Paired Comparison Preference Models

The prefmod Package: Day 5

Pattern Models - Missing values – Composite Link

based on:
Missing Observations in Paired Comparison Data
Dittrich, Francis, Hatzinger and Katzenbeisser
to appear in Statistical Modelling

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What is Composite Link?

example given by Thompson and Baker (1981):

In a sample of 422 people we observe 4 blood groups:
A = 42% , AB ~ 2%, O = 48%, B = 8%

the blood groups (A, AB, O, B) of the child are determined by alleles (a,o,b) of father and mother
e.g. father allele a and mother allele o gives blood group A

observed table

group	counts
A	179
AB	6
O	202
B	35

complete table

alleles	father		
mother	a	o	b
a	A	A	AB
o	A	O	B
b	AB	B	B

- we want to estimate the probabilities for p_a, p_o, p_b

(same for mother and father)

We look at patttern (aa), which gives blood group A:

alleles	father		
mother	a	o	b
a	p_a^2		
o			
b			

the probability for pattern (aa) is:

$$p(aa) = p_a\, p_a = p_a^2$$

the expected number for pattern (aa) is

$$
\begin{aligned}
m_{aa} &= N\, p_a^2 \\
\ln m_{aa} &= \ln N + 2 \ln p_a && \text{log link} \\
&= \mu \quad + 2\, \beta_a && \text{linear predictor } \eta_1 \\
m_{aa} &= \exp(\mu + 2\, \beta_a) && \text{inverse link}
\end{aligned}
$$

all patterns which give blood group A
(9 possible patterns):

alleles	father		
mother	a	o	b
a	p_a^2	$p_o p_a$	
o	$p_o p_a$		
b			

ℓ	genotype	group	μ	x_a	x_o	x_b	expected frequency	m_ℓ
1	aa	A	1	2	0	0	$\exp(\mu + 2\, \beta_a)$	$= \exp(\eta_1)$
2	ao	A	1	1	1	0	$\exp(\mu + 1\, \beta_a + 1\, \beta_o)$	$= \exp(\eta_2)$
3	ab	AB	1	1	0	1		
4	oa	A	1	1	1	0	$\exp(\mu + 1\, \beta_a + 1\, \beta_o)$	$= \exp(\eta_4)$
5	oo	0	1	0	2	0		
6	ob	B	1	0	1	1		
7	ba	AB	1	1	0	1		
8	bo	B	1	0	1	1		
9	bb	B	1	0	0	2		

$$p_{obs}(A) = p_{compl}(aa) + p_{compl}(oa) + p_{compl}(ao)$$

$$p(A) = \frac{\exp(\mu+2\,\beta_a)+\exp(\mu+1\,\beta_a+1\,\beta_o)+\exp(\mu+1\,\beta_a+1\,\beta_o)}{\sum_\ell \exp(\mu+x_a\,\beta_a+x_o\beta_o+x_b\beta_b)}$$

for estimating β_a, β_o, β_b and
to get estimated probabilities for blood groups (A, AB, O, B)

- we compose (add up) specific links
– that's where the name composite link comes from

$$p(A) = \frac{\exp(\eta_1)+\exp(\eta_2)+\exp(\eta_4)}{\sum_\ell \exp(\eta_\ell)} \qquad p(AB) = \frac{\exp(\eta_3)+\exp(\eta_7)}{\sum_\ell \exp(\eta_\ell)}$$

$$p(0) = \frac{\exp(\eta_5)}{\sum_\ell \exp(\eta_\ell)} \qquad p(B) = \frac{\exp(\eta_6)+\exp(\eta_8)+\exp(\eta_9)}{\sum_\ell \exp(\eta_\ell)}$$

How can we fit such a model?
- the data are the counts of the blood groups: y_A, y_{AB}, y_O, y_B

```
> y <- c(179, 6, 202, 35)
```

create design matrix X

```
> X<-matrix(c(
+ 1,1,1,1,1,1,1,1,1,
+ 2,1,1,1,0,0,1,0,0,
+ 0,1,0,1,2,1,0,1,0,
+ 0,0,1,0,0,1,1,1,2
+ ),nr=4,b=T)
> X<-t(X)    #transponieren

   mu xa xo xb
aa  1  2  0  0
ao  1  1  1  0
ab  1  1  0  1
oa  1  1  1  0
oo  1  0  2  0
ob  1  0  1  1
ba  1  1  0  1
bo  1  0  1  1
bb  1  0  0  2
```



```
> Xdf
  genotyp gruppe mu xa xo xb
1      aa      A  1  2  0  0
2      ao      A  1  1  1  0
3      ab     AB  1  1  0  1
4      oa      A  1  1  1  0
5      oo      O  1  0  2  0
6      ob      B  1  0  1  1
7      ba     AB  1  1  0  1
8      bo      B  1  0  1  1
9      bb      B  1  0  0  2
```

which elements have to be added up for each blood group ?
we create a vector with 9 elements (# of all possible patterns)

```
> s <- c(1, 1, 2, 1, 3, 4, 2, 4, 4)
```

where the numbers represent the observed groups
1 for A, 2 for AB, 3 for O and 4 for B

