Graphical Models with R

4th talk: Mixed Interaction Models

Dhafer Malouche

essai.academia.edu/DhaferMalouche

Table of contents

Mixed Data and CG-densities

Mixed Gaussian Distribution

- V is a finite set, $V = \Delta \cup \Gamma$, Δ is the set of discrete variables and Γ is the set of continuous variables

- $X_V = (I_\Delta, Y_\Gamma)$ where
  - $I_\Delta = (I_v, v \in \Delta)$ and $Y_\Gamma = (Y_v, v \in \Gamma)$.
  - $X_V(\Omega) = \mathcal{I} \bigotimes \mathbb{R}^{|\Gamma|}$
  - $\mathcal{I} = I_\Delta(\Omega) = \bigotimes_{v \in \Delta} \mathcal{I}_v = \bigotimes_{v \in \Delta} \{1, \dots, I_v\}$

- $\forall i \in \mathcal{I}$, $Y_\Gamma \mid I_\Delta = i \sim \mathcal{N}(\mu(i), \Sigma(i))$ and

$$\mathbb{P}(I_\Delta = i) = p(i)$$

- The density of X_V, $\forall x = (i, y) \in \mathcal{I} \bigotimes \mathbb{R}^{|\Gamma|}$

$$f(x) = f(i, y) = p(i) \frac{|K(i)|^{1/2}}{(2\pi)^{|\Gamma|/2}} \exp\left(-\frac{1}{2}(y - \mu)'K(i)(y - \mu)\right)$$

$K(i) = (\Sigma(i))^{-1}$.

- Parameters: $\{p(i), \mu(i), K(i)\}_{i \in \mathcal{I}}$

Mixed Gaussian Distribution, re-parametrization

- Canonical parameters

$$f(x) = f(i, y) = \exp\left\{ g(i) + h(i)'y - \frac{1}{2}y'K(i)y \right\}$$

$\{g(i) \in \mathbb{R}, \, h(i) \in \mathbb{R}^{|\Gamma|}, \, K(i) \in \mathbb{R}^{|\Gamma| \times |\Gamma|}\}$

- Homogeneous model: $\forall i \in \mathcal{I}_\Delta, \, K(i) = K$
- Where

$$\left\{ \begin{array}{rcl} h(i) & = & \Sigma^{-1}\mu(i) \\ g(i) & = & \log p(i) - \frac{1}{2}\log\det(\Sigma) \\ & & -\frac{1}{2}\mu(i)'\Sigma^{-1}\mu(i) - \frac{|\Gamma|}{2}\log(2\pi) \end{array} \right.$$

and

$$\left\{ \begin{array}{rcl} \mu(i) & = & K^{-1}h(i) \\ p(i) & = & (2\pi)^{|\Gamma|}(\det(K))^{-1/2} \\ & & \times \exp\left\{ g(i) + \frac{1}{2}\mu(i)'K^{-1}\mu(i) \right\} \end{array} \right.$$

- $X_V = (I_\Delta, Y_\Gamma) \sim MI\{(g(i), h(i))_{i \in \mathcal{I}}, K\}$

Example $\Delta = \{A, B\}$ and $\Gamma = \{S, T\}$

- $i = (j, k)$, $y = (s, t)$,

- Density of $X = (A, B, S, T)$, for $x = (j, k, s, t)$

$$
\begin{aligned}
f(x) = f(i, y) &= f(j, k, s, t) \\
&= \exp\left\{ g(i) + h_S(i)s + h_T(i)t - \tfrac{1}{2}(k_{SS}s^2 + 2k_{ST}ts + k_{TT}t^2) \right\}
\end{aligned}
$$

- Log-linear decomposition:

$$
\begin{aligned}
g(i) &= g(j, k) &=& \ u_\emptyset + u_j^A + u_k^B + u_{jk}^{AB} \\
h_S(i) &= h_S(j, k) &=& \ v_\emptyset(S) + v_j^A(S) + v_k^B(S) + v_{jk}^{AB}(S) \\
h_T(i) &= h_T(j, k) &=& \ v_\emptyset(T) + v_j^A(T) + v_k^B(T) + v_{jk}^{AB}(T)
\end{aligned}
$$

Mixed Interaction Models

- $X_V = (I_\Delta, Y_\Gamma) \sim MI\{(g(i), h(i))_{i \in \mathcal{I}}, K\}$

- $MI\{(g(i), h(i))_{i \in \mathcal{I}}, K\}$ can be parametrized as follows like log-linear models

$$g(i) = \sum_{A \in \mathcal{A}} u^A_{i_A}, \ \forall i \in \mathcal{I}$$

and for some $\forall s \in \Gamma$

$$h_s(i) = \sum_{A \in \mathcal{B}(s)} v^A_{i_A}(s), \ \forall i \in \mathcal{I}$$

where $\mathcal{A}$ and $(\mathcal{B}(s))_{s \in \Gamma} \subseteq \mathcal{P}(\Delta) = \{A, A \subseteq \Delta\} \cup \{\emptyset\}$ and $i_A = (i_a, a \in A)$.

