this page was tested in SAS 9.3.

Zero-truncated negative binomial regression is used to model count data for which the value zero cannot occur and when there is evidence of over dispersion .

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-truncated negative binomial

Example 1.

A study of the length of hospital stay, in days, as a function of age, kind of health insurance and whether or not the patient died while in the hospital. Length of hospital stay is recorded as a minimum of at least one day.

Example 2.

A study of the number of journal articles published by tenured faculty as a function of discipline (fine arts, science, social science, humanities, medical, etc). To get tenure faculty must publish, i.e., there are no tenured faculty with zero publications.

Example 3.

A study by the county traffic court on the number of tickets received by teenagers as predicted by school performance, amount of driver training and gender. Only individuals

who have received at least one citation are in the traffic court files.

Description of the data

Let's pursue Example 1 from above.

We have a hypothetical data file, ztp.sas7bdat with 1,493 observations available here .
The variable describing length of hospital visit is stay.
The variable age gives the age group from 1 to 9 which will be treated as
interval in this example.
The variables hmo and died are binary indicator variables
for HMO insured patients and patients who died while in hospital, respectively. These are the same
data as were used in the ztp example.

Let's look at the data.

```
proc means data=mylib.ztp;
var stay;
run;
```

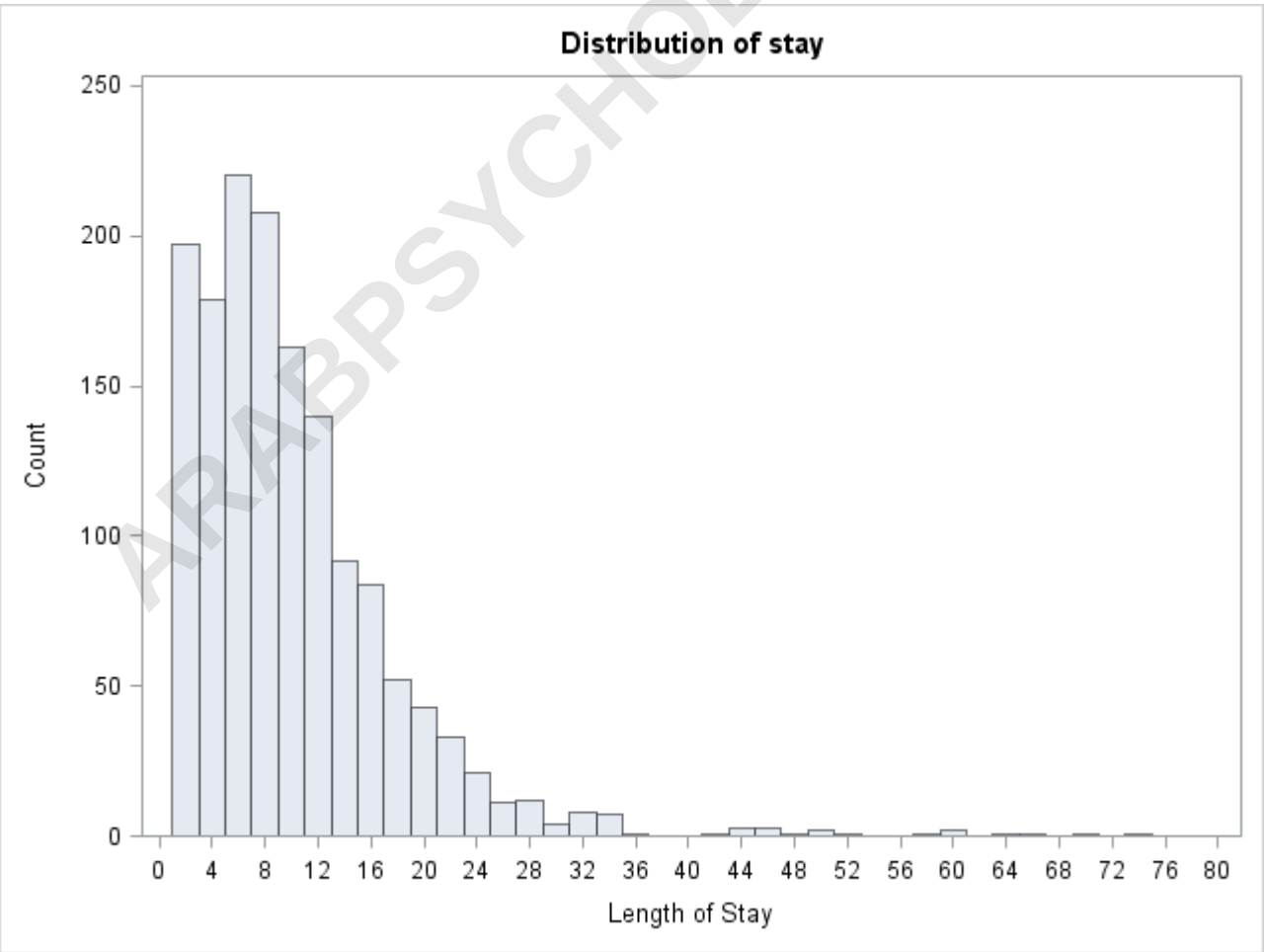
The MEANS Procedure

Analysis Variable : stay Length of Stay

N Mean Std Dev Minimum Maximum

1493 9.7287341 8.1329081 1.0000000 74.0000000

```
proc univariate data=mylib.ztp noprint;
histogram stay / midpoints = 0 to 80 by 2 vscale = count;
run;
```



proc freq data=mylib.ztp;

tables age hmo died;

run;

The FREQ Procedure

Age Group

Cumulative Cumulative

age Frequency Percent Frequency Percent

----

1 6 0.40 6 0.40

2 60 4.02 66 4.42

3 163 10.92 229 15.34

4 291 19.49 520 34.83

5 317 21.23 837 56.06

