

SAS Code:

```
libname thesis 'C:\Users\ejohn82\OneDrive - Emory University\Desktop\Thesis'
;
run;

/* Import an Excel file named 'mydata.xlsx' from your local computer */
proc import datafile= "C:\Users\ejohn82\OneDrive - Emory
University\Desktop\Thesis\Atlanta_AIDSVu_DownloadableDataset_2021.xlsx"
    out=thesis.linkagetocare2021
    dbms=xlsx
    replace;
    sheet="Linkage to Care Data"; /* Specify the sheet name */
    getnames=yes; /* Use first row as variable names */
run;

proc import datafile= "C:\Users\ejohn82\OneDrive - Emory
University\Desktop\Thesis\Atlanta_Dataset_2022-2024 (updated).xlsx"
    out=thesis.atlanta_2018_2022_rcd
    dbms=xlsx
    replace;
    sheet="Receipt of Care Data"; /* Specify the sheet name */
    getnames=yes; /* Use first row as variable names */
run;

/*I just renamed the code as appropriate to not have to copy so much stuff*/

/* editing and sorting data*/

PROC SORT DATA = thesis.atlanta_2018_2022_lcd; BY zip_code; RUN;
PROC SORT DATA = thesis.atlanta_2018_2022_vsd; BY zip_code; RUN;
PROC SORT DATA = thesis.atlanta_2018_2022_sdo; BY zip_code; RUN;
PROC SORT DATA = thesis.atlanta_2018_2022_rcd; BY zip_code; RUN;
PROC SORT DATA = thesis.atlanta_2018_2022_ldd; BY zip_code; RUN;
PROC SORT DATA = thesis.atlanta_2018_2022_ndd; BY zip_code; RUN;

/*notable methods info (missing data)
```

The downloadable datasets may have suppressed/missing values for several reasons. Suppressed and/or missing data are represented as -1, -5, -8, or -9 in the dataset and indicate the following:

-1: Data are not shown to protect privacy because a small number of cases and/or a small population size for reasons listed in the Data Suppression and Rate Stability section of the Data Methods.

-5: City did not authorize sharing this specific type of data

-8: Data are undefined, for example when rate or proportion cannot be calculated because the denominator is 0.

-9: Data are unavailable.

The downloadable datasets include a rate stability variable for each indicator. As is standard in the display of health statistics, rates generated from a numerator less than 12 are considered unreliable and should

be interpreted with caution.

Y: Reliable rates (i.e. those generated with a numerator of 12 or greater)

N: Unreliable rates (i.e. those generated with a numerator less than 12)

Rate stability listed as -9 when rate is unavailable, suppressed, or zero.
*/

/*renaming variables*/

/*fix vsd dataset*/

```
data thesis.atlanta_2018_2022_lcd;  
set thesis.atlanta_2018_2022_lcd;  
rename var5=zip_code_percent  
var6=zip_code_cases;  
run;
```

/*merging data sets, lcd and sdoh*/

```
data atlanta_lcd_reduced;  
set thesis.atlanta_2018_2022_lcd (keep=city zip_code zip_code_percent  
zip_code_cases var13 var14 var16 var17);  
run;
```

```
data atlanta_sdoh_reduced;  
set thesis.atlanta_2018_2022_sdoh (keep=zip_code var5 var7 var8 var9);  
run;
```

```
data atlanta_reduced_merged;  
merge atlanta_lcd_reduced atlanta_sdoh_reduced;  
by zip_code;  
run;
```

/*cleaning merged data set, still temp set til complete*/

```
data atlanta_reduced_cleaned;  
set atlanta_reduced_merged;  
if zip_code_percent in(-1.0 -8.0 -5.0 -9.0) then delete;  
if var14 in(-1.0 -8.0 -5.0 -9.0) then delete;  
if var16 in(-1.0 -8.0 -5.0 -9.0) then delete;  
if var17 in(-1.0 -8.0 -5.0 -9.0) then delete;  
if var5 in(-1.0 -8.0 -5.0 -9.0) then delete;  
if var9 in(-1.0 -8.0 -5.0 -9.0) then delete;  
run;
```

```
data thesis.atlanta_lcd_reduced_cleaned;  
set atlanta_reduced_cleaned;  
run;
```

/*NOTE: There were 323 observations read from the data set
WORK.ATLANTA_REDUCED_MERGED.

