

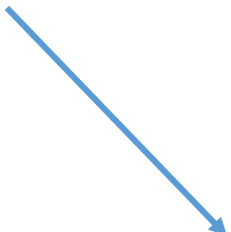
# Phenotypic factor analysis: Small practical

Big 5 dimensions N & E in males and females

Script: fa2efa

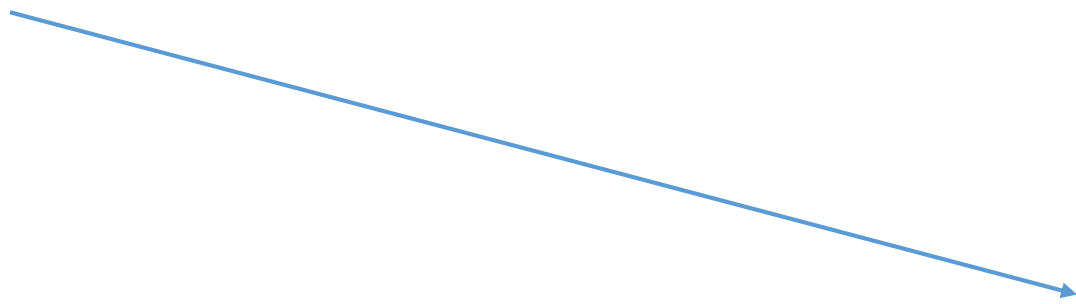
- Efa using R (factanal)

```
# read the data
datf=read.table('rdataf') # read the female data
datm=read.table('rdatam') # read the male data
datb5=rbind(datf,datm) # into 1 data matrix
datb5[,1]=datb5[,1]-1 # recode sex from 1->0(m) and 2->1(f)
# assign variable names
colnames(datb5)=c('sex',
'n1', 'n2', 'n3', 'n4', 'n5', 'n6',
'e1', 'e2', 'e3', 'e4', 'e5', 'e6',
'o1', 'o2', 'o3', 'o4', 'o5', 'o6',
'a1', 'a2', 'a3', 'a4', 'a5', 'a6',
'c1', 'c2', 'c3', 'c4', 'c5', 'c6')
```



**Mean =  $b_0 + b_1 * \text{sex}$**   
**Sex=0 -> mean= $b_0$**   
**Sex=1 -> mean= $b_0 + b_1$**   
**So  $b_1$ =sex difference**

```
# select the variables of interest
isel=c(1:13) # selection of variables sex, n1-n6, e1-e6
datb2=datb5[,isel]
sex=datb5[,1] # sex in a separate vector for convenience
table(sex)
```