6 327 21.90 1164 77.96

7 190 12.73 1354 90.69

8 93 6.23 1447 96.92

9 46 3.08 1493 100.00

hmo

Cumulative Cumulative

hmo Frequency Percent Frequency Percent

---

0 1254 83.99 1254 83.99

1 239 16.01 1493 100.00

died

Cumulative Cumulative

died Frequency Percent Frequency Percent

---

0 981 65.71 981 65.71

1 512 34.29 1493 100.00

Analysis methods you might consider

Before we show how you can analyze these data with a zero-truncated negative binomial analysis, let's consider some other methods that you might use.

Zero-truncated negative binomial regression using proc nlmixed

In order to use procnlmixed to perform truncated negative binomial regression, we must supply it with a likelihood function.

The probability that an observation has count (y) under the negative

binomial distribution (without zero truncation) is given by the equation:

where (alpha)
is the overdispersion parameter and (mu) is the mean of the negative
binomial distribution. With zero truncation, we calculate the probability that (Y=y) conditional on (Y>0),
that is, that (Y) is observed as 0 values are not observed. The probability
of a zero count under the negative binomial distribution is (P(Y=0) =
left(frac{1}{1+alphamu}right)^{frac{1}{alpha}}). The conditional
probability is then:

The log-likelihood function for the zero-truncated negative binomial distribution is thus:

In negative binomial regression, we model (log(mu)), the log of the mean (expected
counts), as a linear combination of a set of predictors: We supply the last two equations to
proc nlmixed to model our data using a zero-truncated negative distribution.

Additionally, proc nlmixed does not support a class statement, so
categorical variables should be dummy-coded before running the analysis.
Unlike other SAS procs, by default the first group is the reference group by
default in procnlmixed.

```
proc nlmixed data = mylib.ztp;
log_mu = intercept + b_age*age + b_died*died + b_hmo*hmo;
mu = exp(log_mu);
het = 1/alpha;
ll = lgamma(stay+het) - lgamma(stay + 1) - lgamma(het) - het*log(1+alpha*mu)
+ stay*log(alpha*mu) - stay*log(1+alpha*mu) - log(1 - (1 + alpha * mu)**-het);
model stay ~ general(ll);
run;
```