NOTE: The data set WORK.ATLANTA_REDUCED_CLEANED has 61 observations and 12
variables.

NOTE: DATA statement used (Total process time):
real time 0.01 seconds

```

        cpu time          0.01 seconds

*/

/*Merging more data, sets receipt of care and sdoh*/

data thesis.atlanta_2018_2022_rcd;
set thesis.atlanta_2018_2022_rcd;
rename Zip_Code=zip_code
var5=zip_code_percent
var6=zip_code_cases
Black__Cases=black_cases
Black__Percent=black_percent;
run;

data atlanta_rcd_reduced;
set thesis.atlanta_2018_2022_rcd (keep= city zip_code_percent zip_code_cases
zip_code black_percent black_cases White__Percent White__Cases);
run;

data atlanta_sdoh_reduced;
set thesis.atlanta_2018_2022_sdoh (keep=zip_code var5 var7 var8 var9);
run; /*can skip this step, already done in last merge*/

data atlanta_rcd_reduced_merged;
merge atlanta_rcd_reduced atlanta_sdoh_reduced;
by zip_code;
run;

/*cleaning merged data set (receipt of care and sdoh), still temp set til
complete*/

data atlanta_rcd_reduced_cleaned;
set atlanta_rcd_reduced_merged;
if zip_code_percent in(-1.0 -8.0 -5.0 -9.0) then delete;
if var5 in(-1.0 -8.0 -5.0 -9.0) then delete;
if var7 in(-1.0 -8.0 -5.0 -9.0) then delete;
if var8 in(-1.0 -8.0 -5.0 -9.0) then delete;
if var9 in(-1.0 -8.0 -5.0 -9.0) then delete;
if black_percent in(-1.0 -8.0 -5.0 -9.0) then delete;
if black_cases in(-1.0 -8.0 -5.0 -9.0) then delete;
if White__Percent in(-1.0 -8.0 -5.0 -9.0) then delete;
if White__Cases in(-1.0 -8.0 -5.0 -9.0) then delete;
run;

data thesis.atlanta_rcd_reduced_cleaned;
set atlanta_rcd_reduced_cleaned;
run;
/*NOTE: There were 146 observations read from the data set
WORK.ATLANTA_RCD_REDUCED_CLEANED.
NOTE: The data set THESIS.ATLANTA_RCD_REDUCED_CLEANED has 145 observations
and 12 variables.
NOTE: DATA statement used (Total process time):
        real time          0.03 seconds
        cpu time           0.01 seconds

*/

```

```

/*attempted linear regression (general group)*/

proc reg data= atlanta_reduced_cleaned;
model zip_code_percent= var5 var7 var8 var9;
run; /*only relevant model for this methodology, no validity*/

proc reg data= atlanta_reduced_cleaned;
model zip_code_cases= var5 var7 var8 var9;
run;

/*linear regression (black group)*/

proc reg data= atlanta_reduced_cleaned;
model var13= var5 var7 var8 var9;
run; /*only relevant model for this methodology, no validity*/

proc reg data= atlanta_reduced_cleaned;
model var14= var5 var7 var8 var9;
run;

/*linear regression (black+zip)*/

proc reg data= atlanta_reduced_cleaned;
model var13= zip_code var5 var7 var8 var9;
run; /*only relevant model for this methodology, no validity*/

proc reg data= atlanta_reduced_cleaned;
model var14= zip_code var5 var7 var8 var9;
run;

/*backwards elimination*/

proc reg data= thesis.atlanta_reduced_cleaned;
model var14= zip_code var5 var7 var8 var9 / selection=backward slstay=0.05;
run;
quit; /*zip_codes and var7 removed*/

/*more backward elimination*/

proc glm data= thesis.atlanta_reduced_cleaned;
model var14= zip_code var5 var7 var8 var9 zip_code*var5 zip_code*var7
zip_code*var8 zip_code*var9 var7*var5 var7*var8 var7*var9;
run;
quit;

proc glm data= thesis.atlanta_reduced_cleaned;
model var14= zip_code var5 var7 var8 var9 zip_code*var5 zip_code*var8
zip_code*var9 var7*var8 var7*var9;
run;
quit;

proc glm data= thesis.atlanta_reduced_cleaned;
model var14= zip_code var5 var7 var8 var9 zip_code*var9 var7*var8 var7*var9;
run;

