# 409 presentation results

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## **Summary stats**

```
\#\# Warning in chisq.test(table(y, g)): Chi-squared approximation may be incorrect
```

 $\hbox{\tt \#\# Warning in chisq.test(table(y, g)): Chi-squared approximation may be incorrect}$ 

Name		Cumpagggd	Ungunnaggad	Total	P-value						
Media (SD)		Suppressed	Unsuppressed		P-varue						
Mean (SD)   25.2 (7.26)   25.6 (6.16)   25.0 [10.0, 40.0]   25.0 [10.0, 51.0]   2		(N=117)	(N=145)	(N=262)							
Median   Min, Max   25.0   10.0, 40.0   26.0   10.0, 40.0   25.0   25.0   10.0, 40.0   25.0   25.0   10.0, 40.0   25.0   25.0   10.0, 40.0   25.0   25.0   10.0   25.0   2				()							
Netra	( )		` /	` /	0.622						
Mean (SD) Median [Min, Max]         23.0 [10.0, 40.0]         24.1 [6.24) [2.0, 40.0]         23.7 [6.18) [2.0, 40.0]         0.282 [2.0] [2.0, 40.0]         23.7 [6.18] [2.0, 40.0]         23.7 [6.18] [2.0, 40.0]         23.5 [6.29] [2.0, 40.0]         0.647           Mean (SD) Median [Min, Max]         24.0 [10.0, 40.0]         23.0 [10.0, 40.0]         23.5 [6.29] [2.0, 40.0]         0.647           HIV clinical utilization 12m           Mean (SD) Median [Min, Max]         1.00 [0, 12.0]         2.94 [5.67] [2.2, 5 [0.0], 51.0]         2.24 [4.41] [2.0, 0.022]         0.022           Median [Min, Max]         1.00 [0, 12.0]         2.00 [0, 51.0]         2.00 [0, 51.0]         0.449           Median [Min, Max]         24.0 [1.0, 0, 112]         21.1 [7.21]         21.5 [9.37]         0.449           Mean (SD) Median [Min, Max]         24.0 [1.0, 112]         21.0 [3.00, 30.0]         22.5 [1.00, 112]         0.499           Dectors office care utilization 12m           Mean (SD)         2.08 (3.31)         1.64 (2.30)         1.84 (2.80)         0.229           Mean (SD)         0.521 (1.06)         0.669 (1.38)         0.603 (1.25)         0.33           Median [Min, Max]         0 [0, 6.00]         0 [0, 10.0]         0 [0, 10.0]         0 [0, 10.0]         0 [0, 10.0]         0 [0, 10.0]         0 [0, 10.0]		25.0 [10.0, 40.0]	26.0 [10.0, 40.0]	25.0 [10.0, 40.0]							
Median [Min, Max]         23.0 [10.0, 40.0]         25.0 [10.0, 40.0]         24.0 [10.0, 40.0]         26.0 [20.0]         0.647           Stigma 12 month           Mean (SD)         23.7 (6.48)         23.3 (6.16)         23.5 (6.29)         0.647           Median [Min, Max]         24.0 [10.0, 40.0]         23.0 [10.0, 40.0]         23.0 [10.0, 40.0]           HIV clinical utilization 12m         0.00 [0, 12.0]         2.94 (5.67)         2.42 (4.41)         0.022           Median [Min, Max]         1.00 [0, 12.0]         2.00 [0, 51.0]         2.00 [0, 51.0]         0.449           Social support           Mean (SD)         22.0 (11.5)         21.1 (7.21)         21.5 (9.37)         0.449           Median [Min, Max]         24.0 [1.00, 112]         21.0 [3.00, 30.0]         22.5 [1.00, 112]         0.449           Doctors office care utilization 12m           Mean (SD)         2.08 (3.31)         1.64 (2.30)         1.84 (2.80)         0.229           Emergency/urgent care utilization 12m           Mean (SD)         0.521 (1.06)         0.669 (1.38)         0.603 (1.25)         0.33           Median [Min, Max]         0 [0, 6.0]         0 [0, 10.0]         0 [0, 10.0] <td <="" colspan="6" td=""><td>_</td><td></td><td></td><td></td><td></td></td>	<td>_</td> <td></td> <td></td> <td></td> <td></td>						_				