The NLMIXED Procedure

Specifications

Data Set MYLIB.ZTP
Dependent Variable stay

Distribution for Dependent Variable General

Optimization Technique Dual Quasi-Newton

Integration Method None

Dimensions

Observations Used 1493

Observations Not Used 0

Total Observations 1493

Parameters 5

Parameters

intercept b_age b_died b_hmo alpha NegLogLike

1 1 1 1 1 10136.7274

Iteration History

Iter Calls NegLogLike Diff MaxGrad Slope

1 3 5203.75757 4932.97 1718.332 -825332

2 6 5130.65185 73.10572 212.6078 -12208.4

3 8 4922.88698 207.7649 1701.184 -735.733

4 9 4862.95248 59.9345 176.3689 -177.538

5 11 4851.81702 11.13546 393.0774 -13.9647

6 12 4838.27102 13.546 179.7832 -7.96192

7 16 4788.46175 49.80926 168.3697 -26.6674

8 17 4774.94754 13.51421 105.3687 -117.309

9 18 4759.72531 15.22222 77.4436 -25.9074

10 20 4755.95435 3.77096 85.88275 -22.2361

11 22 4755.3438 0.610557 39.18804 -2.65095

12 24 4755.29354 0.050252 30.83521 -0.14278

13 26 4755.28066 0.012889 3.944229 -0.03589

14 28 4755.28014 0.000512 0.44716 -0.00416

15 29 4755.27964 0.0005 0.195745 -0.00109

16 31 4755.27962 0.000028 0.007496 -0.00006

17 33 4755.27962 1.109E-7 0.030916 -4.12E-7

NOTE: GCONV convergence criterion satisfied.

The SAS System 09:40 Monday, June 4, 2012 5

The NLMIXED Procedure

Fit Statistics

-2 Log Likelihood 9510.6

AIC (smaller is better) 9520.6

AICC (smaller is better) 9520.6

BIC (smaller is better) 9547.1

Parameter Estimates

Standard
Parameter Estimate Error DF t Value Pr > |t| Alpha Lower Upper Gradient

intercept 2.4083 0.07198 1493 33.46

The output looks very much like the output from an OLS regression:

Looking through the results we see the following:

We can also use estimate statments to help understand our model, by examining the predicted or expected length of stay of patients with varying covariate values. For example we can
predict the expected number of days spent at the hospital across age groups for the two hmo statuses for patients who died. The estimate statement for proc nlmixed works
slightly differently from how it works within other procs. Here, each
parameter must be explicitly multiplied by the value at which is to be held for

that estimate statment, and expressions are allowed, such as exponentiation (see code below). Because we would like to predict actual number of days rather than log number of days, we need to exponentiate the estimate. Additionally, the following expected counts are unconditional, meaning these are the expected lengths of stay for patients with the given covariate values in the entire population, not for those patients who we know have stayed at least one day in the hospital (the conditional expectation).

```
proc nlmixed data = mylib.ztp;
log_mu = intercept + b_age*age + b_died*died + b_hmo*hmo;
mu = exp(log_mu);
het = 1/alpha;
ll = lgamma(stay+het) - lgamma(stay + 1) - lgamma(het) - het*log(1+alpha*mu)
+ stay*log(alpha*mu) - stay*log(1+alpha*mu) - log(1 - (1 + alpha * mu)**-het);
model stay ~ general(ll);
estimate 'age 1 died 1 hmo 0' exp(intercept * 1 + b_age * 1 + b_died * 1 + b_hmo * 0);
```

```
estimate 'age 1 died 1 hmo 1' exp(intercept * 1 + b_age * 1 + b_died * 1 + b_hmo * 1);
estimate 'age 3 died 1 hmo 0' exp(intercept * 1 + b_age * 3 + b_died * 1 + b_hmo * 0);
estimate 'age 3 died 1 hmo 1' exp(intercept * 1 + b_age * 3 + b_died * 1 + b_hmo * 1);
estimate 'age 5 died 1 hmo 0' exp(intercept * 1 + b_age * 5 + b_died * 1 + b_hmo * 0);
estimate 'age 5 died 1 hmo 1' exp(intercept * 1 + b_age * 5 + b_died * 1 + b_hmo * 1);
estimate 'age 7 died 1 hmo 0' exp(intercept * 1 + b_age * 7 + b_died * 1 + b_hmo * 0);
estimate 'age 7 died 1 hmo 1' exp(intercept * 1 + b_age * 7 + b_died * 1 + b_hmo * 1);
estimate 'age 9 died 1 hmo 0' exp(intercept * 1 + b_age * 9 + b_died * 1 + b_hmo * 0);
estimate 'age 9 died 1 hmo 1' exp(intercept * 1 + b_age * 9 + b_died * 1 + b_hmo * 1);
run;
```

Additional Estimates

Label	Estimate	Standard Error	DF	t Value	Pr > |t|	Alpha	Lower

Upper

age 1 died 1 hmo 0 8.8010 0.6291 1493 13.99

The expected stay for non-HMO patients in age group 1 who died was 8.8010 days,
while it was 7.5974 days for HMO patients in age group 1 who died.