```

```

quit;

proc glm data= thesis.atlanta_reduced_cleaned;
model var14= zip_code var5 var7 var8 var9 var7*var9;
run;
quit;

proc glm data= thesis.atlanta_reduced_cleaned;
model var14= var5 var7 var8 var9;
run;
quit;

proc glm data= thesis.atlanta_reduced_cleaned;
model var14= var5 var8 var9;
run;
quit;

/*almost final analysis*/

data thesis.atlanta_reduced_cleaned;
set atlanta_reduced_cleaned;
run;

proc reg data= thesis.atlanta_reduced_cleaned;
model zip_code_cases= var5 var7 var8 var9;
run;

proc reg data= thesis.atlanta_reduced_cleaned;
model zip_code_cases= zip_code var5 var7 var8 var9;
run;

proc reg data= thesis.atlanta_reduced_cleaned;
model var14= zip_code var5 var7 var8 var9;
run;

proc reg data= thesis.atlanta_reduced_cleaned;
model var14= var5 var7 var8 var9; /*without zipcode variable*/
run;

/*final analysis with final model (linear regression)*/

proc reg data= thesis.atlanta_reduced_cleaned;
model zip_code_cases= var5 var8 var9;
run;

proc reg data= thesis.atlanta_reduced_cleaned;
model var13= var5 var7 var8 var9;
run;

proc reg data= thesis.atlanta_reduced_cleaned;
model zip_code_percent= var5 var8 var9;
run;

/*final analysis with final model *linkage to care* (poisson
regression/negative binomial regression)*/

proc genmod data=thesis.atlanta_reduced_cleaned;

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```

model var14= var5 var8 var9 / dist=poisson link=log;
run; /*poisson, too much deviance and worse AIC than negative binomial
model*/

proc genmod data=thesis.atlanta_reduced_cleaned;
model zip_code_cases= var5 var8 var9 / dist=negbin link=log;
run; /*Likely final model, good results with validity*/

proc genmod data=thesis.atlanta_reduced_cleaned;
model var14= var5 var8 var9 / dist=negbin link=log;
run; /*Likely final model, good results with validity, specific to black
population*/

/*try adding class*/
proc genmod data=thesis.atlanta_reduced_cleaned;
class zip_code;
model zip_code_cases= var5 var8 var9 / dist=negbin link=log;
run; /*Likely final model, good results with validity*/

proc genmod data=thesis.atlanta_reduced_cleaned;
model var14= var5 var8 var9 / dist=negbin link=log;
run; /*Likely final model, good results with validity, specific to black
population*/

/*final analysis with final model *receipt of care* (poisson
regression/negative binomial regression)*/

proc genmod data=thesis.atlanta_rcd_reduced_cleaned;
model zip_code_cases= var5 var8 var9 / dist=negbin link=log;
run; /*Likely final model, good results with validity*/

proc genmod data=thesis.atlanta_rcd_reduced_cleaned;
model black_cases= var5 var8 var9 / dist=negbin link=log;
run;

/*Trying again with city profile dataset*/

proc reg data= thesis.atlanta_2018_2022_cityprof;
model var57= var130 var132 var133 var134 var135;
run;

proc genmod data=thesis.atlanta_rcd_reduced_cleaned;
model black_cases= var5 var8 var9 / dist=negbin link=log;
run;

/*most up to data analysis*/
/*neg binomial, lcd*/

proc genmod data=thesis.atlanta_lcd_reduced_cleaned;
model zip_code_cases= var5 var7 var8 var9 Gini__Coefficient / dist=negbin
link=log;
run; /*Likely final model, good results with validity*/

/*final.final*/