Name   Signa   12 month   Mean   (Signa   23.7   (6.48)   23.3   (6.16)   23.5   (6.29)   0.647   Median   Min, Max   24.0   10.0, 40.0   23.0   10.0, 40.0   23.0   10.0, 40.0   23.0   10.0, 40.0   23.0   10.0, 40.0   23.0   10.0, 40.0   23.0   10.0, 40.0   23.0   10.0, 40.0   23.0   10.0, 40.0   23.0   10.0, 40.0   23.0   10.0, 40.0   23.0   10.0, 40.0   23.0   10.0, 40.0   23.0   10.0, 40.0   23.0   10.0, 40.0   23.0   10.0, 40.0   23.0   10.0, 40.0   23.0   10.0, 10.0   20.0   0, 51.0   20.0   0, 51.0   20.0   0, 51.0   20.0   0, 51.0   20.0   0, 51.0   20.0   0, 51.0   20.0   0, 51.0   20.0   0, 51.0   20.0   0, 51.0   20.0   0, 51.0   20.0   0, 51.0   20.0   0, 51.0   20.0   0.51.0   20.0   0.51.0   20.0   0.51.0   20.0   0.51.0   20.0   0.51.0   20.0   0.51.0   20.0   0.51.0   20.0   0.51.0   20.0   0.51.0   20.0   0.0	` /	` /		` /	0.282						
$ \begin{array}{ c c c c c c } \hline Mean (SD) & 23.7 (6.48) \\ Median [Min, Max] & 24.0 [10.0, 40.0] & 23.0 [10.0, 40.0] & 23.0 [10.0, 40.0] \\ \hline MIV Clinical utilization 12m \\ \hline Mean (SD) & 1.79 (1.78) & 2.94 (5.67) & 2.42 (4.41) & 0.022 \\ \hline Median [Min, Max] & 1.00 [0, 12.0] & 2.00 [0, 51.0] & 2.00 [0, 51.0] \\ \hline Social support \\ \hline Mean (SD) & 22.0 (11.5) & 21.1 (7.21) & 21.5 (9.37) & 0.449 \\ \hline Mean (SD) & 22.0 (10.0, 112] & 21.0 [3.00, 30.0] & 22.5 [1.00, 112] \\ \hline Doctors office care utilization 12m \\ \hline Mean (SD) & 2.08 (3.31) & 1.64 (2.30) & 1.84 (2.80) & 0.229 \\ \hline Median [Min, Max] & 1.00 [0, 25.0] & 1.00 [0, 18.0] & 1.00 [0, 25.0] \\ \hline Emergency/urgent care utilization 12m \\ \hline Mean (SD) & 0.521 (1.06) & 0.669 (1.38) & 0.603 (1.25) & 0.33 \\ \hline Median [Min, Max] & 0 [0, 6.00] & 0 [0, 10.0] & 0 [0, 10.0] \\ \hline Times admitted to bospital 12m \\ \hline Mean (SD) & 0.188 (0.642) & 0.462 (1.45) & 0.340 (1.17) & 0.0429 \\ \hline Median [Min, Max] & 0 [0, 5.00] & 0 [0, 10.0] & 0 [0, 10.0] \\ \hline Total care utilization \\ \hline Mean (SD) & 4.57 (4.91) & 5.71 (7.91) & 5.20 (6.75) & 0.156 \\ \hline Median [Min, Max] & 3.00 [0, 32.0] & 4.00 [0, 66.0] & 3.00 [0, 66.0] \\ \hline Gender \\ \hline cis & 102 (87.2%) & 129 (89.0\%) & 231 (88.2\%) & 0.902 \\ \hline other & 3 (2.6\%) & 3 (2.1\%) & 6 (2.3\%) & 1.00 \\ \hline cis & 16 (13.7\%) & 23 (15.9\%) & 39 (14.9\%) & 0.245 \\ \hline gay & 72 (61.5\%) & 84 (57.9\%) & 156 (59.5\%) \\ \hline Sexual orientation \\ \hline bi & 16 (13.7\%) & 23 (15.9\%) & 39 (14.9\%) & 0.245 \\ \hline gay & 72 (61.5\%) & 84 (57.9\%) & 156 (59.5\%) \\ \hline Sexual orientation & 1 (0.9\%) & 4 (2.8\%) & 5 (1.9\%) \\ \hline equer & 9 (7.7\%) & 4 (2.8\%) & 5 (1.9\%) & 0.0272 \\ \hline non-latino black & 54 (46.2\%) & 81 (55.9\%) & 135 (51.5\%) & 0.0272 \\ \hline non-latino black & 26 (22.2\%) & 13 (9.0\%) & 39 (14.9\%) & 0.0272 \\ \hline Employment & 4 (3.68\%) & 43 (29.7\%) & 86 (32.8\%) & 0.469 \\ \hline full-time & 43 (36.8\%) & 43 (29.7\%) & 86 (32.8\%) & 0.469 \\ \hline full-time & 43 (36.8\%) & 43 (29.7\%) & 86 (32.8\%) & 0.469 \\ \hline full-time & 43 (36.8\%) & 43 (29.7\%) & 55 (20.2\%) & 55 (20.2\%) \\ \hline extendent & 6 (5.1\%) & 85 (55\%) & 14 (5.3\%) & 14 (5.3\%) & 14 (5.3\%) $		23.0 [10.0, 40.0]	25.0 [10.0, 40.0]	24.0 [10.0, 40.0]							