We can also test whether the effect of HMO is significant at each level of age
for patients who died. We can simply subtract the two estimates that vary by hmo
at each level of age.

```
proc nlmixed data = mylib.ztp;
log_mu = intercept + b_age*age + b_died*died + b_hmo*hmo;
mu = exp(log_mu);
het = 1/alpha;
ll = lgamma(stay+het) - lgamma(stay + 1) - lgamma(het) - het*log(1+alpha*mu)
+ stay*log(alpha*mu) - stay*log(1+alpha*mu) - log(1 - (1 + alpha * mu)**-het);
model stay ~ general(ll);
```

```
estimate 'age 1 died 1 hmo 0 vs 1' exp(intercept * 1 + b_age * 1 + b_died * 1 + b_hmo * 0) - exp(intercept * 1 + b_age * 1 + b_died * 1 + b_hmo * 1);
estimate 'age 3 died 1 hmo 0 vs 1' exp(intercept * 1 + b_age * 3 + b_died * 1 + b_hmo * 0) - exp(intercept * 1 + b_age * 3 + b_died * 1 + b_hmo * 1);
estimate 'age 5 died 1 hmo 0 vs 1' exp(intercept * 1 + b_age * 5 + b_died * 1 + b_hmo * 0) - exp(intercept * 1 + b_age * 5 + b_died * 1 + b_hmo * 1);
estimate 'age 7 died 1 hmo 0 vs 1' exp(intercept * 1 + b_age * 7 + b_died * 1 + b_hmo * 0) - exp(intercept * 1 + b_age * 7 + b_died * 1 + b_hmo * 1);
estimate 'age 9 died 1 hmo 0 vs 1' exp(intercept * 1 + b_age * 9 + b_died * 1 + b_hmo * 0) - exp(intercept * 1 + b_age * 9 + b_died * 1 + b_hmo * 1);
run;
```

Additional Estimates

Label	Estimate	Standard Error	DF	t Value	Pr > |t|	Alpha	Lower	Upper
age 1 died 1 hmo 0 vs 1	1.2036	0.4698	1493	2.56	0.0105	0.05	0.2820	2.1251

age 3 died 1 hmo 0 vs 1 1.1664 0.4511 1493 2.59 0.0098 0.05 0.2816 2.0512
age 5 died 1 hmo 0 vs 1 1.1303 0.4350 1493 2.60 0.0095 0.05 0.2770 1.9837
age 7 died 1 hmo 0 vs 1 1.0954 0.4215 1493 2.60 0.0094 0.05 0.2686 1.9222
age 9 died 1 hmo 0 vs 1 1.0616 0.4103 1493 2.59 0.0098 0.05 0.2568 1.8664

The effect of hmo is significant for each age group tested.

It may be illustrative for us to plot the predicted number of days stayed as a function of age and hmo status.
To do this, we must tell SAS to save this table of predicted values as a dataset. Tables and graphics produced by
procedures are given names upon creation. We will need the name of this prediction table to tell SAS to save it.
Place odstraceon and odstraceoff statements around the procedure which produced this table to obtain its name.
Output from the odstrace statements is located in the

