

# Multivariate Log-binomial (and Poisson) Regression between Years since Quitting Smoking and Self-reported Oral Health:

## A Sample of Work in SAS

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### Methods

This study used data from the Canadian Community Health Survey (CCHS), Annual Component, from 2015-2016. A subset was taken of the CCHS, consisting of 13 variables:

- Sex
- Age
- Education
- BMI (self-reported)
- Diabetes
- Number of years since stopped smoking completely (**← the exposure**)
  - o Levels: 0 (<1 year), 2 (1 to 2 years), 3 (3 to 5 years), 4 (>=11 years)
- Self-perceived oral health (**← the outcome**)
  - o Levels: 1 (poor), 2 (fair), 3 (good), 4 (very good), 5 (excellent)
- Frequency of tooth brushing
- Frequency of dental visits
- Diet
- Alcohol
- Drug use
- Income

The sample contained 109,659 observations in total (including missing values).

## Data Analysis:

```
/*//////////////////// .csv IMPORT and SAS file MERGING //////////////////*/
LIBNAME smoking "C:/Users/namakuto/Documents/Data Management/Assignment 4";
FILENAME REFFILE "C:/Users/namakuto/Documents/Data Management/Assignment
4/cchs.csv";
PROC IMPORT DATAFILE=REFFILE
    DBMS=CSV OUT=smoking.data1; GETNAMES=YES; RUN;
data smoking.data1; set smoking.data1;
rename ALC_015=Alcohol CCC_095=Diabetes DEN_030=DentalVisits
DEN_010A=Toothbrushing DHHGAGE=Age DHH_SEX=Sex DRMDVLAY=Drugs
EHG2DVR3=Education FDCDVAVD=Food HWTGDBCC=BMI INCDGPER=Income OHT_005=OralH
SMKDGSTP=StopSmoking; run;

*** Loop to group "Valid skip", "don't know", "refused", "did not state"
etc., responses together. Also group oral health "(oralh)" into good/poor
categories. ;
data smoking.dataoralh; set smoking.data1;
array x education bmi diabetes oralh toothbrushing
dentalvisits food stopsmoking drugs;
do i=1 to dim(x);
if x[i]>=6 and x[i]<=9 then x[i]=.; end; drop i;
if alcohol>=96 then alcohol=.;
if income>=96 then income=.;
if oralh<=3 and oralh>=1 then oralh = 1;
else if oralh>3 and oralh<6 then oralh = 0;
run;

**** Make and assign value labels. Then, apply the labels;
proc format;
value sex_1 1="Male" 2="Female";
value age_1 1="12 to 14"
           2="15 to 17"
           3="18 and 19"
           4="20 to 24"
           5="25 to 29"
           6="30 to 34"
           7="35 to 39"
           8="40 to 44"
           9="45 to 49"
          10="50 to 54"
          11="55 to 59"
          12="60 to 64"
          13="65 to 69"
          14="70 to 74"
          15="75 to 79"
          16=">= 80";
value edu_1 1="< high school"
           2="Graduated high school, no post-secondary"
           3="Post-secondary diploma or degree";
value bmi_1 1="Underweight"
           2="Normal weight"
```

```

3="Overweight"
4="Obese - Class I, II, III";
value diab_1 1="Yes"
2="No";
value oralh_1 0="Poor"
1="Good";
value teethfreq_1 1="At least 1x day"
2="At least 1x week"
3="At least 1x month"
4="At least 1x year";
value dentalvisit_1 1="> 1x a year"
2="About 1x a year"
3="< 1x a year"
4="Only for emergency care"
5="Never";
value food_1 1="Avoids foods - fat, salt, cholesterol, calories"
2="Does not avoid foods - fat, salt, cholesterol, calories";
value smokestop_1 0="< 1 year"
1="1 to 2 years"
2="3 to 5 years"
3="6 to 10 years"
4=">= 11 years";
value alcohol_1 1="< 1x a month"
2="1x a month"
3="2 to 3x a month"
4="1x a week"
5="2 to 3x a week"
6="4 to 6x a week"
7="1x a day";
value drugs_1 1="Used drugs - 12 months"
2="No drugs - 12 months";
value income_1 1="No income, or income loss"
2="< $20,000"
3="$20,000 to $39,999"
4="$40,000 to $59,999"
5="$60,000 to $79,999"
6=">= $80,000" ; run;

data smoking.dataoralh; set smoking.dataoralh; format Alcohol alcohol_1.
Diabetes diab_1. DentalVisits dentalvisit_1. Toothbrushing teethfreq_1.
Age Age_1. Sex Sex_1. Drugs Drugs_1. Education edu_1. Food Food_1. BMI bmi_1.
Income income_1. OralH oralh_1. StopSmoking smokestop_1.; run;

*** Descriptive statistics of data (all categorical);
proc freq data=smoking.dataoralh; tables _ALL_/missing; run;

*** Dichotomize smoking status. Then quick bivariate analysis. . . ;
data modsmoke; set smoking.dataoralh;
if stopsmoking=. then stopsmoking2="Non-former"; else stopsmoking2 =
"former"; run;

*. . .1) between exposure status and all variables (minus the outcome);
proc freq data=modsmoke;