- Let $\mathcal{A}_m = \{a \subseteq \Delta, a = \cup_{a' \subseteq a} a'\}$ and $(\mathcal{B}(s)_m = \{a \cup \{s\}, a = \cup_{a' \subseteq a} a'\})_{s \in \Gamma}$ are the generators of Mixed interaction models.

- $D = \{st, s, t \in \Gamma \text{ s.t. } k_{st} \neq 0\}$

- Log-linear parametrization: $(\mathcal{A}, (\mathcal{B}(s))_{s \in \Gamma}, D)$

- $A \perp\!\!\!\perp S \mid B, T \iff f(j, k, s, t) = h(j, k, t) \times h(k, s, t)$

- If $v_j^A(S) = v_{jk}^{AB}(S) = 0$, then

$$
\begin{aligned}
f(j, k, s, t) &= \exp\{u_\emptyset + u_j^A + u_k^B + u_{jk}^{AB} + [v_\emptyset(S) + v_k^B(S)]\, s \\
&\quad + [v_\emptyset(T) + v_j^A(T) + v_k^B(T) + v_{jk}^{AB}(T)]\, t \\
&\quad - \tfrac{1}{2}(k_{SS}s^2 + 2k_{ST}ts + k_{TT}t^2)\} \\
&\propto \exp\left\{u_\emptyset + u_j^A + u_k^B + u_{jk}^{AB} + [v_\emptyset(T) + v_j^A(T) + v_k^B(T) + v_{jk}^{AB}(T)]\, t\right\} \\
&\quad \times \exp\left\{[v_\emptyset(S) + v_k^B(S)]\, s - \tfrac{1}{2}(k_{SS}s^2 + 2k_{ST}ts)\right\} \\
&= h(j, k, t) \times h(k, s, t)
\end{aligned}
$$

- $v_j^A(S) = v_{jk}^{AB}(S) = 0 \iff A \perp\!\!\!\perp S \mid B, T$

- $B \perp\!\!\!\perp T \mid A, S \iff v_k^B(T) = w_{jk}^{AB}(T) = 0$

- $S \perp\!\!\!\perp T \mid A, B \iff k_{ST} = 0.$

- $A \perp\!\!\!\perp B \mid S, T \iff u_{jk}^{AB} = 0$

```
> library(gRbase)
> data(milkcomp1)
> colnames(milkcomp1)
[1] "treat"   "fat"      "protein" "dm"       "lactose"
> head(milkcomp1,3)
  treat  fat protein    dm lactose
1     d 6.16    6.65 18.55    5.06
2     c 4.06    5.44 18.32    5.23
3     f 9.25    5.67 20.68    5.15
```

Example with R

```
> library(gRim)
> SS <- CGstats(milkcomp1)
> SS
$n.obs

a b c d e f g
8 8 8 8 8 7 8

$center
              a        b        c        d        e         f         g
fat      6.64125  8.01000  7.0525  7.40125  8.13375  7.518571  6.97375
protein  5.48750  5.28750  5.4750  5.81750  5.26250  5.295714  5.58000
dm      18.36375 19.38125 18.9750 19.25375 19.52125 18.732857 18.55000
lactose  5.49125  5.48875  5.4675  5.31375  5.40625  5.382857  5.41500

$cov
                fat     protein          dm     lactose
fat      2.31288338  0.19928422   2.3425294 -0.07028198
protein  0.19928422  0.12288675   0.3072388 -0.03035208
dm       2.34252938  0.30723883   2.6293253 -0.10382831
lactose -0.07028198 -0.03035208  -0.1038283  0.04529896

$cont.names
[1] "fat"     "protein" "dm"      "lactose"

$disc.names
[1] "treat"

$disc.levels
[1] 7
```

Example with R

```
> can.parms<-CGstats2mmodParms(SS,type="ghk")
> can.parms
$g
         a          b          c          d          e          f          g
 -973.5146  -954.1249  -981.7727  -962.5882  -939.0944  -923.0635  -955.8872

$h
          [,1]       [,2]       [,3]       [,4]       [,5]       [,6]       [,7]
[1,] -50.22894 -49.02083 -51.48436 -49.12735 -49.15246 -47.91322 -48.75867
[2,]  36.04849  33.20831  33.95960  39.01610  32.14528  34.44229  37.76233
[3,]  55.17976  54.78307  56.76543  54.08196  54.98826  53.27740  53.67301
[4,] 193.92119 192.92813 193.68393 191.18410 190.66071 189.68467 192.21384

$K
          [,1]       [,2]       [,3]       [,4]
[1,]  6.211785  5.085329 -6.171950 -1.101489
[2,]  5.085329 16.832881 -6.311932  4.701271
[3,] -6.171950 -6.311932  6.675696  1.496041
[4,] -1.101489  4.701271  1.496041 26.945650

$gentype
[1] "mixed"

$gentype
[1] "mixed"

$cont.names
[1] "fat"     "protein" "dm"      "lactose"

$disc.names
[1] "treat"

$disc.levels
[1] 7
```

