Material de Apoyo Docente

Universidad de Talca Facultad de Psicología

MODELOS LONGITUDINALES CON VARIABLES LATENTES PARA LA INVESTIGACIÓN EN PSICOLOGÍA

Modelos de ecuaciones estructurales (SEM) Fabiola Gómez 01 de octubre 2024

Paquetes a utilizar en esta sesión.

- a. lavaan: Un paquete para la estimación de modelos de variables latentes como CFA, además permite realizar path analysis, modelación de ecuaciones estructurales, curvas de crecimiento latente, etc.
- b. psych: Paquete que incluye funciones útiles para la investigación en psicología.
- c. MVN: Paquete que usaremos para evaluar normalidad multivariada.

Durante esta sesión trabajaremos con una base de datos que contiene información de 543 jóvenes mayores de 18 años. Estos datos contienen información sobre el sexo de los participantes (hombre= 0 y mujer= 1), edad (años cumplidos) y nivel de religiosidad. Además contiene los resultados en las siguientes escalas: Justificación del Sistema (3 ítems) y Homonegatividad Moderna (7 ítems). Todas las escalas están medidas con una escala likert de cinco puntos.

Los investigadores están interesados en evaluar el efecto que tiene la religiososdad y la justificación del sistema sobre los niveles de homonegatividad moderna. Adicionalmente, quieren evaluar si este modelo es invariante entre hombres y mujeres.

Ellos hipotetizan que estas dos variables tendrán un efecto positivo y significativo sobre los niveles de homonegatividad hacia los hombres gays. Además, se espera que el nivel de medición de esta escala sea invariante entre hombres y mujeres.

Cargar la base de datos y exploración de las variables

"sexo"

"si 03"

##

##

[1] "CASE"

[6] "sj 02"

```
setwd("/Users/fa/Dropbox/Docencia/2024/Doctorado/Optativo Doctorado UTalca/Clases/Clase
base<- read.csv("sem.csv", header = T, sep = ";", na= -9)
names(base) # nombre de las variables</pre>
```

"edad"

"homo1 gay"

"religiosidad" "sj_01"
"homo2 gay" "homo3 gay"