```

```
tables stopsmoking2*(age income alcohol diabetes dentalvisits toothbrushing
sex drugs education food bmi oralh)/nopercent nocol nofreq nocum missing
chisq; run;
```

\*. . . 2) between outcome status and all variables (minus the exposure);

```
proc freq data=modsmoke;
tables oralh*(age income alcohol diabetes dentalvisits toothbrushing sex
drugs education food bmi stopsmoking)/nopercent nocol nofreq nocum missing
chisq; run;
```

\*. . . 3) between the exposure and the outcome (using a crude log-binomial model);

```
proc genmod data=smoking.dummies descending;
class oralh (param=ref ref="Poor") stopsmoking (ref="< 1 year");
model oralh=stopsmoking/ dist=bin link=log lrci; estimate "RR Good vs Poor"
stopsmoking 1-1
/exp;run;
```

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		DF	Estimate	Standard Error	Likelihood Ratio 95% Confidence Limits		Wald Chi-Square	Pr > ChiSq
Intercept		1	-0.1961	0.0516	-0.3192	-0.1135	14.46	0.0001
StopSmoking	1 to 2 years	1	-0.1224	0.1135	-0.3963	0.0699	1.16	0.2809
StopSmoking	3 to 5 years	1	-0.0663	0.1285	-0.4101	0.1286	0.27	0.6058
StopSmoking	6 to 10 years	1	-0.0046	0.1216	-0.3487	0.1755	0.00	0.9697
StopSmoking	>= 11 years	1	0.0544	0.0662	-0.0793	0.1943	0.68	0.4111
Scale		0	1.0000	0.0000	1.0000	1.0000		

Note: The scale parameter was held fixed.

Contrast Estimate Results									
Label	Mean Estimate	Mean		L'Beta Estimate	Standard Error	Alpha	L'Beta		Chi-Square
		Confidence Limits					Confidence Limits		
RR Good vs Poor	0.9455	0.6385	1.4000	-0.0561	0.2003	0.05	-0.4487	0.3365	0.08
Exp(RR Good vs Poor)				0.9455	0.1894	0.05	0.6385	1.4000	

\*\*\* Non-significant.

\*\*\* Regardless, all other variables seem to be associated with the exposure and outcome (could be due to the extremely large sample size) from the Chi-squared test.

\*\*\* Trying log-binomial models of the other factors' associations with the outcome (first trying "age" modeled with outcome): ;

```
proc genmod data=smoking.dummies descending;
```

```
class oralh (param=ref ref="Poor")
age (ref="12 to 14");
model oralh=age/ dist=bin link=log lrci;
estimate "RR Good vs Poor" age 1-1/exp;run;
```

\*\*\* Proper entry of dummies for age? ;

Class Level Information														
Class	Value	Design Variables												
Age	12 to 14	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1
	15 to 17	1	0	0	0	0	0	0	0	0	0	0	0	0
	18 and 19	0	1	0	0	0	0	0	0	0	0	0	0	0
	20 to 24	0	0	1	0	0	0	0	0	0	0	0	0	0
	25 to 29	0	0	0	1	0	0	0	0	0	0	0	0	0
	30 to 34	0	0	0	0	1	0	0	0	0	0	0	0	0
	35 to 39	0	0	0	0	0	1	0	0	0	0	0	0	0
	40 to 44	0	0	0	0	0	0	1	0	0	0	0	0	0
	45 to 49	0	0	0	0	0	0	0	1	0	0	0	0	0
	50 to 54	0	0	0	0	0	0	0	0	1	0	0	0	0
	55 to 59	0	0	0	0	0	0	0	0	0	1	0	0	0
	60 to 64	0	0	0	0	0	0	0	0	0	0	1	0	0
	65 to 69	0	0	0	0	0	0	0	0	0	0	0	1	0
	70 to 74	0	0	0	0	0	0	0	0	0	0	0	0	1
	75 to 79	0	0	0	0	0	0	0	0	0	0	0	0	1
	>= 80	0	0	0	0	0	0	0	0	0	0	0	0	1

\*\*\* Yes. But model found to be non-convergent.