$$A, B//ABX, AZ, Y//XY, XZ$$

$$
\begin{aligned}
g(i) &= u_\emptyset + u_j^A + u_k^B \\
h_X(i) &= v_\emptyset(X) + v_j^A(X) + v_k^B(X) + v_{jk}^{AB}(X) \\
h_Z(i) &= v_\emptyset(Z) + v_j^A(Z) \\
h_Y(i) &= v_\emptyset(Y)
\end{aligned}
\quad \text{and}
$$

$$
K = \begin{pmatrix}
k_{XX} & k_{XY} & k_{XZ} \\
k_{XY} & k_{YY} & 0 \\
k_{XZ} & 0 & k_{ZZ}
\end{pmatrix}
$$

Model Formula

- Let $\mathcal{C} = \{C_1, \ldots, C_q\}$ is the formula of the $MI\{(g(i), h(i))_{i \in \mathcal{I}}, K\}$ and Log-linear parametrization $\{\mathcal{A}, (\mathcal{B}(s))_{s \in \Gamma}, D\}$

$$\sim C_1 + C_2 + \ldots + C_q \qquad \text{(with R)}$$

- Any $C \in \mathcal{C}$ should satisfy one of the following statements

  i. $C \in \mathcal{A}_m$

  ii. if $C \in \mathcal{C} \setminus \mathcal{A}_m$ and $C \cap \Delta \neq \emptyset$ then $\forall s \in C \cap \Gamma$, $\exists B \in \mathcal{B}_m(s)$ s.t. $B \subseteq C \setminus \Gamma$.

  iii. if $C \in \mathcal{C} \setminus \mathcal{A}_m$ and $C \cap \Delta = \emptyset$ then $\forall st \in \Gamma \times \Gamma$ s.t. $k_{st} = 0$, $\{s, t\} \nsubseteq C$.

$\Delta = \{A\}$ and $\Gamma = \{X\}$

```
> data(Nutrimouse, package='gRbase')
> head(Nutrimouse[,1:5],2)
  genotype diet X36b4 ACAT1 ACAT2
1       wt  lin -0.42 -0.65 -0.84
2       wt  sun -0.44 -0.68 -0.91
> dtX=Nutrimouse[,1:5]
> colnames(dtX)=c("A","B","X","Y","Z")
> summary(dtX)
    A          B           X                  Y                  Z
 wt  :20   coc :8   Min.   :-0.5800   Min.   :-0.7500   Min.   :-1.1000
 ppar:20   fish:8   1st Qu.:-0.5025   1st Qu.:-0.6900   1st Qu.:-0.8800
           lin :8   Median :-0.4600   Median :-0.6600   Median :-0.7950
           ref :8   Mean   :-0.4552   Mean   :-0.6552   Mean   :-0.7668
           sun :8   3rd Qu.:-0.4200   3rd Qu.:-0.6200   3rd Qu.:-0.6450
                    Max.   :-0.3000   Max.   :-0.5200   Max.   :-0.3900
> g1<-mmod(~A+X,data=dtX)
> g1$fitinfo$parms[c("g","h","K")]
$g

      wt      ppar
-22.45077 -22.45077

$h
          [,1]      [,2]
[1,] -103.4674 -103.4674

$K
         [,1]
[1,] 227.276
```

$\Delta = \{A\}$ and $\Gamma = \{X\}$

```
> g1<-mmod(~A*X,data=dtX)
> g1$fitinfo$parms[c("g","h","K")]
$g
       wt      ppar
-22.17036 -22.84452

$h
         [,1]      [,2]
[1,] -102.9759 -104.4568

$K
         [,1]
[1,] 227.8229
```

$\Delta = \{A\}$ and $\Gamma = \{X, Y\}$

```
> g2<-mmod(~A+X*Y,data=dtX)
> g2$fitinfo$parms[c("g","h","K")]
$g
        wt      ppar
-78.79175 -78.79175

$h
            [,1]       [,2]
[1,]   -46.97397  -46.97397
[2,] -217.57641 -217.57641

$K
            [,1]       [,2]
[1,]   254.5892 -105.1931
[2,] -105.1931  405.1363
```

```
> g2<-mmod(~A*X+A*Y,data=dtX)
> g2$fitinfo$parms[c("g","h","K")]
$g
        wt      ppar
-101.75043  -98.41564

$h
           [,1]      [,2]
[1,] -102.9759 -104.4568
[2,] -246.0255 -239.9073

$K
          [,1]      [,2]
[1,] 227.8229    0.0000
[2,]   0.0000  370.7995
```

$\Delta = \{A\}$ and $\Gamma = \{X, Y\}$

```
> g2<-mmod(~A*X*Y,data=dtX)
> g2$fitinfo$parms[c("g","h","K")]
$g
        wt      ppar
-81.89446 -78.48745

$h
          [,1]      [,2]
[1,]  -42.32771  -45.84449
[2,] -227.67400 -220.03108

$K
          [,1]      [,2]
[1,]  257.5701 -111.6714
[2,] -111.6714  419.2155
```

- $X_V = (I_\Delta, Y_\Gamma) \sim MI\{(g(i), h(i))_{i \in \mathcal{I}}, K\}$ with formula $\mathcal{C}$.