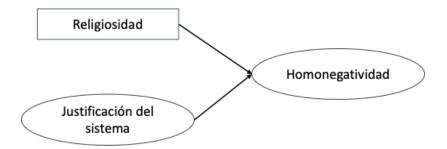
```
## [11] "homo4 gay" "homo5 gay" "homo6 gay" "homo7 gay"
str(base) # estructura de la base de datos y variables
## 'data.frame': 543 obs. of 14 variables:
## $ CASE
                : int 524 34 564 576 540 77 115 272 294 457 ...
## $ sexo
                 : int 1 1 1 1 1 1 0 1 1 1 ...
## $ edad
                 : int 24 24 24 23 23 22 22 22 22 ...
## $ religiosidad: int 5 1 6 7 4 3 1 4 2 5 ...
                 : int 2 1 2 3 3 3 3 1 2 2 ...
##
   $ sj 01
##
   $ sj 02
                : int 2 1 3 2 2 2 2 3 1 2 ...
                : int 1 1 3 4 4 2 2 2 1 3 ...
## $ sj 03
## $ homo1_gay
                 : int 2 3 3 1 1 3 2 3 1 2 ...
## $ homo2 gay : int 3 2 2 1 1 2 1 1 1 2 ...
## $ homo3 gay : int 2 2 4 2 5 2 1 3 1 4 ...
## $ homo4_gay : int 3 2 4 4 3 2 1 1 1 3 ...
## $ homo5 gay : int 3 2 3 2 1 2 1 2 1 3 ...
## $ homo6 gay : int 4 2 3 1 1 3 2 2 1 2 ...
## $ homo7 gay : int 3 2 4 1 1 3 1 1 1 3 ...
library(psych)
describe(base[3:14]) # descriptivos
##
                               sd median trimmed mad min max range skew
                     n mean
## edad
                  1 540 21.33 2.12
                                      21
                                           21.28 2.97
                                                      18
                                                          25
                                                                7 0.17
                  2 541 3.17 1.82
                                                           7
                                                                6 0.34
## religiosidad
                                       3
                                           3.03 2.97
                                                       1
## sj 01
                  3 543 2.15 0.87
                                       2
                                           2.13 1.48 1
                                                           5
                                                                4 0.26
                  4 543
                       2.23 0.97
                                       2
## sj 02
                                           2.15 1.48 1
                                                           5
                                                                4 0.62
## sj 03
                  5 541
                        1.90 0.94
                                       2 1.77 1.48 1
                                                           5
                                                                4 0.97
## homo1 gay
                  6 541
                        1.99 1.07
                                       2
                                         1.85 1.48 1
                                                           5
                                                                4 0.78
                 7 541
                                       1
                                                           5
## homo2 gay
                        1.53 0.99
                                           1.29 0.00
                                                      1
                                                                4 2.16
## homo3 gay
                 8 540
                        2.45 1.30
                                       2
                                           2.34 1.48 1 5
                                                               4 0.41
## homo4 gay
                 9 541
                        2.09 1.19
                                       2
                                         1.92 1.48 1
                                                           5
                                                                4 0.89
## homo5_gay
                 10 540
                        2.24 1.27
                                       2
                                           2.09 1.48 1 5
                                                                4 0.72
                                       2
                        2.15 1.23
                                           1.99 1.48 1 5
                                                                4 0.77
## homo6_gay
                 11 540
                 12 541
                        2.14 1.26
                                       2
                                          1.97 1.48 1
                                                           5
                                                                4 0.76
## homo7 gay
##
               kurtosis
                         se
## edad
                  -1.030.09
## religiosidad
                  -1.07 0.08
## sj 01
                  -0.480.04
## sj 02
                  -0.230.04
                 0.39 0.04
## sj 03
```

```
## homo1 gay
                   -0.29 0.05
## homo2 gay
                   4.17 0.04
## homo3 gay
                   -1.01 0.06
## homo4 gay
                   -0.23 0.05
## homo5 gay
                   -0.63 0.05
## homo6 gay
                   -0.40 0.05
## homo7 gay
                   -0.59 0.05
library(MVN)
mvn(base[4:14], desc = F)
## $multivariateNormality
##
              Test
                        HZ p value MVN
## 1 Henze-Zirkler 2.891059
                                  O NO
##
## $univariateNormality
##
                  Test
                          Variable Statistic p value Normality
## 1 Anderson-Darling religiosidad
                                      17.9995 < 0.001
                                                           NO
## 2 Anderson-Darling
                         sj 01
                                      31.3253 < 0.001
                                                           NO
## 3 Anderson-Darling
                          sj 02
                                      30.5472
                                              <0.001
                                                           NO
## 4 Anderson-Darling
                          sj_03
                                      38.1744
                                              <0.001
                                                           NO
## 5 Anderson-Darling homo1 gay
                                      37.5046
                                              <0.001
                                                          NO
## 6 Anderson-Darling homo2_gay
                                      88.9063
                                              <0.001
                                                           NO
## 7 Anderson-Darling homo3 gay
                                      23.4981
                                              <0.001
                                                           NO
## 8 Anderson-Darling homo4_gay
                                      35.4575
                                              <0.001
                                                           NO
## 9 Anderson-Darling homo5 gay
                                      31.0099
                                              <0.001
                                                           NO
## 10 Anderson-Darling homo6 gay
                                      33.5500 < 0.001
                                                           NO
## 11 Anderson-Darling homo7 gay
                                      37.5804
                                              <0.001
                                                           NO
```

Principales operadores usados en SEM

Lavaan	Mplus	Significado	Ejemplo
~	on	Predicción, se utiliza para la regresión de resultados observados a predictores observados	y ~ x y ON x
=~	by	Indicador, se utiliza para la variable latente a indicador observado en modelos de medición de análisis factorial	f=~ q+r+s f BY q+r+s
~~	with	Covarianza	x ~~ x ; x ~~ y x WITH x; x WITH y
~1	[]	Intercepto o media (estima la media de)	x ~ 1 [x]