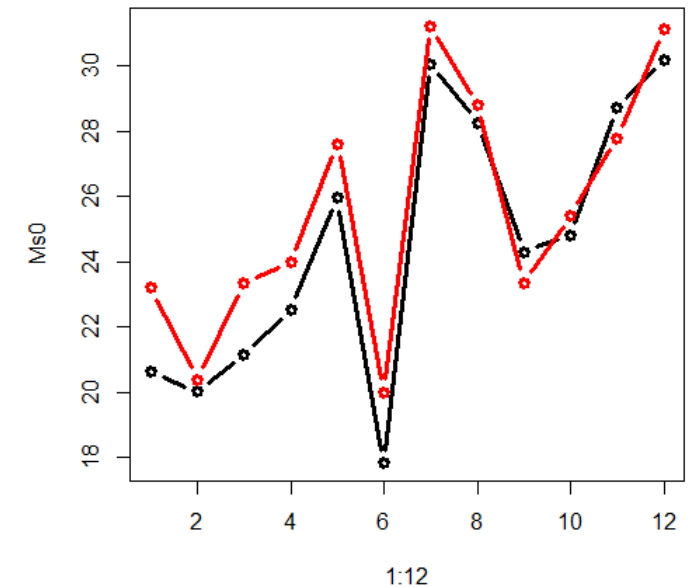
sex	
0	1
139	361

```

Ss0=cov(datb2[sex==0,2:13])      # calculate the covariance matrix in males
Ss1=cov(datb2[sex==1,2:13])      # calculate the covariance matrix in females
Ms0=apply(datb2[sex==0,2:13],2,mean) # males means
Ms1=apply(datb2[sex==1,2:13],2,mean) # females means

#
mi=min(Ms0,Ms1)
ma=max(Ms0,Ms1)
plot(1:12,Ms0,type='b',col=1,lwd=3,ylim=c(mi,ma))
lines(1:12,Ms1,type='b',col=2,lwd=3,ylim=c(mi,ma))

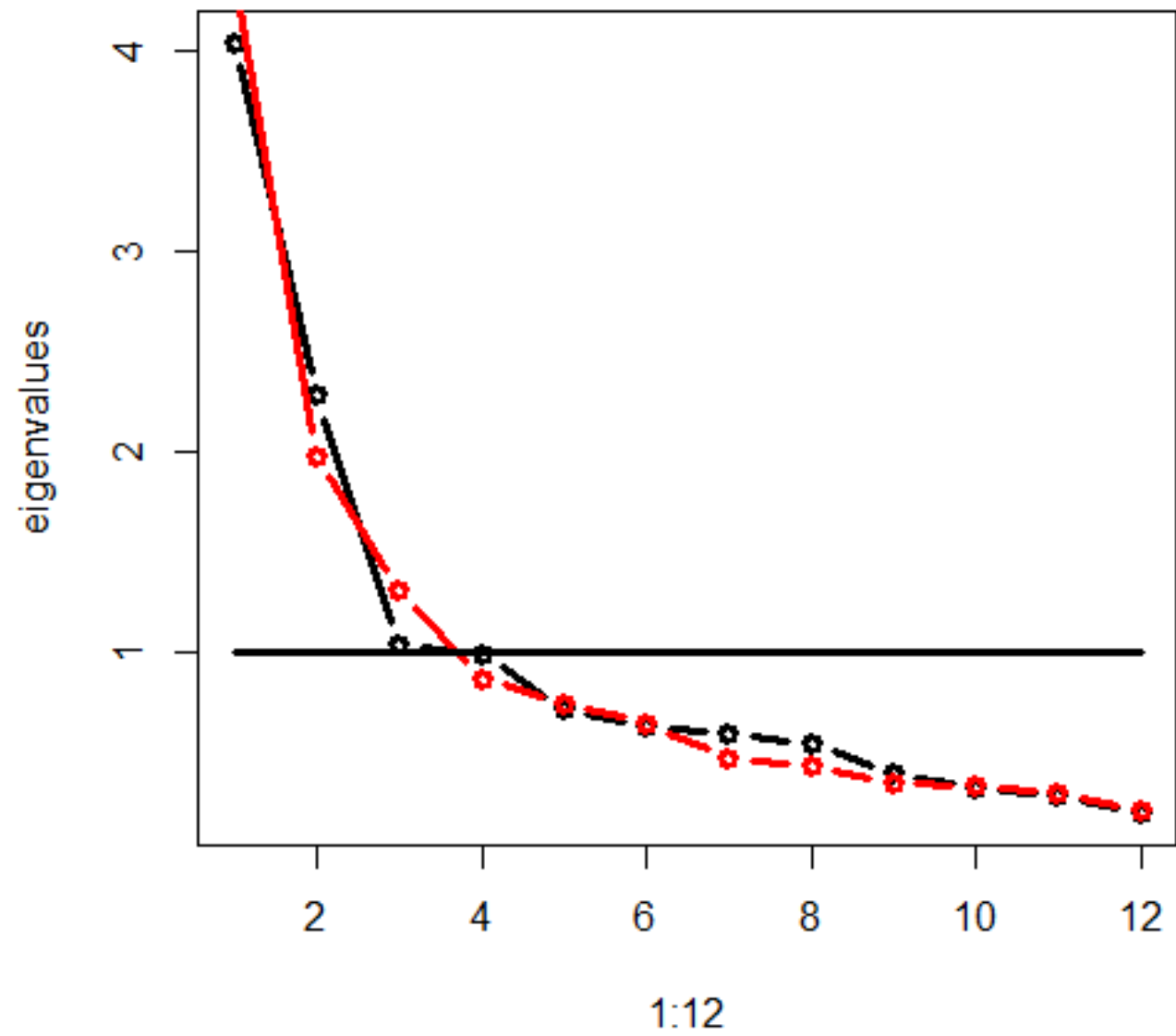
```