Median [Min, Max]         24.0 [10.0, 40.0]         23.0 [10.0, 40.0]         23.0 [10.0, 40.0]         Colspan="6">Colspan="6"	_	()	( )								
Mean (SD)			` /		0.647						
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Median [Min, Max]   1.00 [0, 12.0]   2.00 [0, 51.0]   2.00 [0, 51.0]     Social support											
Social support           Mean (SD)         22.0 (11.5)         21.1 (7.21)         21.5 (9.37)         0.449           Median [Min, Max]         24.0 [1.00, 112]         21.0 [3.00, 30.0]         22.5 [1.00, 112]         1.00           Doctors office care utilization 12m           Mean (SD)         2.08 (3.31)         1.64 (2.30)         1.84 (2.80)         0.229           Median [Min, Max]         1.00 [0, 25.0]         1.00 [0, 18.0]         1.00 [0, 25.0]         0.229           Emergency/urgent care utilization 12m           Mean (SD)         0.521 (1.06)         0.669 (1.38)         0.603 (1.25)         0.33           Median [Min, Max]         0 [0, 6.00]         0 [0, 10.0]         0 [0, 10.0]         0           Times admitted to hospital 12m           Mean (SD)         0.188 (0.642)         0.462 (1.45)         0.340 (1.17)         0.0429           Median [Min, Max]         0 [0, 5.00]         0 [0, 10.0]         0 [0, 10.0]         10           Times admitted to hospital 12m           Mean (SD)         0.188 (0.642)         0.462 (1.45)         0.340 (1.17)         0.0429           Median [Min, Max]         3 (0, 5.00]         0 [0, 10.0]         0 [0, 10.0]         0 [0, 10.0]         0 [0		` /			0.022						
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Mean (SD)   2.08 (3.31)   1.64 (2.30)   1.84 (2.80)   0.229     Median [Min, Max]   1.00 [0, 25.0]   1.00 [0, 18.0]   1.00 [0, 25.0]     Emergency/urgent care utilization 12m	` /	` /	` /	\ /	0.449						
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$			21.0 [3.00, 30.0]	22.5 [1.00, 112]							
Median [Min, Max]         1.00 [0, 25.0]         1.00 [0, 18.0]         1.00 [0, 25.0]           Emergency/urgent care utilization 12m         Mean (SD)         0.521 (1.06)         0.669 (1.38)         0.603 (1.25)         0.33           Median [Min, Max]         0 [0, 6.00]         0 [0, 10.0]         0 [0, 10.0]         0         0.01.00           Times admitted to hospital 12m           Mean (SD)         0.188 (0.642)         0.462 (1.45)         0.340 (1.17)         0.0429           Median [Min, Max]         0 [0, 5.00]         0 [0, 10.0]         0 [0, 10.0]         0.0429           Median [Min, Max]         0 [0, 5.00]         0 [0, 10.0]         0 [0, 10.0]         0.0429           Median [Min, Max]         3.00 [0, 5.00]         0 [0, 10.0]         0 [0, 10.0]         0 [0, 10.0]           Total care utilization           Mean (SD)         4.57 (4.91)         5.71 (7.91)         5.20 (6.75)         0.156           Median [Min, Max]         3.00 [0, 32.0]         4.00 [0, 66.0]         3.00 [0, 66.0]         0.156           Gender           cis         102 (87.2%)         129 (89.0%)         231 (88.2%)         0.902           other         3 (2.6%)         3 (2.1%)         6 (2.3%)         0.902      <			1 0 1 (0 00)	1 0 1 (0 00)							