Especificación del modelo



Estimación y evaluación de ajuste del modelo estructural

```
library(lavaan)
## This is lavaan 0.6-18
## lavaan is FREE software! Please report any bugs.
##
## Attaching package: 'lavaan'
## The following object is masked from 'package:psych':
##
##
       cor2cov
mod1<- 'justif=~ sj 01 + sj 02 + sj 03
        homoneg=~ homo1_gay + homo2_gay + homo3_gay +
                  homo4_gay + homo5_gay + homo6_gay +
                  homo7_gay
       homoneg~ justif + religiosidad
\#\# std.lv= T, sample.mean = T, meanstructure=T
fit1<- sem(mod1, estimator = "MLR",
            data=base)
## std.lv = T, sample.mean = T
summary(fit1, fit.measures = T, standardized = T, rsquare = T)
## lavaan 0.6-18 ended normally after 33 iterations
##
                                                        ML
## Estimator
```

##	Optimization method Number of model parameters	NLMINB 22		
##	wamber of moder parameters	22		
##		Used	Total	
##	Number of observations	534	543	
##	Number of observations	334	040	
	Model Test User Model:			
##	model lest osel model.	Standard	Scaled	
##	Test Statistic	181.222		
##	Degrees of freedom	43	43	
##		0.000	0.000	
	P-value (Chi-square)	0.000	1.119	
##	Scaling correction factor		1.119	
##	Yuan-Bentler correction (Mplus variant)			
	Model Test Baseline Model:			
##	Hodel lest baseline Model.			
##	Test statistic	2394.616	1894.431	
##	Degrees of freedom	55	55	
##	P-value	0.000	0.000	
##	Scaling correction factor	0.000	1.264	
##	boaring outlooding ractor		1.201	
	User Model versus Baseline Model:			
##				
##	Comparative Fit Index (CFI)	0.941	0.935	
##	Tucker-Lewis Index (TLI)	0.924		
##	- 40-10-1	0.022	0.02.	
##	Robust Comparative Fit Index (CFI)		0.943	
##	Robust Tucker-Lewis Index (TLI)		0.927	
##	,			
	Loglikelihood and Information Criteria:			
##				
##	Loglikelihood user model (HO)	-6934.841	-6934.841	
##	Scaling correction factor		1.451	
##	for the MLR correction			
##	Loglikelihood unrestricted model (H1)	-6844.230	-6844.230	
##	Scaling correction factor		1.231	
##	for the MLR correction			
##				
##	Akaike (AIC)	13913.681	13913.681	
##	Bayesian (BIC)	14007.850		
##	Sample-size adjusted Bayesian (SABIC)	13938.015	13938.015	
##	1			

```
## Root Mean Square Error of Approximation:
##
##
    RMSEA
                                                  0.078
                                                              0.072
    90 Percent confidence interval - lower
##
                                                  0.066
                                                              0.061
##
    90 Percent confidence interval - upper
                                                  0.089
                                                              0.083
##
    P-value H O: RMSEA <= 0.050
                                                  0.000
                                                              0.001
    P-value H 0: RMSEA >= 0.080
##
                                                  0.381
                                                              0.125
##
    Robust RMSEA
##
                                                              0.076
##
    90 Percent confidence interval - lower
                                                              0.064
##
    90 Percent confidence interval - upper
                                                              0.089
##
    P-value H O: Robust RMSEA <= 0.050
                                                              0.000
##
    P-value H O: Robust RMSEA >= 0.080
                                                              0.319
##
## Standardized Root Mean Square Residual:
##
##
    SRMR
                                                  0.063
                                                              0.063
##
## Parameter Estimates:
##
##
    Standard errors
                                                Sandwich
##
    Information bread
                                                Observed
    Observed information based on
##
                                                Hessian
##
## Latent Variables:
##
                     Estimate Std.Err z-value P(>|z|) Std.lv Std.all
##
    justif =~
                                                           0.486
##
     sj 01
                                                                    0.562
                        1.000
##
      sj_02
                        1.355
                                 0.187
                                         7.258
                                                  0.000
                                                           0.659
                                                                    0.677
                                                  0.000
                                                           0.533
##
      sj 03
                        1.097
                                 0.168
                                          6.540
                                                                    0.571
##
    homoneg =~
##
      homo1 gay
                        1.000
                                                           0.775
                                                                    0.733
##
      homo2_gay
                        0.476
                                0.071
                                        6.734
                                                  0.000
                                                           0.369
                                                                    0.389
##
      homo3 gay
                                0.073 17.980
                        1.313
                                                  0.000
                                                          1.017
                                                                    0.790
##
      homo4 gay
                        1.145
                                0.086
                                        13.362
                                                  0.000
                                                           0.887
                                                                    0.745
##
      homo5 gay
                        1.452
                                0.073 19.775
                                                  0.000 1.125
                                                                   0.894
                                                           0.761
##
      homo6_gay
                                0.078 12.613
                                                  0.000
                                                                    0.621
                        0.982
##
                                                  0.000
      homo7_gay
                        1.402
                                 0.083
                                        16.890
                                                           1.086
                                                                    0.869
##
## Regressions:
##
                     Estimate Std.Err z-value P(>|z|)
                                                          Std.lv Std.all
##
    homoneg ~
```