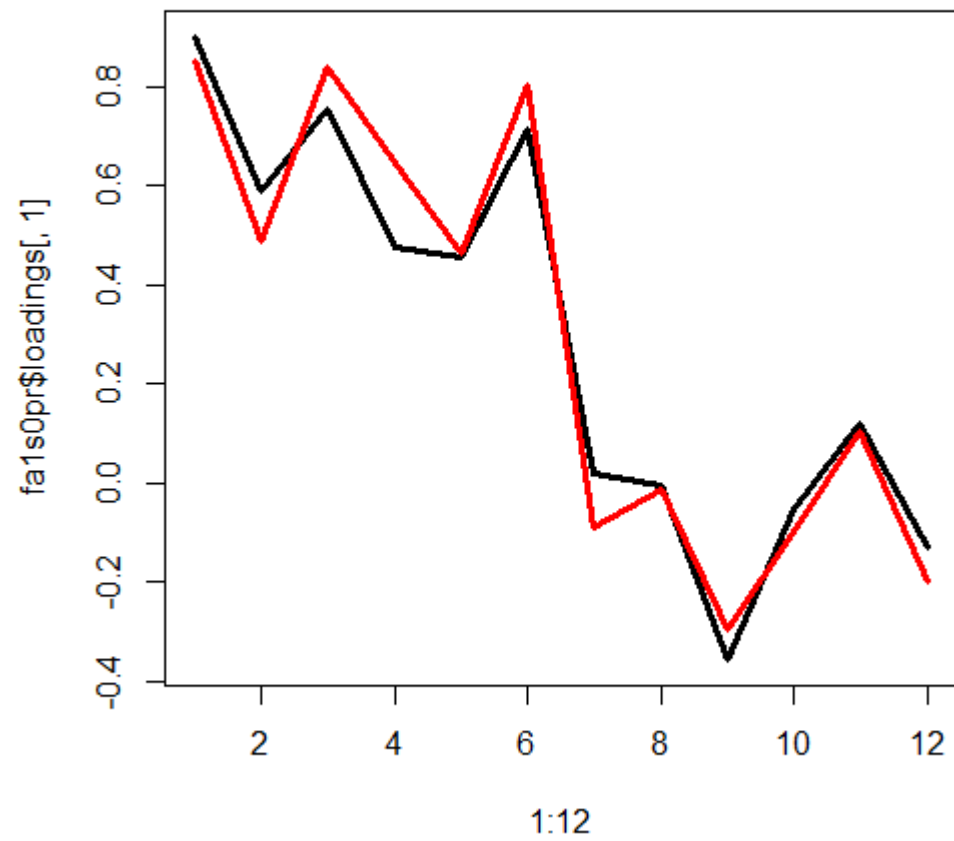
```
alpha=.05/12; Stest=matrix(0,1,12)
for (j in 2:13) {
tmp=lm(datb2[,j]~(sex))
pval=summary(tmp)$coefficients[2,4]
Stest[1,j-1]=(pval<alpha)}
colnames(Stest)=colnames(datb2)[2:13]
print(Stest)
```

<b>n1</b>	<b>n2</b>	<b>n3</b>	<b>n4</b>	<b>n5</b>	<b>n6</b>	<b>e1</b>	<b>e2</b>	<b>e3</b>	<b>e4</b>	<b>e5</b>	<b>e6</b>
1	0	1	1	1	1	1	0	0	0	0	0