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$		` /	, ,	\ /	0.229						
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$			-	$1.00 \ [0, \ 25.0]$							
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$				0.000 (4.05)	0.00						
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	` /	` /	` /	` /	0.33						
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$			0 [0, 10.0]	0 [0, 10.0]							
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$		<del>-</del>	0.400 (4.45)	0.040 (4.45)	0.0400						
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$		` /			0.0429						
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$			0 [0, 10.0]	0 [0, 10.0]							
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$\begin{array}{c ccccccccccccccccccccccccccccccccccc$		` '	` /		0.156						
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	•	3.00 [0, 32.0]	4.00 [0, 00.0]	5.00 [0, 00.0]							
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$		100 (07 007)	100 (00 007)	091 (00 007)	0.000						
trans $12\ (10.3\%)$ $13\ (9.0\%)$ $25\ (9.5\%)$ Sexual orientation $16\ (13.7\%)$ $23\ (15.9\%)$ $39\ (14.9\%)$ $0.245$ gay $72\ (61.5\%)$ $84\ (57.9\%)$ $156\ (59.5\%)$ other $1\ (0.9\%)$ $4\ (2.8\%)$ $5\ (1.9\%)$ queer $9\ (7.7\%)$ $4\ (2.8\%)$ $13\ (5.0\%)$ straight $19\ (16.2\%)$ $30\ (20.7\%)$ $49\ (18.7\%)$ Race/ethnicitylatino $25\ (21.4\%)$ $36\ (24.8\%)$ $61\ (23.3\%)$ $0.0272$ non-latino black $54\ (46.2\%)$ $81\ (55.9\%)$ $135\ (51.5\%)$ $0.0272$ other/mixed $12\ (10.3\%)$ $15\ (10.3\%)$ $27\ (10.3\%)$ $0.0272$ white $26\ (22.2\%)$ $13\ (9.0\%)$ $39\ (14.9\%)$ Employment $0.469$ disabled $10\ (8.5\%)$ $11\ (7.6\%)$ $21\ (8.0\%)$ $0.469$ full-time $43\ (36.8\%)$ $43\ (29.7\%)$ $86\ (32.8\%)$ part-time $18\ (15.4\%)$ $35\ (24.1\%)$ $53\ (20.2\%)$ student $6\ (5.1\%)$ $8\ (5.5\%)$ $14\ (5.3\%)$		,	,	,	0.902						
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$		,	, ,	,							
$\begin{array}{cccccccccccccccccccccccccccccccccccc$		12 (10.370)	13 (9.070)	20 (9.070)							
$\begin{array}{cccccccccccccccccccccccccccccccccccc$		16 (12 7%)	23 (15 0%)	30 (14 0%)	0.245						
$\begin{array}{cccccccccccccccccccccccccccccccccccc$		,		,	0.249						
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$\begin{array}{cccccccccccccccccccccccccccccccccccc$	•	25 (21.4%)	36 (24.8%)	61 (23.3%)	0.0272						
$\begin{array}{cccccccccccccccccccccccccccccccccccc$				, ,	0.02.1						
white $26 (22.2\%)$ $13 (9.0\%)$ $39 (14.9\%)$ Employment  disabled $10 (8.5\%)$ $11 (7.6\%)$ $21 (8.0\%)$ $0.469$ full-time $43 (36.8\%)$ $43 (29.7\%)$ $86 (32.8\%)$ part-time $18 (15.4\%)$ $35 (24.1\%)$ $53 (20.2\%)$ student $6 (5.1\%)$ $8 (5.5\%)$ $14 (5.3\%)$	other/mixed	\ /	\ /								
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	•	, ,	,								
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	Employment										
$\begin{array}{llllllllllllllllllllllllllllllllllll$		10~(8.5%)	$11 \ (7.6\%)$	21~(8.0%)	0.469						
student $6 (5.1\%)$ $8 (5.5\%)$ $14 (5.3\%)$	full-time	, ,	, ,								
	_		,	,							
unemployed 40 (34.2%) 48 (33.1%) 88 (33.6%)		, ,	'	'							
	unemployed	40 (34.2%)	48 (33.1%)	88 (33.6%)							

