

```

1  ## Test if the chisq difference test applies when missing data are available
2  ## Generate data in R and analyze data in Mplus
3  ## The chisq value is read in for density plot.
4
5  library(mvtnorm)
6
7  gen.model<-function(T){
8  ## generate mplus scripts for data analysis
9  ## Mplus input scripts
10 mplus.null<-'m1null.inp'
11 mplus.alt<-'m2alt.inp'
12
13 ## for null model
14 cat('TITLE: Null model\n',file=mplus.null);
15 cat('DATA:\n',file=mplus.null, append=T);
16 cat(' FILE=data.txt;\n',file=mplus.null, append=T);
17 cat('VARIABLE: \n',file=mplus.null, append=T);
18 cat(' NAMES ARE y1-y',T, ' x;\n', sep='', file=mplus.null, append=T);
19 cat(' USEVARIABLES ARE y1-y',T, ' x;\n', sep='', file=mplus.null, append=T);
20 cat(' MISSING = ALL(999);\n',file=mplus.null, append=T);
21
22 cat('ANALYSIS: \n',file=mplus.null, append=T);
23 cat(' COVERAGE=.01;\n',file=mplus.null, append=T);
24
25 cat('MODEL: \n',file=mplus.null, append=T);
26 cat(' i s q| ',file=mplus.null, append=T);
27 for (i in 1:T){
28   cat('y',i,'@',i-1, ', ',sep='',file=mplus.null,append=T)
29 }
30 cat('; \n',file=mplus.null,append=T)
31
32 cat(' [i * 50, s *, q * ]; \n',file=mplus.null, append=T);
33 cat(' i * 100, s *, q * ; \n',file=mplus.null, append=T);
34 cat(' q on x; \n',file=mplus.null, append=T);
35 cat(' i with s * 0; \n',file=mplus.null, append=T);
36 cat(' i with q * 0; \n',file=mplus.null, append=T);
37 cat(' s with q * 0; \n',file=mplus.null, append=T);
38 cat(' y1-y',T, ' (10);\n', sep='', file=mplus.null, append=T);
39 cat(' [y1-y',T, '@0];\n', sep='', file=mplus.null, append=T);
40
41 cat('SAVEDATA:\n', sep='', file=mplus.null, append=T);
42 cat(' results=res.txt;\n', sep='', file=mplus.null, append=T);
43
44 ## for alternative model
45 cat('TITLE: Null model\n',file=mplus.alt);
46 cat('DATA:\n',file=mplus.alt, append=T);
47 cat(' FILE=data.txt;\n',file=mplus.alt, append=T);
48 cat('VARIABLE: \n',file=mplus.alt, append=T);
49 cat(' NAMES ARE y1-y',T, ' x;\n', sep='', file=mplus.alt, append=T);
50 cat(' USEVARIABLES ARE y1-y',T, ' x;\n', sep='', file=mplus.alt, append=T);
51 cat(' MISSING = ALL(999);\n',file=mplus.alt, append=T);
52

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Function to generate Mplus scripts for M0 and M1
This function require the input of number of measurement occasions

```

53 cat('ANALYSIS: \n',file=mplus.alt, append=T);
54 cat(' COVERAGE=.01; \n',file=mplus.alt, append=T);
55
56 cat('MODEL: \n',file=mplus.alt, append=T);
57 cat(' i s q| ',file=mplus.alt, append=T);
58 for (i in 1:T){
59   cat('y',i,'@',i-1,' ',sep='',file=mplus.alt,append=T)
60 }
61 cat('; \n',file=mplus.alt,append=T)
62
63 cat(' [i * 50, s *, q *]; \n',file=mplus.alt, append=T);
64 cat(' i * 100, s *, q *; \n',file=mplus.alt, append=T);
65 cat(' q on x @ 0; \n',file=mplus.alt, append=T);
66 cat(' i with s * 0; \n',file=mplus.alt, append=T);
67 cat(' i with q * 0; \n',file=mplus.alt, append=T);
68 cat(' q with s * 0; \n',file=mplus.alt, append=T);
69 cat(' y1-y',T, ' (10); \n', sep='', file=mplus.alt, append=T);
70 cat(' [y1-y',T, '@0]; \n', sep='', file=mplus.alt, append=T);
71
72 cat('SAVEDATA: \n', sep='', file=mplus.alt, append=T);
73 cat(' results=res.txt; \n', sep='', file=mplus.alt, append=T);
74 }
75
76 ## Data generation
77
78 ## quadratic model with covariate
79 grm.quadratic<-function(N, T, R){
80 ## Constants and parameters
81 mL<-50
82 vL<-100
83 mS<-5
84 vS<-25
85 vLS<-0
86 mQ<--1
87 vQ<-9
88 vLQ<-0
89 vSQ<-0
90
91 bQ<-0
92
93 vE<-25
94
95 sigma<-array(c(vL,vLS,vLQ, vLS,vS,vSQ, vLQ,vSQ,vQ), dim=c(3,3))
96
97
98 y<-array(NA, dim=c(N, T))
99 x<-rep(c(0,1),N/2)
100
101 for (i in 1:N){
102   mu<-c(mL,mS,mQ+x[i]*bQ)
103   LSQ<-rmvnorm(1, mu, sigma)
104   for (j in 1:T){
105     y[i, j] <- LSQ[1] + LSQ[2]*(j-1)/(T-1) + LSQ[3]*((j-1)/(T-1))^2 + rnorm(1, 0, sqrt(vE))

```

Function to generate complete data for the quadratic growth curve model
The population parameter values