```

```

proc genmod data=thesis.atlanta_lcd_reduced_cleaned;
model var14= var5 var7 var8 var9 Gini__Coefficient / dist=negbin link=log;
run; /*Likely final model, good results with validity, specific to black
population*/

proc genmod data=thesis.atlanta_lcd_reduced_cleaned;
model zip_code_cases= var5 var8 var9 / dist=negbin link=log;
run; /*Likely final model, good results with validity*/

proc genmod data=thesis.atlanta_lcd_reduced_cleaned;
model var14= var5 var8 var9 / dist=negbin link=log;
run; /*Likely final model, good results with validity, specific to black
population*/

/*tried linear regression again*/
proc reg data= thesis.atlanta_lcd_reduced_cleaned;
model var13= var5 var7 var8 var9;
run;
proc reg data= thesis.atlanta_lcd_reduced_cleaned;
model var16= var5 var7 var8 var9;
run;

/*final analysis*/
proc genmod data=thesis.atlanta_lcd_reduced_cleaned;
model var14= var5 var7 var8 var9 / dist=negbin link=log;
run; /*Likely final model, good results with validity, specific to black
population*/

proc genmod data=thesis.atlanta_lcd_reduced_cleaned;
model zip_code_cases= var5 var7 var8 var9/ dist=negbin link=log;
run; /*Likely final model, total population*/

proc genmod data=thesis.atlanta_lcd_reduced_cleaned;
model var17= var5 var7 var8 var9 / dist=negbin link=log;
run; /*Likely final model,specific to white population*/

/*rcd*/

proc genmod data=thesis.atlanta_rcd_reduced_cleaned;
model black_cases= var5 var7 var8 var9 / dist=negbin link=log;
run; /*Likely final model, good results with validity, specific to black
population*/

proc genmod data=thesis.atlanta_rcd_reduced_cleaned;
model zip_code_cases= var5 var7 var8 var9/ dist=negbin link=log;
run; /*Likely final model, total population*/

proc genmod data=thesis.atlanta_rcd_reduced_cleaned;
model White_Cases= var5 var7 var8 var9 / dist=negbin link=log;
run; /*Likely final model,specific to white population*/

/*making table 1 and then final analysis with all sdoh variables and
character variables*/ /*add var 16/17*/

```

```

proc means data=thesis.atlanta_lcd_reduced_cleaned n mean median stddev min
max maxdec=1;
    var zip_code_percent zip_code_cases var13 var14 var16 var17 var5 var7
var8 var9;
run;

proc means data=thesis.atlanta_rcd_reduced_cleaned n mean median stddev min
max maxdec=1;
    var zip_code_percent zip_code_cases black_percent black_cases
White__Percent White__Cases var5 var7 var8 var9;
run;

/*making table 2 lcd*/

ods output ParameterEstimates=black_model_params1;
proc genmod data=thesis.atlanta_lcd_reduced_cleaned;
model var14= var5 var7 var8 var9 / dist=negbin link=log;
run;

ods output ParameterEstimates=white_model_params1;
proc genmod data=thesis.atlanta_lcd_reduced_cleaned;
model var17= var5 var7 var8 var9 / dist=negbin link=log;
run;

data black_table1;
    set black_model_params1;
    model = "Black LCD HIV Cases";
    Estimate_CI = cats(put(Estimate, 6.3), " (",
                        put(LowerWaldCL, 6.3), ", ",
                        put(UpperWaldCL, 6.3), ")");
    keep model Parameter Estimate_CI ProbChiSq;
    rename Parameter=Variable ProbChiSq=P_value;
run;

data white_table1;
    set white_model_params1;
    model = "White LCD HIV Cases";
    Estimate_CI = cats(put(Estimate, 6.3), " (",
                        put(LowerWaldCL, 6.3), ", ",
                        put(UpperWaldCL, 6.3), ")");
    keep model Parameter Estimate_CI ProbChiSq;
    rename Parameter=Variable ProbChiSq=P_value;
run;

data combined_table1;
    set black_table1 white_table1;
run;

/*making table 2 rcd*/

ods output ParameterEstimates=black_model_params2;
proc genmod data=thesis.atlanta_rcd_reduced_cleaned;
model black_cases= var5 var7 var8 var9 / dist=negbin link=log;
run;