- $\mathcal{G} = (V = \Delta \cup \Gamma, E)$ is the Mixed graph associated X_V

$$\alpha \not\sim \beta \iff$$

If $\alpha, \beta \in \Delta$, $\forall B \supseteq uv$ and $B \subseteq \Delta$ we have
$u^B_{i_B} = 0$
and $\forall b \in \Gamma, v^B_{i_B}(b) = 0$

If $\alpha, \in \Delta, \beta \in \Gamma$ $\forall B \ni u$ and $B \subseteq \Delta$
$v^B_{i_B}(\beta) = 0$

If $\alpha, \beta \in \Gamma,$ $k_{\alpha\beta} = 0$

- We say that the $MI\{(g(i), h(i))_{i \in \mathcal{I}}, K\}$ associated to $\mathcal{G}$ is Graphical if $\mathcal{C}$ is the set of cliques of $\mathcal{G}$.

- $(A, B, S) \subset V$ (pairwise disjoint) is a decomposition of $\mathcal{G}$ if
    i. $V = A \cup S \cup B$.
    ii. A and B are separated by S in $\mathcal{G}$.
    iii. S is complete
    iv. $S \subset \Delta$ or $B \subset \Gamma$.

- A graph with mixed variables $\mathcal{G}$ is called decomposable if it is complete or it can be successively decomposed into complete graphs.

- $(A, B, S) \subset V$ (pairwise disjoint) is a decomposition of $\mathcal{G}$ if
  i. $V = A \cup S \cup B$.
  ii. A and B are separated by S in $\mathcal{G}$.
  iii. S is complete
  iv. $S \subset \Delta$ or $B \subset \Gamma$.

- A graph with mixed variables $\mathcal{G}$ is called decomposable if it is complete or it can be successively decomposed into complete graphs.

- A forbidden path is a path between two non-adjacent discrete vertices that passes through only continuous vertices

Proposition
A graph is decomposable if and only if it is triangulated and has no no forbidden paths.

Decomposition in $\mathcal{G}$

- $(A, B, S) \subset V$ (pairwise disjoint) is a decomposition of $\mathcal{G}$ if
    i. $V = A \cup S \cup B$.
    ii. A and B are separated by S in $\mathcal{G}$.
    iii. S is complete
    iv. $S \subset \Delta$ or $B \subset \Gamma$.

- A graph with mixed variables $\mathcal{G}$ is called decomposable if it is complete or it can be successively decomposed into complete graphs.

- The *star* graph $\mathcal{G}^\star$ associated to $\mathcal{G}$: Add a vertex $\star$ and connect $\star$ with an edge to all discrete variables.

Proposition

A graph is decomposable if and only if its *star* graph is decomposable.

Examples
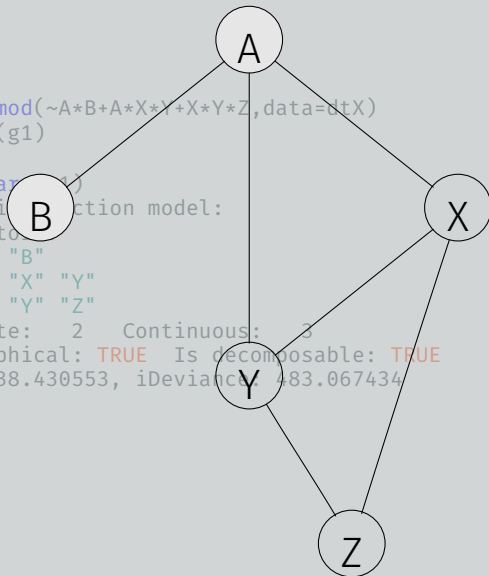
```
> g1=mmod(~A*B+A*X*Y+X*Y*Z,data=dtX)
> plot(g1)

> summary(g1)
Mixed interaction model:
Generators:
  :"A" "B"
  :"A" "X" "Y"
  :"X" "Y" "Z"
Discrete:   2   Continuous:   3
Is graphical: TRUE   Is decomposable: TRUE
logL: 38.430553, iDeviance: 483.067434
```

```
> g1=mmod(~A*B+A*X*Y+X*Y*Z,data=dtX)
> plot(g1)

> summary(g1)
Mixed interaction model:
Generators:
  :"A" "B"
  :"A" "X" "Y"
  :"X" "Y" "Z"
Discrete:  2   Continuous:  3
Is graphical: TRUE  Is decomposable: TRUE
logL: 38.430553, iDeviance: 483.067434
```