\*\*\* Try with Poisson instead-- Poisson can approximate binomial distribution;

```
data smoking.dummies; set smoking.dummies;
by age notsorted; if age then id+1;run;
proc genmod data=smoking.dummies; class id;
model oralh=age/ dist=poisson link=log lrci;
repeated subject=id;
estimate "RR Good vs Poor" age 1-1/exp;run;
```

\*\*\* We'll use  $p < .10$  as our threshold for potential confounding. Age here not "significantly" associated with the outcome (oralh), however.

\*\*\* Chisq again to see if oralh differs across only some ages: ;

```
proc freq data=smoking.dummies;
tables oralh*age/ chisq; run;
```

\*\*\* Some differences in oralh at the extremes of age. Testing if dichotomizing age results in a "significant" model at  $p < .10$ : ;

```
data smoking.dummies2; set smoking.dummies;
if age<=8 then age_bin = 0;
else if age>8 then age_bin = 1; run;
proc genmod data=smoking.dummies2 descending;
class oralh (param=ref ref="Poor")
age_bin (ref="0");
model oralh=age_bin/ dist=bin link=log lrci;
estimate "RR Good vs Poor" age_bin 1-1/exp;run;
```

\*\* Algorithm convergence. But  $p > .10$ . Leave age out of full model.

\*\* Use genmod again to test all other remaining factors in log-binomial (or Poisson) models with oralh at p>.10 significance (potential confounders): ;

```
proc genmod . . .
```

\*\* . . . only education, bmi, and drug use associated with oralh at p<.10. Place these factors in log-bin model with oralh and the exposure: ;

```
proc genmod data=smoking.dummies descending;
class oralh(param=ref ref="Poor")
drugs(ref="Used drugs - 12 months")
BMI(ref="Obese - Class I, II, III")
stopsmoking(ref("< 1 year");
model oralh=stopsmoking education bmi drugs / dist=bin link=log lrci;
estimate "RR Good vs Poor" stopsmoking 1-1/exp;run;
```

\*\*\* Non-convergence. Trying multivariate Poisson regression instead. ;

```
data smoking.dummies; set smoking.dummies;
by drugs notsorted; if drugs then id+1;run;
proc genmod data=smoking.dummies; class id;
model oralh=stopsmoking bmi drugs / dist=poisson link=log lrci;
repeated subject=id;
estimate "RR Good vs Poor" stopsmoking 1-1/exp;run;
```

Analysis Of GEE Parameter Estimates						
Empirical Standard Error Estimates						
Parameter	Estimate	Standard Error	95% Confidence Limits		Z	Pr >  Z
Intercept	-0.5024	0.2816	-1.0543	0.0494	-1.78	0.0744
StopSmoking	-0.0218	0.0298	-0.0803	0.0366	-0.73	0.4643
BMI	-0.0188	0.0612	-0.1388	0.1012	-0.31	0.7592
Drugs	0.2601	0.1473	-0.0286	0.5487	1.77	0.0774

Contrast Estimate Results										
Label	Mean Estimate	Mean		L'Beta Estimate	Standard Error	Alpha	L'Beta		Chi-Square	Pr > ChiSq
		Confidence Limits					Confidence Limits			
RR Good vs Poor	0.9784	0.9229	1.0373	-0.0218	0.0298	0.05	-0.0803	0.0366	0.54	0.4643
Exp(RR Good vs Poor)				0.9784	0.0292	0.05	0.9229	1.0373		

\*\*\* Convergence. But still not significant. Could try removing variables anyhow and checking if the estimate (beta coefficient) for StopSmoking changes by ~±20%.

\*\*\* One could also compute changes in the mean squared error (MSE) of StopSmoking, as per the recent paper by Greenland et al. (2016), as an alternative method of testing for potential confounders.