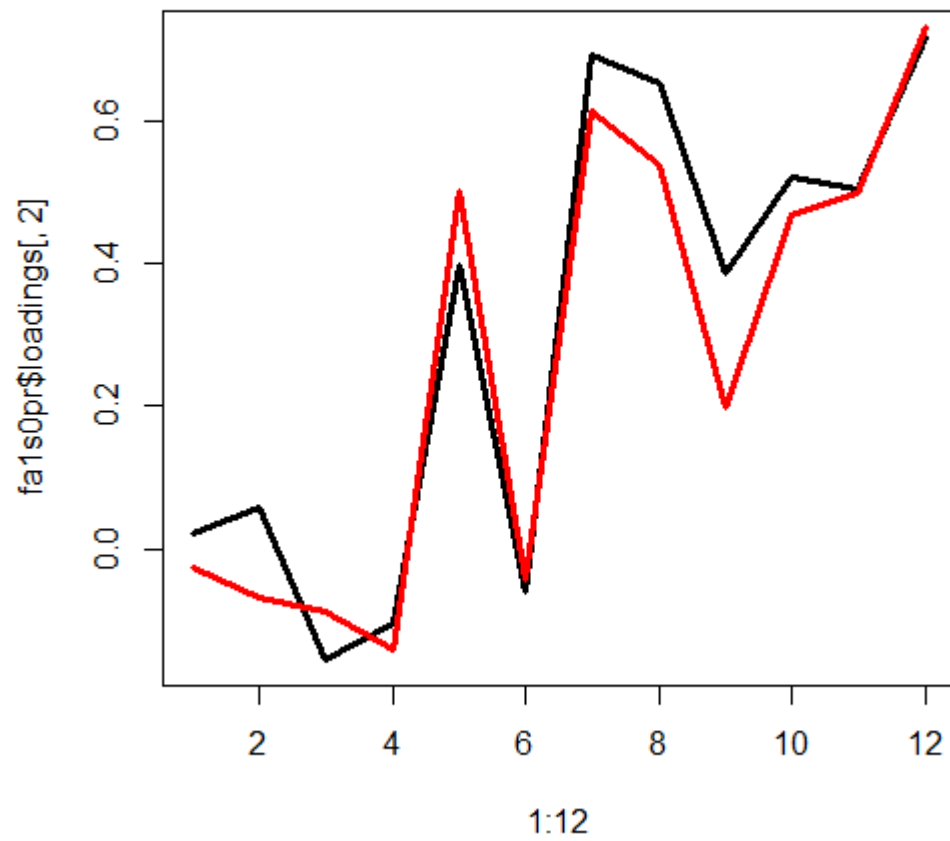
# SCREEPLOT



factor#1 loadings



factor#2 loadings



Uniquenesses:

n1	n2	n3	n4	n5	n6	e1	e2	e3	e4	e5	e6
0.199	0.670	0.339	0.736	0.738	0.461	0.528	0.571	0.645	0.709	0.766	0.413

Loadings:

	Factor1	Factor2
n1	0.901	
n2	0.588	
n3	0.754	-0.156
n4	0.473	-0.106
n5	<u>0.457</u>	<u>0.398</u>
n6	0.714	
e1		0.693
e2		0.653
e3	<u>-0.357</u>	<u>0.385</u>
e4		0.522
e5	0.120	0.505
e6	-0.130	0.718

$$\Sigma_y = \Lambda \Psi \Lambda^t + \Theta$$

Factor Correlations:

	Factor1	Factor2
Factor1	1.000	0.288
Factor2	0.288	1.000

MALES



Uniquenesses:

n1

0.199

Loadings:

Factor1 Factor2

n1 0.901 ~0

$$\lambda_1^2 \sigma_{\eta}^2 + \sigma_{\varepsilon}^2 = 1$$

$$.901^2 * 1 + .199 \approx 1$$

MALES

Uniquenesses:

n1	n2	n3	n4	n5	n6	e1	e2	e3	e4	e5	e6
0.259	0.735	0.237	0.496	0.705	0.330	0.574	0.707	0.831	0.738	0.780	0.321

Loadings:

