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Using GENMOD to Analyze Correlated Data on Military Health System Beneficiaries Receiving Inpatient Behavioral Health Care in South Carolina Health Care Systems

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Abstract

The SAS procedure, GENMOD, was used to analyze a large, correlated dataset of Military Health Care (MHS) system beneficiaries who received inpatient behavioral health (BH) care in South Carolina (SC) Health Care Systems from 2005 to 2014. BH was defined by Major Diagnostic Code (MDC) 19 (mental disorders and diseases) and 20 (alcohol/drug use). MDCs are formed by dividing all possible principal diagnoses from the International Classification Diagnostic (ICD-9) codes into 25 mutually exclusive diagnostic categories. The sample included a total of 6,783 BH hospitalizations and 4,827 unique military service members, veterans, and their adult and child dependents who had MHS insurance coverage. Type of BH hospitalization (mental health or substance abuse) was the dependent variable; and gender, race, age group, and discharge year were predictors. Gender was significant with both independent correlation ($p = .0001$) and exchangeable structure ($p = .0003$). However, age group was significant using the independent correlation ($p = .0160$), but non-significant using the exchangeable correlation structure ($p = .0584$).

Introduction

When analyzing large, correlated datasets with categorical outcomes, it is challenging for new investigators to determine what type of statistical procedures to use and which statistical software is most powerful and efficient. SAS is a powerful statistical software program that provides multiple efficient procedures for investigators to analyze large, correlated data. The SAS GENMOD procedure is used to perform general linear models as well as nonlinear and complex models including loglinear, logistic, or count models for categorical outcomes.

Purpose

The SAS GENMOD procedure was used to analyze a large, correlated dataset of Military Health Care system (MHS) beneficiaries who received inpatient behavioral health (mental health/substance use) care in South Carolina Health Care Systems from 2005 to 2014.

Methodology

This study used South Carolina Revenue and Fiscal Affairs Office (RFA) data, which includes medical claims from all health care systems in South Carolina (SC). The study period was from January 1, 2005 to December 31, 2014. The study outcome was behavioral health (BH; mental health/substance abuse) hospitalizations. PROC MEANS and PROC FREQ were used to describe patient characteristics by BH group. Chi-square tests examined associations between patient characteristics and BH group. PROC GENMOD analyzed correlated data using a multivariate GEE model with gender, race, age, and discharge year as predictors of BH hospitalizations.

Results

Table 1 shows descriptive statistics for BH group, gender, race, age group, and discharge year. Approximately eighty three percent of MHS hospitalizations had a primary diagnosis of mental health, 77.98% white, 60.21% female, 31.01% were for 30-59 year olds, and 63.78% received inpatient BH care between 2005 and 2014.

Table 1: Frequency distribution of hospitalization characteristics from 2005 to 2014.

BEHAVIORAL HEALTH GROUP	Frequency	Percent	Cumulative Frequency	Cumulative Percent
Mental Health	5653	83.34	5653	83.34
Substance Abuse	1130	16.66	6783	100.00

RACE	Frequency	Percent	Cumulative Frequency	Cumulative Percent
White	5288	77.98	5288	77.98
African-American	1204	17.76	6492	95.74
Other	289	4.26	6781	100.00

SEX	Frequency	Percent	Cumulative Frequency	Cumulative Percent
Female	4084	60.21	4084	60.21
Male	2699	39.79	6783	100.00

AGE	Frequency	Percent	Cumulative Frequency	Cumulative Percent
Under 18	1295	19.09	1295	19.09
18-29 yr	1481	21.84	2776	40.93
30-59 yr	2103	31.01	4879	71.94
60 and over	1903	28.06	6782	100.00

DISCHARGE YEAR	Frequency	Percent	Cumulative Frequency	Cumulative Percent
2005 - 2009	4326	63.78	4326	63.78
2010-2014	2457	36.22	6783	100.00

Table 2 displays descriptive statistics of age and age by BH group. Overall, the average age of MHS patients was 42.25 years. The average age for MHS beneficiaries with mental health diagnoses was 40.71 years compared to 49.97 years for those with substance abuse diagnoses.

Table 2: Descriptive statistics of age and age by behavioral health group from 2005 to 2014

AGE				
N	Mean	Std Dev	Minimum	Maximum
6783	42.25	23.72	2.00	112.00

	AGE				
Behavioral Health Group	N	Mean	Std Dev	Minimum	Maximum
Mental Health	5653	40.71	24.33	2.00	112.00
Substance Abuse	1130	49.97	18.56	14.00	94.00

Table 3 shows estimates for GEE analysis from GENMOD procedures with different correlation structures and BH hospitalization as the dichotomous outcome (mental health/substance abuse). Gender was significant for both the independent correlation ($p = .0001$) and exchangeable structure ($p = .0003$).

However, age was significant for the independent correlation ($p = .0160$), but non-significant for the exchangeable correlation structure ($p = .0584$). Discharge year and race were significant in both the independent correlation and exchangeable structure models. The unstructured correlation structure was examined, but the model did not converge.

Table 3: GEE Analysis for GENMOD procedure with different distributions of correlation structure

Variables	DF	Independent X² Value	P-Value	Exchangeable X² Value	P-Value
DISCHARGE YEAR (ref=2005-2009)	1	1.14	0.2848	.13	.7209
SEX (ref=male)	1	16.53	<.0001	13.14	0.0003
RACE (ref=white)	2	1.55	0.4599	1.07	0.5292
AGE (ref=0-17)	3	10.32	0.0160	7.47	0.0584

SAS Syntax

```
ods rtf; ods listing close;
proc freq data=three;
tables bh *(sex raceg yearg ageg) / chisq;
title ' Frequency tables  '; run;

proc means data=three maxdec=2;
 var age;   TITLE1 'Mean / by group';   run;
ods rtf close;
ods listing;
quit;
run;

ods rtf;
ods listing close;
proc genmod data=three descending;
        class hid race (ref="White") sex (ref="M") ageg (ref="under 18") yearg (ref="2005 - 2009") /    param=ref ;
model bh = yearg sex raceg ageg / dist=bin link=logit type3 scale=deviance;
repeated  subject = hid /corr=ind ;
title ' genmod model /uncorrelated'; run;
proc genmod data=three descending
class hid raceg (ref="White") sex (ref="M") ageg (ref="under 18") yearg (ref="2005 - 2009") /param=ref ;
        model bh = yearg sex raceg ageg / dist=bin link=logit type3 scale=deviance  ;
        repeated  subject = hid /corr=exch ;
        title ' genmode model/ exchangeable correlated' ; run;
ods rtf close;
ods listing;
quit;
run;
```

Conclusions

GENMOD is a powerful SAS procedure for analyzing generalized linear models as well as generalized estimating equations when the data are correlated. This study indicated that, when adjustments for correlated data are not made, results may differ. It is also prudent to examine different correlation structures and distributions when the outcome is dichotomous. SAS is one of the most powerful statistical programs for the analysis of large, correlated datasets.

Acknowledgements

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