```

106 }
107 }
108
109 data.file<-paste('Q-N-',N,'-T-',T,'-',R,'.txt',sep='')
110 write.table(cbind(y,x), data.file, row.names=F, col.names=F)
111
112 }
113
114
115 for (i in 1:10000){
116   grm.quadratic(500,5,i)
117 }
118
119 ## process data
120 data.gen<-function(i,N,T, r=0.5, alpha=0){
121   ##read in data
122   data.file<-paste('Q-N-500-T-5-',i,'.txt',sep='')
123   y<-read.table(data.file)
124   ##missing data or complete data
125   if (r>0){
126     for (i in 2:T){
127       ## find which element is mssing for y[,t-1]
128       ind.c<-NULL
129       ind.m<-NULL
130       for (j in 1:N){
131         if (!is.na(y[j,i-1])){
132           ind.c<-c(ind.c,j)
133         }else{
134           ind.m<-c(ind.m,j)}
135       }
136
137       if (length(ind.m)!=0){
138         y[ind.m,i]<-NA }
139
140       cut.r<-quantile(y[1:N,i-1],r,na.rm=T)
141
142       for (k in 1:N){
143         if ( !is.na(y[k,i])){
144           if (y[k,i-1]>cut.r){
145             if (runif(1)<r*alpha){y[k,i]<-NA}
146           }else{
147             if (runif(1)<1-alpha+r*alpha){y[k,i]<-NA}
148           }
149         }
150       }
151     }
152   }
153   write.table(cbind(y[1:N,1:T],y[1:N,6]),'data.txt',row.names=F,col.names=F,na='999')
154 }
155
156 ## Run Mplus and get the chi-square statistics
157 ptm <- proc.time()
158 R<-10000

```

Save generated data into a file

Generate 10000 sets of complete data

Generate missing data according to missing data rates and missing mechanisms
alpha=0 for MAR
alpha=1 for MANR
alpha=0.5 for mixture of MAR and MNAR

Procedure to run the simulation and obtain chi-square statistics

| | |
|--|--|
| <pre> 159 160 N.v<-c(500,400, 300, 200, 100) 161 T.v<-4:5 162 alpha.v<-c(0, 0.5, 1) 163 r.v<-c(.3,.1, 0) 164 165 for (T in T.v){ 166 gen.model(T) 167 for (N in N.v){ 168 for (r in r.v){ 169 170 for (alpha in alpha.v){ 171 res.file<-paste('res-N',N,'-T',T,'-alpha',alpha,'-R',r,'-a.txt',sep='') 172 for (i in 1:R){ 173 data.gen(i,N,T,r,alpha) 174 ## Model 1 175 system("c:\\progra~1\\mplus\\mplus.exe m1null.inp",show.output.on.console=F) 176 if (file.exists('res.txt')){ 177 m1.out<-scan('res.txt') 178 unlink('res.txt') 179 }else{ m1.out<-NA} 180 181 system("c:\\progra~1\\mplus\\mplus.exe m2alt.inp",show.output.on.console=F) 182 if (file.exists('res.txt')){ 183 m2.out<-scan('res.txt') 184 unlink('res.txt') 185 unlink('data.txt') 186 }else{ m2.out<-NA} 187 188 cat(c(i,m1.out,m2.out), file=res.file,append=T) 189 cat("\n", file=res.file,append=T) 190 } 191 } 192 } 193 } 194 } 195 } 196 proc.time()-ptm </pre> | <pre> sample sizes number of measurement occasions missing mechanisms missing data rate Generate mplus model scripts Name of the file to save the results from mplus generate missing data Run Mplus for data analysis Read saved estimates from Mplus </pre> |
|--|--|