	Factor1	Factor2
n1	0.851	
n2	0.486	
n3	0.838	
n4	0.647	-0.140
n5	<u>0.464</u>	<u>0.501</u>
n6	0.801	
e1		0.614
e2		0.537
e3	<u>-0.294</u>	<u>0.199</u>
e4		0.466
e5	0.102	0.497
e6	-0.198	0.731

$$\Sigma_y = \Lambda \Psi \Lambda^t + \Theta$$

$$\lambda_1^2 \sigma_\eta^2 + \sigma_\varepsilon^2 = 1$$

Factor Correlations:

	Factor1	Factor2
Factor1	1.000	-0.368
Factor2	-0.368	1.000

FEMALES

```

Ly=mxMatrix(type='Full',nrow=ny,ncol=ne,free=
  matrix(c(
    T,F,
    T,F,
    T,F,
    T,F,
    T,F, # T,T
    T,F,
    F,T,
    F,T,
    T,T, # F,T
    F,T,
    F,T,
    F,T),ny,ne,byrow=T),
  value=c(4,4,4,4,4,4,0,0,0,0,0,0,
          0,0,0,0,0,0,4,4,4,4,4,4),name='Ly') #
read column-wise
labels=matrix(c(
  'f11','f12',
  'f21','f22',
  'f31','f32',
  'f41','f42',
  'f51','f52',
  'f61','f62',
  'f71','f72',
  'f81','f82',
  'f91','f92',
  'f101','f102',
  'f111','f112',
  'f121','f122'),ny,ne,byrow=T)

```

Define factor loading matrix  $\Lambda$

$$\Sigma_y = \Lambda \Psi \Lambda^t + \Theta$$

```
Te=mxMatrix(type='Diag',nrow=ny,ncol=ny,free=TRUE,value=10,name='Te')
```

Define covariance matrix of residuals  $\Theta$

$$\Sigma_y = \Lambda \Psi \Lambda^t + \Theta$$

```
## latent correlation matrix
Ps0=mxMatrix(type='Symm',nrow=ne,ncol=ne,
             free=c(FALSE,TRUE,FALSE),
             labels=c('v1_0','r12_0', 'v2_0'),values=c(1,-.1,1),name='Ps0')
Ps1=mxMatrix(type='Symm',nrow=ne,ncol=ne,
             free=c(FALSE,TRUE,FALSE),
             labels=c('v_1','r12_1', 'v2_1'),values=c(0,0,0),name='Ps1')
```