```

```

ods output ParameterEstimates=white_model_params2;
proc genmod data=thesis.atlanta_rcd_reduced_cleaned;
model White__Cases= var5 var7 var8 var9 / dist=negbin link=log;
run;

data black_table2;
set black_model_params2;
model = "Black RCD HIV Cases";
Estimate_CI = cats(put(Estimate, 6.3), " (",
                    put(LowerWaldCL, 6.3), ", ",
                    put(UpperWaldCL, 6.3), ")");
keep model Parameter Estimate_CI ProbChiSq;
rename Parameter=Variable ProbChiSq=P_value;
run;

data white_table2;
set white_model_params2;
model = "White RCD HIV Cases";
Estimate_CI = cats(put(Estimate, 6.3), " (",
                    put(LowerWaldCL, 6.3), ", ",
                    put(UpperWaldCL, 6.3), ")");
keep model Parameter Estimate_CI ProbChiSq;
rename Parameter=Variable ProbChiSq=P_value;
run;

data combined_table2;
set black_table2 white_table2;
run;

/*Running sensitivity analysis before final analysis*/

data atlanta_lcd_reduced;
set thesis.atlanta_2018_2022_lcd (keep=city zip_code zip_code_percent
zip_code_cases var13 var14 var16 var17);
run;

data atlanta_sdoH_reduced;
set thesis.atlanta_2018_2022_sdoH (keep=zip_code var5 var7 var8 var9
Gini__Coefficient);
run;

data atlanta_reduced_merged;
merge atlanta_lcd_reduced atlanta_sdoH_reduced;
by zip_code;
run;

data atlanta_rcd_reduced;
set thesis.atlanta_2018_2022_rcd (keep= city zip_code_percent zip_code_cases
zip_code black_percent black_cases White__Percent White__Cases);
run;

data atlanta_sdoH_reduced;
set thesis.atlanta_2018_2022_sdoH (keep=zip_code var5 var7 var8 var9
Gini__Coefficient);
run;

```

```

data atlanta_reduced_merged_rcd;
merge atlanta_rcd_reduced atlanta_sdoh_reduced;
by zip_code;
run;

proc genmod data=atlanta_reduced_merged;
model var14= var5 var7 var8 var9 Gini__Coefficient;
run;
proc genmod data=atlanta_reduced_merged;
model var16= var5 var7 var8 var9 Gini__Coefficient;
run;
proc genmod data=atlanta_reduced_merged;
model zip_code_cases= var5 var7 var8 var9 Gini__Coefficient;
run;
proc genmod data=atlanta_reduced_merged_rcd;
model black_cases= var5 var7 var8 var9 Gini__Coefficient;
run;
proc genmod data=atlanta_reduced_merged_rcd;
model White__Cases= var5 var7 var8 var9 Gini__Coefficient;
run;
proc genmod data=atlanta_reduced_merged_rcd;
model zip_code_cases= var5 var7 var8 var9 Gini__Coefficient;
run;

/*Rerunning of analysis with linear regression for pertage dependent
variables (all four analysis) and individual genmod regressions for
individual independent variables, final analysis at the end*/

/*linear regression*/
proc reg data= thesis.atlanta_lcd_reduced_cleaned; /*black percentage*/
model var13= var5 var7 var8 var9/clb;
run;
proc reg data= thesis.atlanta_lcd_reduced_cleaned; /*white percentage*/
model var16= var5 var7 var8 var9/clb;
run;
proc reg data= thesis.atlanta_lcd_reduced_cleaned; /*Total percentage*/
model zip_code_percent= var5 var7 var8 var9/clb;
run;
proc reg data= thesis.atlanta_rcd_reduced_cleaned; /*black percentage*/
model black_percent= var5 var7 var8 var9/clb;
run;
proc reg data= thesis.atlanta_rcd_reduced_cleaned; /*white percentage*/
model White__Percent= var5 var7 var8 var9/clb;
run;
proc reg data= thesis.atlanta_rcd_reduced_cleaned; /*Total percentage*/
model zip_code_percent= var5 var7 var8 var9/clb;
run;

/*lcd, neg binomial, individual variables, black*/
proc genmod data=thesis.atlanta_lcd_reduced_cleaned;
model var14= var5 / dist=negbin link=log;
run; /*Likely final model, good results with validity, specific to black
population*/
proc genmod data=thesis.atlanta_lcd_reduced_cleaned;
model var14= var7 / dist=negbin link=log;