Examples

```
> g2=mmod(~A*B+A*X+A*Y+X*Y*Z,data=dtX)
> plot(g2)

> summary(g2)
Mixed interaction model:
Generators:
  :"A" "B"
  :"A" "X"
  :"A" "Y"
  :"X" "Y" "Z"
Discrete:   2   Continuous:   3
Is graphical: FALSE  Is decomposable: FALSE
logL: 38.430553, iDeviance: 483.067434
```
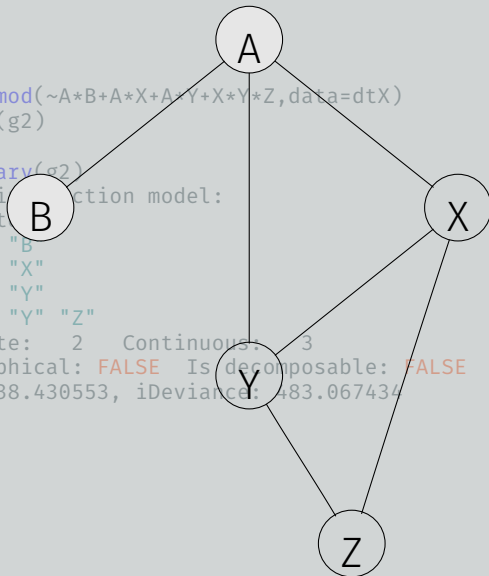
```
> g2=mmod(~A*B+A*X+A*Y+X*Y*Z,data=dtX)
> plot(g2)

> summary(g2)
Mixed interaction model:
Generators:
  :"A" "B"
  :"A" "X"
  :"A" "Y"
  :"X" "Y" "Z"
Discrete:  2   Continuous:  3
Is graphical: FALSE   Is decomposable: FALSE
logL: 38.430553, iDeviance: 483.067434
```

```
> g3=mmod(~A*B+A*X+A*Y+Y*Z+X*Z,data=dtX)
> plot(g3)

> summary(g3)
Mixed interaction model:
Generators:
  :"A" "B"
  :"A" "X"
  :"A" "Y"
  :"Y" "Z"
  :"X" "Z"
Discrete:  2   Continuous:   3
Is graphical: TRUE  Is decomposable: FALSE
logL: 35.707492, iDeviance: 477.621311
```
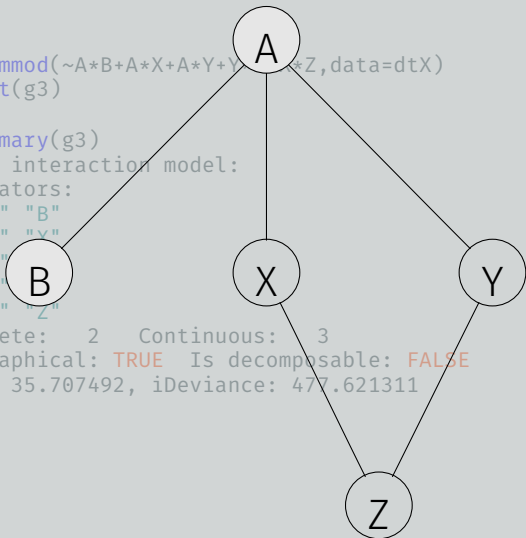
Examples

```
> g4=mmod(~A*X+B*Y+Y*X*Z,data=dtX)
> plot(g4)

> summary(g4)
Mixed interaction model:
Generators:
  :"A" "X"
  :"B" "Y"
  :"Y" "X" "Z"
Discrete:   2   Continuous:   3
Is graphical: TRUE  Is decomposable: FALSE
logL: 39.358463, iDeviance: 484.923254
```
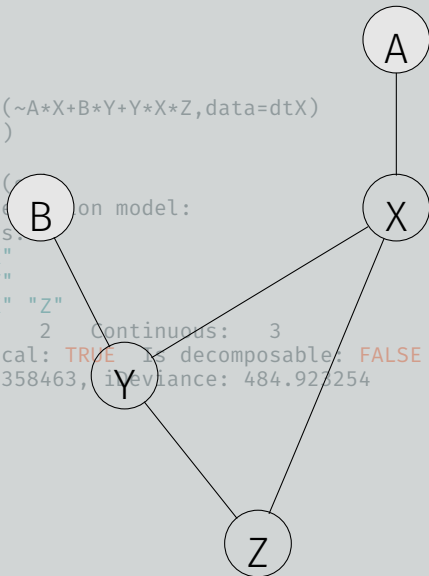
```
> g4=mmod(~A*X+B*Y+Y*X*Z,data=dtX)
> plot(g4)

> summary(
Mixed inte      on model:
Generators
  :"A" "X"
  :"B" "Y"
  :"Y" "X" "Z"
Discrete:   2    Continuous:    3
Is graphical: TRUE   Is decomposable: FALSE
logL: 39.358463,  deviance: 484.923254
```

Maximum Likelihood Estimation

Log-likelihood

- Data: $X^1 = (I^1, Y^1), \ldots, X^N = (I^N, Y^N) \sim MI\left(\{p(i), \mu(i)\}_{i \in \mathcal{I}}, K\right)$