### Regressions

```
# Viral suppression
mod = glm(ViralSupp ~ CAREHV06.12m + stigmasum_6m + stigmasum_baseline,
         family = binomial(), data = d)
summary(mod)
##
## Call:
## glm(formula = ViralSupp ~ CAREHV06.12m + stigmasum_6m + stigmasum_baseline,
##
      family = binomial(), data = d)
##
## Deviance Residuals:
     Min
                             3Q
                                    Max
           1Q Median
## -1.285 -1.110 -0.935 1.213
                                  1.791
##
## Coefficients:
##
                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)
                      0.575762 0.579074 0.994 0.3201
## CAREHVO6.12m
                     -0.120155
                               0.061514 -1.953
                                                 0.0508 .
## stigmasum_6m
                     -0.017362
                               0.025061 -0.693
                                                   0.4885
                                0.023462 -0.204
                                                  0.8381
## stigmasum_baseline -0.004793
## Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' 1
## (Dispersion parameter for binomial family taken to be 1)
##
      Null deviance: 360.21 on 261 degrees of freedom
##
## Residual deviance: 352.80 on 258 degrees of freedom
## AIC: 360.8
##
## Number of Fisher Scoring iterations: 5
# clinical utilization
mod = glm(CAREHV06.12m ~ stigmasum_6m + stigmasum_baseline,
         family = poisson(), data = d)
summary(mod)
##
## Call:
  glm(formula = CAREHV06.12m ~ stigmasum_6m + stigmasum_baseline,
##
      family = poisson(), data = d)
##
## Deviance Residuals:
##
                    Median
      Min
                1Q
                                 3Q
                                         Max
## -3.1616 -1.2074 -0.4917 0.1385 14.1171
##
## Coefficients:
##
                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)
                     0.007874 5.995 2.04e-09 ***
## stigmasum_6m
                     0.047206
```

```
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## (Dispersion parameter for poisson family taken to be 1)
##
      Null deviance: 878.17 on 261 degrees of freedom
## Residual deviance: 832.07 on 259 degrees of freedom
## AIC: 1416.5
## Number of Fisher Scoring iterations: 6
# stigma
mod = glm(stigmasum_6m ~ stigmasum_baseline,
         family = gaussian(), data = d)
summary(mod)
##
## Call:
## glm(formula = stigmasum_6m ~ stigmasum_baseline, family = gaussian(),
      data = d
##
## Deviance Residuals:
       Min
             1Q
                      Median
                                   3Q
                                            Max
## -21.4043 -2.8784 -0.1628
                                3.1270
                                        16.5546
##
## Coefficients:
                    Estimate Std. Error t value Pr(>|t|)
                    10.43823
                              1.24650
                                       8.374 3.49e-15 ***
## (Intercept)
## stigmasum baseline 0.52415
                               0.04749 11.038 < 2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## (Dispersion parameter for gaussian family taken to be 26.11461)
##
      Null deviance: 9971.4 on 261 degrees of freedom
## Residual deviance: 6789.8 on 260 degrees of freedom
## AIC: 1602.3
## Number of Fisher Scoring iterations: 2
```