```

```

run; /*Likely final model, good results with validity, specific to black
population*/
proc genmod data=thesis.atlanta_lcd_reduced_cleaned;
model var14= var8 / dist=negbin link=log;
run; /*Likely final model, good results with validity, specific to black
population*/
proc genmod data=thesis.atlanta_lcd_reduced_cleaned;
model var14=var9 / dist=negbin link=log;
run; /*Likely final model, good results with validity, specific to black
population*/

/*lcd, neg binomial, individual variables, white*/
proc genmod data=thesis.atlanta_lcd_reduced_cleaned;
model var17= var5 / dist=negbin link=log;
run; /*Likely final model,specific to white population*/
proc genmod data=thesis.atlanta_lcd_reduced_cleaned;
model var17= var7 / dist=negbin link=log;
run; /*Likely final model,specific to white population*/
proc genmod data=thesis.atlanta_lcd_reduced_cleaned;
model var17= var8 / dist=negbin link=log;
run; /*Likely final model,specific to white population*/
proc genmod data=thesis.atlanta_lcd_reduced_cleaned;
model var17=var9 / dist=negbin link=log;
run; /*Likely final model,specific to white population*/

/*lcd, neg binomial, individual variables, total*/
proc genmod data=thesis.atlanta_lcd_reduced_cleaned;
model zip_code_cases= var5/ dist=negbin link=log;
run; /*Likely final model, total population*/
proc genmod data=thesis.atlanta_lcd_reduced_cleaned;
model zip_code_cases= var7/ dist=negbin link=log;
run; /*Likely final model, total population*/
proc genmod data=thesis.atlanta_lcd_reduced_cleaned;
model zip_code_cases=var8/ dist=negbin link=log;
run; /*Likely final model, total population*/
proc genmod data=thesis.atlanta_lcd_reduced_cleaned;
model zip_code_cases= var9/ dist=negbin link=log;
run; /*Likely final model, total population*/

/*rcd, neg binomial, individual variables, black*/
proc genmod data=thesis.atlanta_rcd_reduced_cleaned;
model black_cases= var5 / dist=negbin link=log;
run; /*Likely final model, good results with validity, specific to black
population*/
/*rcd, neg binomial, individual variables, black*/
proc genmod data=thesis.atlanta_rcd_reduced_cleaned;
model black_cases= var7 / dist=negbin link=log;
run; /*Likely final model, good results with validity, specific to black
population*/
/*rcd, neg binomial, individual variables, black*/
proc genmod data=thesis.atlanta_rcd_reduced_cleaned;
model black_cases=var8 / dist=negbin link=log;
run; /*Likely final model, good results with validity, specific to black
population*/
/*rcd, neg binomial, individual variables, black*/
proc genmod data=thesis.atlanta_rcd_reduced_cleaned;
model black_cases=var9 / dist=negbin link=log;
run; /*Likely final model, good results with validity, specific to black
population*/