- $n(i) = \sum_{j=1}^{N} \mathbb{1}_{I_j = i}$, hence $\sum_i n(i) = N$

- Log of the density

$$
\begin{aligned}
\log f(i, y) = {} & \log p(i) - |\Gamma| \log(2\pi)/2 - \log \det(\Sigma)/2 \\
& - (y - \mu(i))' \Sigma^{-1} (y - \mu(i))/2
\end{aligned}
$$

- Log-likelihood

$$
\begin{aligned}
l = {} & \sum_i n(i) p(i) - N|\Gamma| \log(2\pi)/2 - N \log \det(\Sigma)/2 \\
& - N \mathrm{tr}(S\Sigma^{-1}) - \sum_i n(i)(\bar{y}(i) - \mu(i))' \Sigma^{-1} (\bar{y}(i) - \mu(i))/2
\end{aligned}
$$

MLE for the complete homogeneous model

- $\widehat{p}(i) = \dfrac{n(i)}{N}$

- $\widehat{\mu}(i) = \overline{y}(i) = \dfrac{1}{n(i)} \displaystyle\sum_{j=1, I^j=i}^{N} Y^j$

- $\widehat{\Sigma} = S = \displaystyle\sum_{i} \dfrac{n(i)S(i)}{N}$

  where
  $$S(i) = \frac{1}{n(i)} \sum_{j=1, I^j=i}^{N} (Y^j - \overline{y}(i))(Y^j - \overline{y}(i))'$$

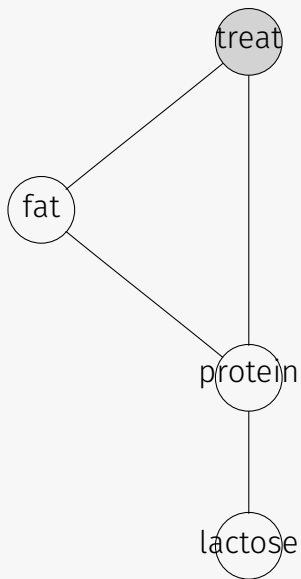 is the covariance sample on the sub-sample $\{j,\ I^j = i\}$

IPS-Algorithm

To be skipped

Model selection

```
> colnames(milkcomp1)
[1] "treat"   "fat"       "protein" "dm"        "lactose"
> glist <- ~treat:fat:protein+protein:lactose
> m1 <- mmod(glist, data=milkcomp1)
> summary(m1)
Mixed interaction model:
Generators:
  :"treat" "fat" "protein"
  :"protein" "lactose"
Discrete:   1   Continuous:   3
Is graphical: TRUE   Is decomposable: TRUE
logL: -214.233011, iDeviance: 241.774364
```

```
> coef(m1, type="ghk")
$g
         a          b          c          d          e          f          g
-676.0550  -666.0859  -675.0546  -690.9918  -664.9730  -666.7805  -680.0217

$h
             [,1]         [,2]         [,3]         [,4]         [,5]         [,6]
[1,]    -1.134727   -0.2838037   -0.9178505   -1.021725   -0.2012326   -0.5374842
[2,]    84.348819   81.3413696   83.8953921   86.850963   81.0040255   81.8196051
[3,]   164.633541  164.6335413  164.6335413  164.633541  164.6335413  164.6335413
             [,7]
[1,]    -1.043008
[2,]    84.952805
[3,]   164.633541

$K
             [,1]         [,2]         [,3]
[1,]    0.5025868   -0.815040     0.000000
[2,]   -0.8150400   10.762254     5.666744
[3,]    0.0000000    5.666744    24.645834
```

Getting the canonical parameters

```
$gentype
[1] "mixed"

$cont.names
[1] "fat"      "protein" "lactose"

$disc.names
[1] "treat"

$disc.levels
[1] 7

$N
[1] 55

$SSD
            [,1]      [,2]      [,3]
[1,] 127.208586 10.960632 -3.865509
[2,]  10.960632  6.758771 -1.669364
[3,]  -3.865509 -1.669364  2.491443

$SS
             fat  protein  lactose
fat     3143.500 2227.141 2199.895
protein 2227.141 1648.827 1627.220
lactose 2199.895 1627.220 1620.993
```