##	justif	0.262	0.105	2.488	0.013	0.165	0.165	
##	religiosidad	0.100	0.020	4.901	0.000	0.129	0.234	
##								
##	Variances:							
##		Estimate	Std.Err	z-value	P(> z)	Std.lv	Std.all	
##	.sj_01	0.513	0.045	11.468	0.000	0.513	0.684	
##	.sj_02	0.513	0.071	7.265	0.000	0.513	0.542	
##	.sj_03	0.589	0.063	9.397	0.000	0.589	0.674	
##	.homo1_gay	0.517	0.044	11.854	0.000	0.517	0.463	
##	$. {\tt homo2_gay}$	0.760	0.101	7.520	0.000	0.760	0.848	
##	.homo3_gay	0.623	0.067	9.320	0.000	0.623	0.376	
##	$. {\tt homo4_gay}$	0.631	0.069	9.141	0.000	0.631	0.445	
##	.homo5_gay	0.319	0.040	7.895	0.000	0.319	0.201	
##	.homo6_gay	0.921	0.070	13.120	0.000	0.921	0.614	
##	.homo7_gay	0.382	0.045	8.457	0.000	0.382	0.245	
##	justif	0.236	0.048	4.951	0.000	1.000	1.000	
##	.homoneg	0.551	0.064	8.549	0.000	0.918	0.918	
##								
##	R-Square:							
##		Estimate						
##	sj_01	0.316						
##	sj_02	0.458						
##	sj_03	0.326						
##	homo1_gay	0.537						
##	homo2_gay	0.152						
##	homo3_gay	0.624						
##	homo4_gay	0.555						
##	homo5_gay	0.799						
##	homo6_gay	0.386						
##	homo7_gay	0.755						
##	homoneg	0.082						