#### SEM

The DAG we are interested in is

```
}')
plot(g1)
```

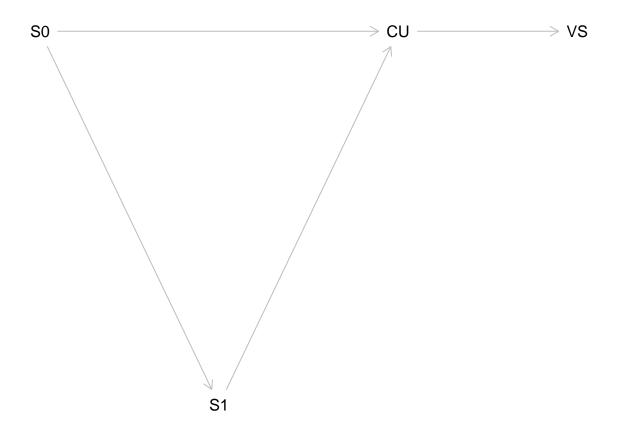
$$S0 \longrightarrow S1 \longrightarrow CU \longrightarrow VS$$

Let's fit using piecewiseSEM and see how well this models the data.

```
##
## Structural Equation Model of sem_g1
##
## Call:
## ViralSupp ~ CAREHV06.12m
## CAREHV06.12m ~ stigmasum_6m
## stigmasum_6m ~ stigmasum_baseline
##
```

```
##
       AIC
                BIC
   57.926
             82.904
##
##
##
##
  Tests of directed separation:
##
                               Independ.Claim Test.Type DF Crit.Value P.Value
##
##
     CAREHVO6.12m ~ stigmasum_baseline + ...
                                                   coef 259
                                                                -6.0681 0.0000 ***
        ViralSupp ~ stigmasum_baseline + ...
##
                                                   coef 259
                                                                -0.7423
                                                                         0.4579
##
              ViralSupp ~ stigmasum_6m + ...
                                                   coef 258
                                                                -0.6928 0.4885
##
  Global goodness-of-fit:
##
##
     Fisher's C = 43.926 with P-value = 0 and on 6 degrees of freedom
##
##
## ---
  Coefficients:
##
##
##
         Response
                            Predictor Estimate Std.Error DF Crit.Value P.Value
##
        ViralSupp
                         CAREHV06.12m -0.1185
                                                  0.0607 260
                                                                 -1.9534 0.0508
##
     CAREHVO6.12m
                         stigmasum_6m
                                        0.0195
                                                  0.0064 260
                                                                  3.0483 0.0023
##
     stigmasum_6m stigmasum_baseline
                                        0.5242
                                                  0.0475 260
                                                                 11.0377 0.0000
##
     Std.Estimate
          -0.2769
##
##
##
           0.5649 ***
##
     Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05
##
##
##
##
  Individual R-squared:
##
##
         Response
                      method R.squared
##
        ViralSupp nagelkerke
                                   0.03
##
     CAREHVO6.12m nagelkerke
                                   0.03
##
     stigmasum_6m
                                   0.32
                        none
```

Goodness of fit p-value is 0, which suggests DAG g1 is not a good fit for the data. The independence claim that seems to be causing the issue is baseline stigma and care utilization. Let's try fitting a model that includes that path, i.e. following DAG g2.



##

##

##

## ##

##

## ## ---

## Call: ## Vir:

AIC

18.995

ViralSupp ~ CAREHV06.12m

BIC

47.542

## Tests of directed separation:

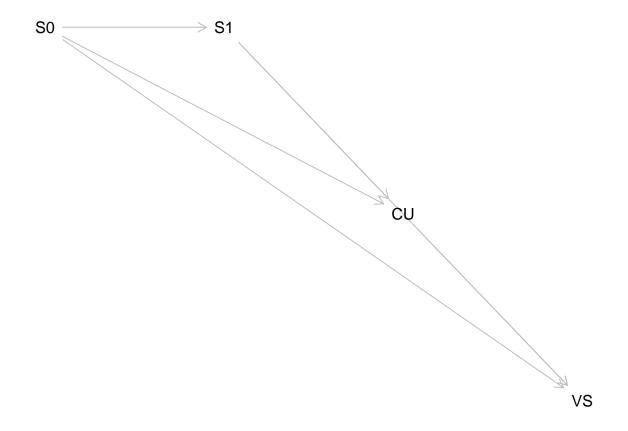
stigmasum\_6m ~ stigmasum\_baseline

CAREHVO6.12m ~ stigmasum\_6m + stigmasum\_baseline

```
##
##
                           Independ.Claim Test.Type DF Crit.Value P.Value
##
     ViralSupp ~ stigmasum baseline + ...
                                               coef 259
                                                            -0.7423 0.4579
           ViralSupp ~ stigmasum_6m + ...
                                                            -0.6928 0.4885
##
                                                coef 258
##
## Global goodness-of-fit:
##
     Fisher's C = 2.995 with P-value = 0.559 and on 4 degrees of freedom
##
##
##
##
  Coefficients:
##
                           Predictor Estimate Std.Error DF Crit.Value P.Value
##
         Response
                                                                -1.9534 0.0508
        ViralSupp
                        CAREHV06.12m -0.1185
##
                                                  0.0607 260
##
     CAREHV06.12m
                        stigmasum_6m
                                        0.0472
                                                  0.0079 259
                                                                 5.9950 0.0000
##
     CAREHVO6.12m stigmasum_baseline
                                      -0.0445
                                                  0.0073 259
                                                                -6.0681
                                                                          0.0000
##
     stigmasum_6m stigmasum_baseline
                                                  0.0475 260
                                                                11.0377 0.0000
                                        0.5242
##
     Std.Estimate
##
          -0.2769
##
##
##
           0.5649 ***
##
##
     Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05
##
##
##
  Individual R-squared:
##
##
         Response
                      method R.squared
##
        ViralSupp nagelkerke
                                   0.03
##
     CAREHVO6.12m nagelkerke
                                   0.16
##
     stigmasum_6m
                        none
                                   0.32
```