log, not the output.

```
ods trace on;
proc nlmixed data = mylib.ztp;
log_mu = intercept + b_age*age + b_died*died + b_hmo*hmo;
mu = exp(log_mu);
het = 1/alpha;
ll = lgamma(stay+het) - lgamma(stay + 1) - lgamma(het) - het*log(1+alpha*mu)
+ stay*log(alpha*mu) - stay*log(1+alpha*mu) - log(1 - (1 + alpha * mu)**-het);
model stay ~ general(ll);
estimate 'age 1 died 1 hmo 0' exp(intercept * 1 + b_age * 1 + b_died * 1 + b_hmo * 0);
estimate 'age 1 died 1 hmo 1' exp(intercept * 1 + b_age * 1 + b_died * 1 + b_hmo * 1);
estimate 'age 3 died 1 hmo 0' exp(intercept * 1 + b_age * 3 + b_died * 1 + b_hmo * 0);
estimate 'age 3 died 1 hmo 1' exp(intercept * 1 + b_age * 3 + b_died * 1 + b_hmo * 1);
estimate 'age 5 died 1 hmo 0' exp(intercept * 1 + b_age * 5 + b_died * 1 + b_hmo * 0);
estimate 'age 5 died 1 hmo 1' exp(intercept * 1 + b_age *
```

```
5 + b_died * 1 + b_hmo * 1);
estimate 'age 7 died 1 hmo 0' exp(intercept * 1 + b_age *
7 + b_died * 1 + b_hmo * 0);
estimate 'age 7 died 1 hmo 1' exp(intercept * 1 + b_age *
7 + b_died * 1 + b_hmo * 1);
estimate 'age 9 died 1 hmo 0' exp(intercept * 1 + b_age *
9 + b_died * 1 + b_hmo * 0);
estimate 'age 9 died 1 hmo 1' exp(intercept * 1 + b_age *
9 + b_died * 1 + b_hmo * 1);
run;
ods trace off;

Output Added:
-------------
Name: AdditionalEstimates
Label: Additional Estimates
Template: Stat.NLM.AdditionalEstimates
Path: Nlmixed.AdditionalEstimates
-------------
NOTE: PROCEDURE NLMIXED used (Total process
time):
real time 0.23 seconds
cpu time 0.17 seconds
```

```
105 ods trace off;
```

Towards the end of the log we find the name of this table, which as expected by its heading in the output above, is "AdditionalEstimates".
We can now tell SAS to save this output table as the dataset "mylib.addest" using an
odsoutput statement.

```
ods output AdditionalEstimates = mylib.addest;
proc nlmixed data = mylib.ztp;
log_mu = intercept + b_age*age + b_died*died + b_hmo*hmo;
mu = exp(log_mu);
het = 1/alpha;
ll = lgamma(stay+het) - lgamma(stay + 1) - lgamma(het) - het*log(1+alpha*mu)
+ stay*log(alpha*mu) - stay*log(1+alpha*mu) - log(1 - (1 + alpha * mu)**-het);
model stay ~ general(ll);
estimate 'age 1 died 1 hmo 0' exp(intercept * 1 + b_age * 1 + b_died * 1 + b_hmo * 0);
estimate 'age 1 died 1 hmo 1' exp(intercept * 1 + b_age * 1 + b_died * 1 + b_hmo * 1);
```

```
estimate 'age 3 died 1 hmo 0' exp(intercept * 1 + b_age * 3 + b_died * 1 + b_hmo * 0);
estimate 'age 3 died 1 hmo 1' exp(intercept * 1 + b_age * 3 + b_died * 1 + b_hmo * 1);
estimate 'age 5 died 1 hmo 0' exp(intercept * 1 + b_age * 5 + b_died * 1 + b_hmo * 0);
estimate 'age 5 died 1 hmo 1' exp(intercept * 1 + b_age * 5 + b_died * 1 + b_hmo * 1);
estimate 'age 7 died 1 hmo 0' exp(intercept * 1 + b_age * 7 + b_died * 1 + b_hmo * 0);
estimate 'age 7 died 1 hmo 1' exp(intercept * 1 + b_age * 7 + b_died * 1 + b_hmo * 1);
estimate 'age 9 died 1 hmo 0' exp(intercept * 1 + b_age * 9 + b_died * 1 + b_hmo * 0);
estimate 'age 9 died 1 hmo 1' exp(intercept * 1 + b_age * 9 + b_died * 1 + b_hmo * 1);
run;
```