$$SS = \sum_{j=1}^{N} (Y^j)' Y^j$$

$$SSD = S = \sum_{i \in \mathcal{I}} \frac{n(i)S(i)}{N}$$

where

$$S(i) = \frac{1}{n(i)} \sum_{j=1, i^j=i}^{N} (Y^j - \bar{y}(i))(Y^j - \bar{y}(i))'$$

```
            fat   protein  lactose
fat     3143.500 2227.141 2199.895
protein 2227.141 1648.827 1627.220
lactose 2199.895 1627.220 1620.993
```

```
> m2 <- update(m1, list(add.edge=~fat:lactose,
+ drop.edge=~treat:protein))
> m2
Model: A mModel with 4 variables
 -2logL    :          446.17 mdim :   21 aic :        488.17
 ideviance :           10.12 idf  :   10 bic :        530.33
 deviance  :           10.96 df   :   12
> summary(m2)
Mixed interaction model:
Generators:
  :"fat" "lactose" "protein"
  :"treat" "fat"
Discrete:   1   Continuous:   3
Is graphical: TRUE  Is decomposable: TRUE
logL: -223.086367, iDeviance: 224.067653
> plot(m2)
```
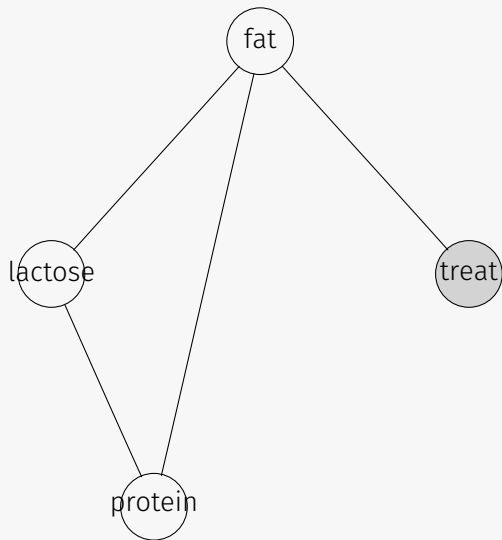
Conditional Independence Test

- Testing $u \perp\!\!\!\perp v \mid V \setminus \{u, v\}$

```
> ciTest(milkcomp1, set=~treat+fat+protein+dm)
set: [1] "treat"   "fat"      "protein" "dm"
CHK: Make usual LR-test - edge = {treat, fat}
Testing treat _|_ fat | protein dm
Statistic (DEV):    8.352 df: 6 p-value: 0.2134 method: CHISQ
```

- Testing $u \perp\!\!\!\perp v \mid W, W \subset V \setminus \{u, v\}$

```
> ciTest(milkcomp1, set=~treat+fat+dm)
set: [1] "treat" "fat"   "dm"
CHK: Make usual LR-test - edge = {treat, fat}
Testing treat _|_ fat | dm
Statistic (DEV):    13.899 df: 6 p-value: 0.0308 method: CHISQ
```

- Testing $u \perp\!\!\!\perp v$ (marginal independence)

```
> ciTest(milkcomp1, set=~treat+fat)
set: [1] "treat" "fat"
CHK: Make usual LR-test - edge = {treat, fat}
Testing treat _|_ fat
Statistic (DEV):    5.982 df: 6 p-value: 0.4253 method: CHISQ
```

```
> as(m1,"igraph")
IGRAPH UNW- 4 4 --
+ attr: name (v/c), label (v/c), weight (e/n)
+ edges (vertex names):
[1] treat  --fat      treat  --protein fat     --protein protein--lactose
> getInEdges(m1$glist)
     [,1]        [,2]
[1,] "treat"    "fat"
[2,] "treat"    "protein"
[3,] "fat"      "protein"
[4,] "protein"  "lactose"
> testInEdges(m1,getInEdges(m1$glist))
 statistic df      p.value        aic      V1       V2 action
1 11.06071  6 0.086518199 -0.9392919   treat      fat      +
2 18.68943  6 0.004721598  6.6894264   treat  protein      -
3  8.27794  1 0.004012963  6.2779399     fat  protein      -
4 10.24527  1 0.001370352  8.2452747 protein  lactose      -
> testdelete(m1, c("treat","fat"))
CHK: Make usual LR-test - edge = {treat, fat}
dev:   11.061 df:  6 p.value: 0.08652 AIC(k=2.0):   -0.9 edge: treat:fat
Notice: Test perfomed by comparing likelihood ratios
```

Testing adding or dropping a set of edges

```
> getOutEdges(m1$glist)
     [,1]    [,2]
[1,] "treat" "lactose"
[2,] "fat"   "lactose"
> testOutEdges(m1,getOutEdges(m1$glist))
  statistic df   p.value      aic   V1      V2 action
1 3.8928582  6 0.6911730 8.107142 treat lactose      -
2 0.9827155  1 0.3215293 1.017285   fat lactose      -
> testadd(m1, c("treat","lactose"))
dev:    3.893 df:  6 p.value: 0.69117 AIC(k=2.0):    8.1 edge: treat:lactos
Notice: Test perfomed by comparing likelihood ratios
```