Análisis Multigrupo

```
config <- sem(mod1, data=base, std.lv= F,</pre>
              estimator = "MLR", meanstructure=T, sample.mean = T,
              group="sexo")
summary(config, fit.measures = T, standardized = T, rsquare = T)
## lavaan 0.6-18 ended normally after 65 iterations
##
##
     Estimator
                                                        ML
     Optimization method
                                                    NLMINB
##
     Number of model parameters
##
                                                         64
##
##
     Number of observations per group:
                                                      Used
                                                                  Total
##
                                                       347
                                                                    353
       0
##
                                                       187
                                                                    190
##
## Model Test User Model:
##
                                                  Standard
                                                                 Scaled
    Test Statistic
                                                   242.169
                                                                223.107
##
##
     Degrees of freedom
                                                         86
                                                                     86
     P-value (Chi-square)
                                                     0.000
                                                                  0.000
##
     Scaling correction factor
                                                                  1.085
      Yuan-Bentler correction (Mplus variant)
##
     Test statistic for each group:
##
##
      1
                                                   163.242
                                                                150.393
##
       0
                                                    78.926
                                                                 72.714
##
## Model Test Baseline Model:
##
    Test statistic
                                                  2424.359
                                                              1976.905
##
##
    Degrees of freedom
                                                       110
                                                                    110
##
     P-value
                                                     0.000
                                                                  0.000
##
     Scaling correction factor
                                                                  1.226
##
## User Model versus Baseline Model:
##
     Comparative Fit Index (CFI)
##
                                                     0.933
                                                                  0.927
##
    Tucker-Lewis Index (TLI)
                                                     0.914
                                                                  0.906
##
##
     Robust Comparative Fit Index (CFI)
                                                                  0.935
     Robust Tucker-Lewis Index (TLI)
##
                                                                  0.917
```

```
##
## Loglikelihood and Information Criteria:
##
    Loglikelihood user model (HO)
##
                                               -6872.257
                                                            -6872.257
##
    Scaling correction factor
                                                                1.286
##
         for the MLR correction
##
    Loglikelihood unrestricted model (H1) -6751.173
                                                            -6751.173
    Scaling correction factor
##
                                                                1.171
##
         for the MLR correction
##
    Akaike (AIC)
##
                                                13872.514
                                                            13872.514
##
    Bayesian (BIC)
                                                14146.460
                                                            14146.460
##
                                                13943.304
                                                            13943.304
     Sample-size adjusted Bayesian (SABIC)
##
## Root Mean Square Error of Approximation:
##
    RMSF.A
##
                                                    0.082
                                                                0.077
    90 Percent confidence interval - lower
##
                                                    0.070
                                                                0.065
##
    90 Percent confidence interval - upper
                                                    0.095
                                                                0.089
    P-value H O: RMSEA <= 0.050
##
                                                    0.000
                                                                0.000
     P-value H_0: RMSEA >= 0.080
                                                    0.642
##
                                                                0.365
##
##
    Robust RMSEA
                                                                0.081
##
    90 Percent confidence interval - lower
                                                                0.068
    90 Percent confidence interval - upper
##
                                                                0.094
##
     P-value H O: Robust RMSEA <= 0.050
                                                                0.000
##
     P-value H_0: Robust RMSEA >= 0.080
                                                                0.539
##
## Standardized Root Mean Square Residual:
##
##
     SRMR
                                                    0.064
                                                                0.064
##
## Parameter Estimates:
##
    Standard errors
                                                 Sandwich
##
   Information bread
##
                                                 Observed
##
    Observed information based on
                                                  Hessian
##
##
## Group 1 [1]:
##
## Latent Variables:
```