```

```

/*rcd, neg binomial, individual variables, White*/
proc genmod data=thesis.atlanta_rcd_reduced_cleaned;
model White__Cases= var5 / dist=negbin link=log;
run; /*Likely final model,specific to white population*/
proc genmod data=thesis.atlanta_rcd_reduced_cleaned;
model White__Cases= var7/ dist=negbin link=log;
run; /*Likely final model,specific to white population*/
proc genmod data=thesis.atlanta_rcd_reduced_cleaned;
model White__Cases= var8 / dist=negbin link=log;
run; /*Likely final model,specific to white population*/
proc genmod data=thesis.atlanta_rcd_reduced_cleaned;
model White__Cases=var9 / dist=negbin link=log;
run; /*Likely final model,specific to white population*/

/*rcd, neg binomial, individual variables, Total*/
proc genmod data=thesis.atlanta_rcd_reduced_cleaned;
model zip_code_cases= var5/ dist=negbin link=log;
run; /*Likely final model, total population*/
proc genmod data=thesis.atlanta_rcd_reduced_cleaned;
model zip_code_cases= var7/ dist=negbin link=log;
run; /*Likely final model, total population*/
proc genmod data=thesis.atlanta_rcd_reduced_cleaned;
model zip_code_cases=var8/ dist=negbin link=log;
run; /*Likely final model, total population*/
proc genmod data=thesis.atlanta_rcd_reduced_cleaned;
model zip_code_cases=var9/ dist=negbin link=log;
run; /*Likely final model, total population*/

/*Testing for Collinearity (linear regression) before final analysis*/
proc reg data= thesis.atlanta_lcd_reduced_cleaned;
model var14= var5 var7 var8 var9 / vif collin;
run; /*no evidence of significant colinearity*/
proc reg data= thesis.atlanta_lcd_reduced_cleaned;
model var17= var5 var7 var8 var9 / vif collin;
run; /*no evidence of significant colinearity*/
proc reg data= thesis.atlanta_lcd_reduced_cleaned;
model zip_code_cases= var5 var7 var8 var9 / vif collin;
run; /*no evidence of significant colinearity*/
proc reg data= thesis.atlanta_rcd_reduced_cleaned;
model black_cases= var5 var7 var8 var9 / vif collin;
run; /*no evidence of significant colinearity*/
proc reg data= thesis.atlanta_rcd_reduced_cleaned;
model White__Cases= var5 var7 var8 var9 / vif collin;
run; /*no evidence of significant colinearity*/
proc reg data= thesis.atlanta_rcd_reduced_cleaned;
model zip_code_cases= var5 var7 var8 var9 / vif collin;
run; /*no evidence of significant colinearity*/

/*final analyses, fr this time*/
proc genmod data=thesis.atlanta_lcd_reduced_cleaned;
model var14= var5 var7 var8 var9 / dist=negbin link=log;
run; /*Likely final model, good results with validity, specific to black
population*/

proc genmod data=thesis.atlanta_lcd_reduced_cleaned;
model var17= var5 var7 var8 var9 / dist=negbin link=log;

```

```

run; /*Likely final model,specific to white population*/

proc genmod data=thesis.atlanta_lcd_reduced_cleaned;
model zip_code_cases= var5 var7 var8 var9/ dist=negbin link=log;
run; /*Likely final model, total population*/

/*rzd*/
proc genmod data=thesis.atlanta_rcd_reduced_cleaned;
model black_cases= var5 var7 var8 var9 / dist=negbin link=log;
run; /*Likely final model, good results with validity, specific to black
population*/

proc genmod data=thesis.atlanta_rcd_reduced_cleaned;
model White__Cases= var5 var7 var8 var9 / dist=negbin link=log;
run; /*Likely final model,specific to white population*/

proc genmod data=thesis.atlanta_rcd_reduced_cleaned;
model zip_code_cases= var5 var7 var8 var9/ dist=negbin link=log;
run; /*Likely final model, total population*/

/*writing methods, getting version number*/
proc setinit;run;

```