The model now fits the data according to the goodness of fit statistic.

Finally, we should compare to the fully saturated model given by DAG g3.



```
##
## Structural Equation Model of sem_g3
##
## Call:
     ViralSupp ~ CAREHV06.12m + stigmasum_6m + stigmasum_baseline
##
     CAREHVO6.12m ~ stigmasum_6m + stigmasum_baseline
##
     stigmasum_6m ~ stigmasum_baseline
##
##
##
       AIC
                BIC
    20.000
##
             55.683
##
##
## Tests of directed separation:
##
## No independence claims present. Tests of directed separation not possible.
```

```
##
## Global goodness-of-fit:
##
##
    Fisher's C = 0 with P-value = 1 and on 0 degrees of freedom
##
##
  Coefficients:
##
##
##
         Response
                            Predictor Estimate Std.Error DF Crit.Value P.Value
##
        ViralSupp
                         CAREHVO6.12m
                                       -0.1202
                                                   0.0615 258
                                                                  -1.9533 0.0508
##
        ViralSupp
                         stigmasum_6m
                                       -0.0174
                                                   0.0251 258
                                                                  -0.6928
                                                                           0.4885
##
        ViralSupp stigmasum_baseline
                                        -0.0048
                                                   0.0235 258
                                                                  -0.2043
                                                                           0.8381
##
     CAREHVO6.12m
                         stigmasum_6m
                                        0.0472
                                                   0.0079 259
                                                                   5.9950
                                                                           0.0000
                                                                           0.0000
##
     CAREHVO6.12m stigmasum_baseline
                                        -0.0445
                                                   0.0073 259
                                                                  -6.0681
##
     stigmasum_6m stigmasum_baseline
                                        0.5242
                                                   0.0475 260
                                                                  11.0377
                                                                           0.0000
##
     Std.Estimate
##
          -0.2796
##
          -0.0566
##
          -0.0168
##
##
##
           0.5649 ***
##
     Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05
##
##
##
   Individual R-squared:
##
##
##
                      method R.squared
         Response
##
        ViralSupp nagelkerke
                                   0.04
##
     CAREHVO6.12m nagelkerke
                                   0.16
##
     stigmasum_6m
                         none
                                   0.32
```

This model is fully specified so no independence claims are tested. Looking at the regression p-values, it does suggest we should get rid of the arrows from stigma to viral suppression. This is exactly what we did in DAG g2.

Let's compare all of our model

```
anova(sem_g1, sem_g2, sem_g3)
## Chi-square Difference Test
##
##
           AIC
                  BIC Fisher.C Fisher.C.Diff DF.diff P.value
##
         57.926 82.904
                          43.926
##
    vs 2 18.995 47.542
                          2.995
                                        40.931
                                                     2
                                                              () ***
##
    vs 3 20.000 55.683
                           0.000
                                        43.926
                                                     6
## ---
## Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05
```

The fully specified model will always fit better by goodness of fit, but look at the AIC/BIC. Model g2 has lower AIC/BIC which suggests it is the better model.

#### Conclusions

For these basic models, it appears that the effect of stigma on viral suppression is primarily mediated through clinical utilization. The effect of baseline stigma on clinical utilization is not fully mediated by 6 month stigma and should be included as a predictor.

Baseline stigma seems to decrease clinical utilization, but 6 month stigma seems to increase it. This might suggest there is some selection bias here. Maybe people who show up to 6 month visits are more likely to go get care? Viral suppression also has a negative relationship with clinical utilization. This is not what I was expecting.

Future analysis should introduce other variables such as demographics in order to address possible confounders of the effects of interest. Another thing to do is to address the possible selection bias induced by only including those with complete data.