##		Estimate	Std.Err	z-value	P(> z)	Std.lv	Std.all	
##	justif =~							
##	sj_01	1.000				0.471	0.550	
##	sj_02	1.555	0.257	6.049	0.000	0.732	0.746	
##	sj_03	1.160	0.184	6.286	0.000	0.546	0.598	
##	homoneg =~							
##	homo1_gay	1.000				0.778	0.766	
##	homo2_gay	0.453	0.088	5.144	0.000	0.353	0.390	
##	homo3_gay	1.213	0.083	14.666	0.000	0.944	0.759	
##	homo4_gay	1.019	0.104	9.797	0.000	0.793	0.689	
##	homo5_gay	1.367	0.076	17.941	0.000	1.063	0.913	
##	homo6_gay	0.898	0.093	9.644	0.000	0.698	0.614	
##	homo7_gay	1.289	0.096	13.442	0.000	1.003	0.852	
##								
##	Regressions:							
##		Estimate	Std.Err	z-value	P(> z)	Std.lv	Std.all	
##	homoneg ~							
##	justif	0.122	0.125	0.979	0.327	0.074	0.074	
##	religiosidad	0.132	0.026	5.153	0.000	0.169	0.311	
##								
##	Intercepts:							
##		Estimate	Std.Err	z-value	P(> z)	Std.lv	Std.all	
##	.sj_01	2.210	0.046	48.160	0.000	2.210	2.585	
##	.sj_02	2.219	0.053	42.173	0.000	2.219	2.264	
##	.sj_03	1.839	0.049	37.532	0.000	1.839	2.015	
##	.homo1_gay	1.403	0.092	15.252	0.000	1.403	1.380	
##	.homo2_gay	1.235	0.061	20.246	0.000	1.235	1.368	
##	.homo3_gay	1.731	0.120	14.461	0.000	1.731	1.392	
##	.homo4_gay	1.515	0.099	15.310	0.000	1.515	1.316	
##	.homo5_gay	1.394	0.119	11.682	0.000	1.394	1.197	
##	.homo6_gay	1.604	0.091	17.564	0.000	1.604	1.411	
##	.homo7_gay	1.383	0.113	12.187	0.000	1.383	1.175	
##								
##	Variances:							
##		Estimate	Std.Err	z-value	P(> z)	Std.lv	Std.all	
##	.sj_01	0.510	0.051	9.929	0.000	0.510	0.697	
##	.sj_02	0.425	0.094	4.547	0.000	0.425	0.443	
##	.sj_03	0.535	0.060	8.900	0.000	0.535	0.642	
##	.homo1_gay	0.428	0.043	9.835	0.000	0.428	0.414	
##	.homo2_gay	0.691	0.125	5.550		0.691	0.848	
##	.homo3_gay	0.655	0.084	7.794	0.000	0.655	0.423	
	_0 7							

```
##
      .homo4 gay
                          0.697
                                    0.094
                                              7.405
                                                       0.000
                                                                 0.697
                                                                          0.526
##
      .homo5 gay
                          0.226
                                    0.038
                                              5.870
                                                       0.000
                                                                 0.226
                                                                          0.166
##
      .homo6_gay
                          0.805
                                    0.083
                                              9.746
                                                       0.000
                                                                 0.805
                                                                          0.623
      .homo7 gay
##
                          0.379
                                    0.057
                                              6.644
                                                       0.000
                                                                 0.379
                                                                          0.274
##
       justif
                          0.221
                                    0.056
                                              3.983
                                                       0.000
                                                                 1.000
                                                                           1.000
##
      .homoneg
                          0.543
                                    0.082
                                              6.646
                                                       0.000
                                                                 0.898
                                                                          0.898
##
## R-Square:
##
                       Estimate
##
       sj 01
                          0.303
##
                          0.557
       sj 02
##
       sj 03
                          0.358
##
       homo1_gay
                          0.586
##
       homo2_gay
                          0.152
##
       homo3 gay
                          0.577
##
       homo4_gay
                          0.474
##
       homo5 gay
                          0.834
##
       homo6 gay
                          0.377
##
       homo7_gay
                          0.726
##
       homoneg
                          0.102
##
##
## Group 2 [0]:
##
## Latent Variables:
##
                       Estimate
                                 Std.Err z-value P(>|z|)
                                                                Std.lv Std.all
##
     justif =~
##
                                                                 0.543
                                                                          0.622
       sj 01
                          1.000
##
       sj_02
                          0.946
                                    0.242
                                              3.911
                                                       0.000
                                                                 0.514
                                                                          0.535
##
       sj 03
                          0.927
                                    0.348
                                              2.662
                                                       0.008
                                                                 0.504
                                                                          0.524
##
     homoneg =~
##
       homo1 gay
                          1.000
                                                                 0.710
                                                                          0.655
##
       homo2 gay
                          0.515
                                    0.137
                                              3.769
                                                       0.000
                                                                 0.365
                                                                          0.362
##
       homo3 gay
                                    0.147
                                              9.979
                                                       0.000
                                                                 1.042
                                                                          0.805
                          1.468
##
       homo4 gay
                                    0.165
                                              8.479
                                                                 0.994
                                                                          0.812
                          1.400
                                                       0.000
##
       homo5 gay
                          1.566
                                    0.158
                                              9.908
                                                       0.000
                                                                 1.111
                                                                          0.850
##
       homo6_gay
                          1.085
                                    0.149
                                              7.307
                                                       0.000
                                                                 0.770
                                                                          0.582
##
                                    0.174
                                              9.398
                                                       0.000
                                                                 1.161
                                                                          0.889
       homo7_gay
                          1.636
##
## Regressions:
##
                                  Std.Err z-value P(>|z|)
                       Estimate
                                                                Std.lv
                                                                        Std.all
##
     homoneg ~
```