Stepwise selection

```
> data(wine)
> head(wine)
  Cult  Alch Mlca  Ash Aloa Mgns Ttlp Flvn Nnfp Prnt Clri  Hue Oodw Prln
1   v1 14.23 1.71 2.43 15.6  127 2.80 3.06 0.28 2.29 5.64 1.04 3.92 1065
2   v1 13.20 1.78 2.14 11.2  100 2.65 2.76 0.26 1.28 4.38 1.05 3.40 1050
3   v1 13.16 2.36 2.67 18.6  101 2.80 3.24 0.30 2.81 5.68 1.03 3.17 1185
4   v1 14.37 1.95 2.50 16.8  113 3.85 3.49 0.24 2.18 7.80 0.86 3.45 1480
5   v1 13.24 2.59 2.87 21.0  118 2.80 2.69 0.39 1.82 4.32 1.04 2.93  735
6   v1 14.20 1.76 2.45 15.2  112 3.27 3.39 0.34 1.97 6.75 1.05 2.85 1450
> mm <- mmod(~.^., data=wine)
> mm2 <- stepwise(mm, k=log(nrow(wine)),criterion = "aic",direction = "back
+                 details=1)
STEPWISE:
 criterion: aic ( k = 5.18 )
 direction: backward
 type     : decomposable
 search   : all
 steps    : 1000
  change.AIC  -10.2499 Edge deleted: Cult Mgns
  change.AIC   -7.5774 Edge deleted: Cult Prnt
  change.AIC   -5.1818 Edge deleted: Alch Mgns
  change.AIC   -5.1700 Edge deleted: Clri Mgns
  change.AIC   -5.1144 Edge deleted: Mlca Mgns
```

```
> data(wine)
> head(wine)
  Cult Alch Mlca  Ash Aloa Mgns Ttlp Flvn Nnfp Prnt Clri Hue Oodw Prln
1   v1 14.23 1.71 2.43 15.6  127 2.80 3.06 0.28 2.29 5.64 1.04 3.92 1065
2   v1 13.20 1.78 2.14 11.2  100 2.65 2.76 0.26 1.28 4.38 1.05 3.40 1050
3   v1 13.16 2.36 2.67 18.6  101 2.80 3.24 0.30 2.81 5.68 1.03 3.17 1185
4   v1 14.37 1.95 2.50 16.8  113 3.85 3.49 0.24 2.18 7.80 0.86 3.45 1480
5   v1 13.24 2.59 2.87 21.0  118 2.80 2.69 0.39 1.82 4.32 1.04 2.93  735
6   v1 14.20 1.76 2.45 15.2  112 3.27 3.39 0.34 1.97 6.75 1.05 2.85 1450
> mm <- mmod(~^., data=wine)
> mm2 <- stepwise(mm,k=log(nrow(wine)),criterion = "aic",direction = "back
+                 details=1)
STEPWISE
 criterion: aic ( k = 5.184 )
 direction: backward
 type     : decomposable
 search   : all
 steps    : 1000
  change.AIC  -10.2499 Edge deleted: Cult Mgns
  change.AIC  -7.5774 Edge deleted: Cult Prnt
  change.AIC  -5.1818 Edge deleted: Alch Mgns
  change.AIC  -5.1700 Edge deleted: Clri Mgns
  change.AIC  -5.1144 Edge deleted: Mlca Mgns
```

33
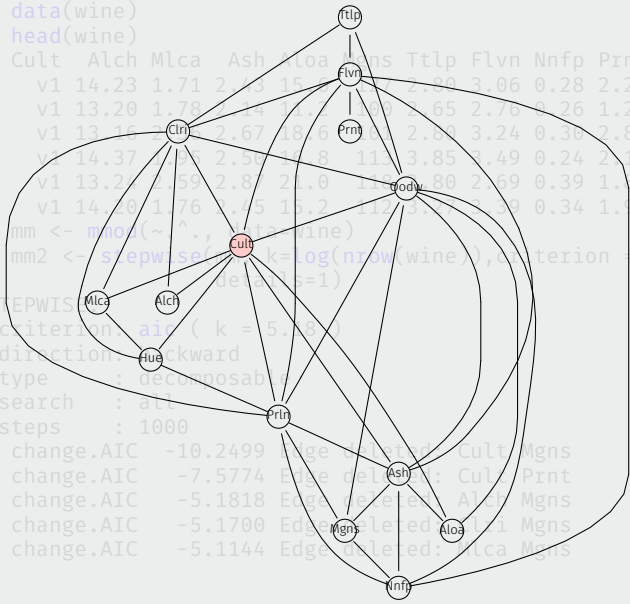
```
> data(Nutrimouse, package='gRbase')
> library(gRapHD)
> block2 <- Nutrimouse[,1:122]
> ## Estimating MI model given the first two variables
> gF1 <- minForest(block2, cond=list(1:2))
> gF1
gRapHD object
Number of edges       = 121
Number of vertices    = 122
Model                 = mixed and homogeneous
Statistic (minForest) = BIC
Statistic (stepw)     =
Statistic (user def.) =
Edges (minForest)     = 1...121
Edges (stepw)         = 0...0
Edges (user def.)     = 1...121
```

```
> ## Stepwise Forward Selection
> gD1 <- stepw(gF1, data=block2,)
> xyD1 <- plot(gD1, numIt=5000, disp=F)
> plot(gF1, numIt=0, coord=xyD1)
> plot(gD1, numIt=0, coord=xyD1)
```