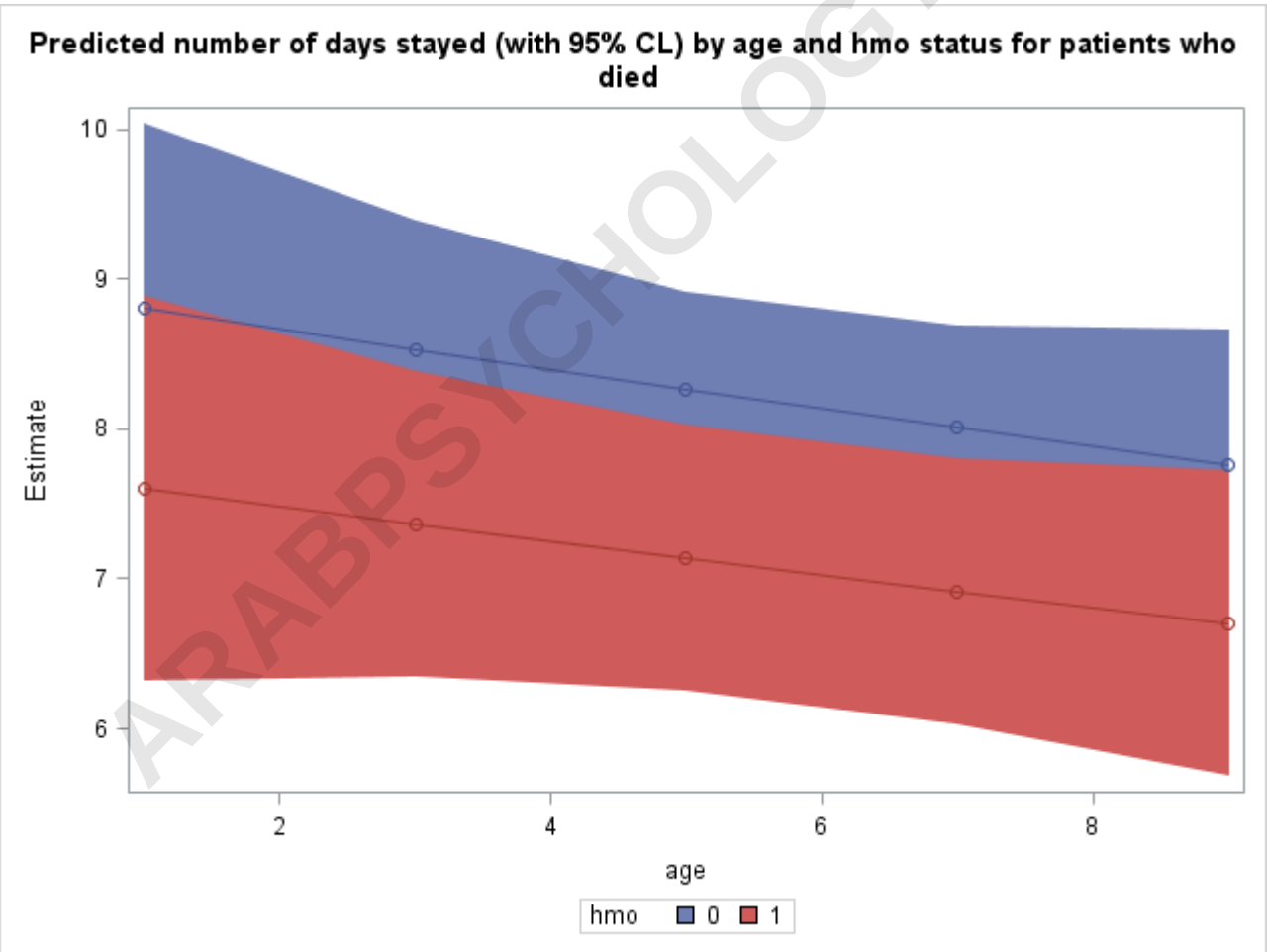
Now we can use this predicted values for plotting. We need to add actual values of
age and hmo to the dataset for plotting as well.

```
data mylib.addest;
set mylib.addest;
```

```
input age hmo;
datalines;
1 0
1 1
3 0
3 1
5 0
5 1
7 0
7 1
9 0
9 1
;
run;
```

Finally, we use procsgplot to plot our predicted number of days stayed as well as 95% confidence interval bands. The predicted values, lines connecting them, and confidence interval bands are all specified separately within
the same procsgplot. The group option will produce separate points, lines, and bands by the grouping variable.

```
proc sgplot data = mylib.addest;
title 'Predicted number of days stayed (with 95% CL) by age and hmo status for patients who died';
band x = age lower = lower upper = upper / group=hmo;
scatter x= age y = estimate / group = hmo;
series x = age y = estimate / group = hmo;
run;
```



Things to consider

References