##	justif	0.386	0.175	2.210	0.027	0.296	0.296	
##	religiosidad	0.114	0.033	3.494	0.000	0.161	0.268	
##								
##	Intercepts:			_	- ()			
##		Estimate	Std.Err	z-value	P(> z)	Std.lv	Std.all	
##	.sj_01	2.037	0.064	31.890	0.000	2.037	2.332	
##	.sj_02	2.225	0.070	31.668	0.000	2.225	2.316	
##	.sj_03	2.027	0.070	28.826	0.000	2.027	2.108	
##	.homo1_gay	1.932	0.111	17.440	0.000	1.932	1.784	
##	.homo2_gay	1.478	0.088	16.757	0.000	1.478	1.464	
##	.homo3_gay	2.355	0.161	14.646	0.000	2.355	1.821	
##	$. {\tt homo4_gay}$	1.900	0.143	13.262	0.000	1.900	1.553	
##	.homo5_gay	2.191	0.158	13.860	0.000	2.191	1.675	
##	.homo6_gay	2.120	0.125	16.991	0.000	2.120	1.603	
##	.homo7_gay	1.971	0.162	12.195	0.000	1.971	1.510	
##								
	Variances:							
##		Estimate	Std.Err	z-value	P(> z)	Std.lv	Std.all	
##	.sj_01	0.468	0.104	4.520	0.000	0.468	0.613	
##	.sj_02	0.659	0.090	7.314	0.000	0.659	0.714	
##	.sj_03	0.671	0.139	4.808	0.000	0.671	0.725	
##	.homo1_gay	0.669	0.089	7.522	0.000	0.669	0.571	
##	.homo2_gay	0.885	0.169	5.228	0.000	0.885	0.869	
##	.homo3_gay	0.588	0.117	5.043	0.000	0.588	0.351	
##	$. {\tt homo4_gay}$	0.509	0.083	6.147	0.000	0.509	0.340	
##	.homo5_gay	0.476	0.089	5.316	0.000	0.476	0.278	
##	.homo6_gay	1.155	0.129	8.936	0.000	1.155	0.661	
##	.homo7_gay	0.357	0.071	5.067	0.000	0.357	0.210	
##	justif	0.295	0.110	2.681	0.007	1.000	1.000	
##	.homoneg	0.423	0.093	4.545	0.000	0.841	0.841	
##								
	R-Square:							
##		Estimate						
##	sj_01	0.387						
##	sj_02	0.286						
##	sj_03	0.275						
##	homo1_gay	0.429						
##	homo2_gay	0.131						
##	homo3_gay	0.649						
##	homo4_gay	0.660						
##	homo5_gay	0.722						
##	homo6_gay	0.339						

```
##
      homo7 gay
                        0.790
##
                        0.159
      homoneg
debil <- sem(mod1, data=base, std.lv= T, estimator = "MLR",
            group="sexo",
            group.equal="loadings")
fuerte <- sem(mod1, data=base, std.lv= T, estimator = "MLR",
             group="sexo",
             group.equal= c("loadings", "intercepts"))
estricta <- sem(mod1, data=base, std.lv= T, estimator = "MLR",
                 group="sexo",
                 group.equal= c("loadings", "intercepts", "residuals"))
## Comparación de ajuste de los modelos
anova(config, debil, fuerte, estricta)
##
## Scaled Chi-Squared Difference Test (method = "satorra.bentler.2001")
## lavaan->lavTestLRT():
     lavaan NOTE: The "Chisq" column contains standard test statistics, not the
     robust test that should be reported per model. A robust difference test is
##
     a function of two standard (not robust) statistics.
##
##
            Df AIC BIC Chisq Chisq diff Df diff Pr(>Chisq)
            86 13872 14146 242.17
## config
           94 13867 14107 252.68
## debil
                                    8.9425
                                                  8
                                                      0.347171
## fuerte 102 13870 14076 272.10
                                    19.3107
                                                  8 0.013284 *
## estricta 112 13892 14054 313.24 25.0882
                                                 10 0.005181 **
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
```