Define covariance matrix of factors  $\Psi$

$$\Psi = \Psi_0 + \text{sex} * \Psi_1$$

$$\Sigma_y = \Lambda \Psi \Lambda^t + \Theta$$

$$\Psi = \Psi_0 + \text{sex} * \Psi_1$$

$$\Psi_0 = \begin{Bmatrix} 1 & \rho_0 \\ \rho_0 & 1 \end{Bmatrix}$$

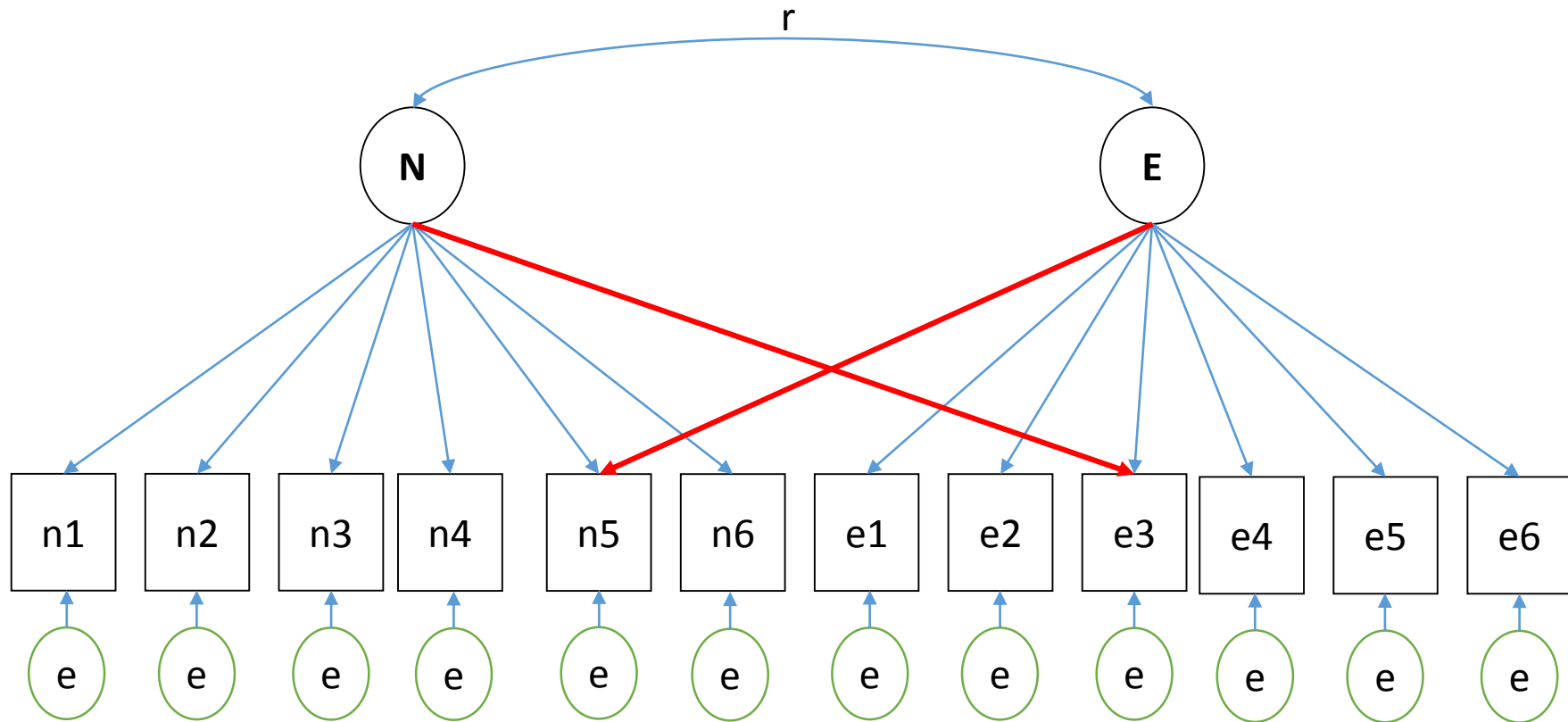


$$\text{Sex} = 0: \quad \rho_0$$

$$\Psi_1 = \begin{Bmatrix} 0 & \rho_1 \\ \rho_1 & 0 \end{Bmatrix}$$

$$\text{Sex} = 1: \quad \rho_0 + \rho_1$$

Allows us to test whether the latent correlation is equal in males and females



Test whether the cross loadings are unequal zero  
 Using a likelihood ratio test

Test whether the correlations are equal  
Using a likelihood ratio test

**Factor Correlations:**

	<b>Factor1</b>	<b>Factor2</b>
<b>Factor1</b>	1.000	0.288
<b>Factor2</b>	0.288	1.000

**Factor Correlations:**

	<b>Factor1</b>	<b>Factor2</b>
<b>Factor1</b>	1.000	-0.368
<b>Factor2</b>	-0.368	1.000



```

> mxCompare(CFM2_out,CFM1_out)
  base comparison ep minus2LL    df      AIC    diffLL diffdf      p
1 CFM1          <NA> 46 33600.68 5954 21692.68      NA      NA      NA
2 CFM1          CFM1 44 33695.92 5956 21783.92 95.24373      2 2.080113e-21

> mxCompare(CFM2_out,CFM3_out)
  base comparison ep minus2LL    df      AIC    diffLL diffdf      p
1 CFM1          <NA> 46 33600.68 5954 21692.68      NA      NA      NA
2 CFM1          CFM1 45 33600.90 5955 21690.90 0.2195677      1 0.6393695

```

Factor loadings are significant (alpha=0.01)

Sex difference in latent correlation is not significant (alpha=0.01)