- we fit the model – use package gllm *Duffy (2010)*

```
> library(gllm)
> res <- gllm(y, s, X[, -1])
> summary(res)
Call:
scoregllm(y = y, s = s, X = X, m = as.array(emgllm(y, s, X, maxit = em.maxit,
    tol = tol)$full.table))


No. cells in observed table: 4
No. cells in complete table: 9
    Mean observed cell size: 106
        Model Deviance (df): 3.17 (1)

   Estimate   S.E. exp(Estimate) Lower 95% CL Upper 95% CL
xa    1.642 0.0686          5.17         4.52         5.91
xo    2.664 0.0344         14.35        13.41        15.35
xb    0.027 0.1539          1.03         0.76         1.39
```

parameter estimates are e.g. $\beta_a = 1.64 = \ln p_a$

by $\exp(\beta)/\sum\exp(\beta)$ (normalising) we get the probabilities for alleles $a, b, 0$

```
> e <- exp(coef(res))
> pr <- e/sum(e)

> names(pr) <- c("pa", "po", "pb")
> round(pr, digits = 2)
  pa   po   pb
0.25 0.70 0.05
```

25% of mothers (fathers) have allele a, 70% allele o and 5% allele b

alleles	father			
mother	a	o	b	
a			$p_a p_b$	$p_a = 0.25$
o				$p_o = 0.7$
b	$p_b p_a$			$p_b = 0.05$
	p_a	p_o	p_b	

the probability for AB is $2 * p_a * p_b = 2 * 0.25 * 0.05 = 0.025$

the estimated counts for AB are $p_{AB} * N = (2 * p_a * p_b) * 422 = 10.6$

the fitted values are the expected numbers
for the blood groups A,AB,O,B

```
> fv <- fitted.values(res)
> names(fv) <- c("A", "AB", "O", "B")
> round(fv, digits = 1)
    A    AB     O     B
175.0  10.6 205.9  30.5
```

the observed numbers are:

```
> names(y) <- c("A", "AB", "O", "B")
> y
  A  AB   O   B
179   6 202  35
```

these are the observed counts where we started from

Missing observations in paired comparisons

missing observations can occur for several reasons:
by design, respondent doesn't know, is unwilling, fatigue, etc.

if NA occurs at random – easily handled in LLBT
since $m_{(y_{jk})}$ depend only on observed values

but we want to use pattern models for several reasons

how can we take account of incomplete response patterns?

- each different missing pattern gives a different design matrix (smaller than design matrix for non-missing data)
- we have to link the observed patterns (incomplete patterns) with complete patterns (all possible patterns)

  ▷ use composite link

Data structure for patterns y in block $[\,]$ – no missings

observed y			*complete patterns*			design η			
y_{12}	y_{13}	y_{23}	(12)	(13)	(23)	μ	x_1	x_2	x_3
1	1	1	1	1	1	1	2	0	-2
1	1	−1	1	1	−1	1	2	-2	0
1	−1	1	1	−1	1	1	0	0	0
1	−1	−1	1	−1	−1	1	0	-2	2
−1	1	1	−1	1	1	1	0	2	-2
−1	1	−1	−1	1	−1	1	0	0	0
−1	−1	1	−1	−1	1	1	-2	2	0
−1	−1	−1	−1	−1	−1	1	-2	0	2

- expected numbers for the patterns y in block $[\,]$:

$$\ln m_{y_{[\,]}} = \mu_1 + \sum_{j=1}^{J} \lambda_j^O x_j = \eta_y \qquad m_{y_{[\,]}} = \exp(\eta_y)$$

$$\ln m_{(1,1,\ 1)} = \mu_1 + 2\lambda_1 - 2\lambda_3 = \eta_{\ell_{(1,1,1)}} \qquad m_{(1,1,\ 1)} = \exp(\eta_{\ell_{(1,1,1)}})$$

$$\ln m_{(1,1,-1)} = \mu_1 + 2\lambda_1 - 2\lambda_2 = \eta_{\ell_{(1,1,-1)}} \qquad m_{(1,1,-1)} = \exp(\eta_{\ell_{(1,1,-1)}})$$

Data structure for observed y in block [23] – y_{23} missing

observed y			complete patterns				design η			
y_{12}	y_{13}	y_{23}		(12)	(13)	(23)	μ	x_1	x_2	x_3
1	1	NA	ℓ_1	1	1	1	2	2	0	-2
			ℓ_2	1	1	–1	2	2	-2	0
1	–1	NA	ℓ_3	1	–1	1	2	0	0	0
			ℓ_4	1	–1	–1	2	0	-2	2
–1	1	NA	ℓ_5	–1	1	1	2	0	2	-2
			ℓ_6	–1	1	–1	2	0	0	0
–1	–1	NA	ℓ_7	–1	–1	1	2	-2	2	0
			ℓ_8	–1	–1	–1	2	-2	0	2

- expected numbers for observed y in block [23]

$$m_{y_{[23]}} = \exp(\eta_{y_{12},y_{13},1}) + \exp(\eta_{y_{12},y_{13},-1})$$

we apply composite link

e.g. expected numbers for $observed\ y_{(1,1,NA)}$

$$m_{obs(1,1,NA)} = \exp\eta_{\ell_1} + \exp\eta_{\ell_2}$$
$$= \exp(\mu_2 + 2\lambda_1 - 2\lambda_3) + \exp(\mu_2 + 2\lambda_1 - 2\lambda_2)$$

Data structure – including NA patterns

	observed y			complete patterns			NA patterns r		
	y_{12}	y_{13}	y_{23}	(12)	(13)	(23)	(12)	(13)	(23)
[]	1	1	1	1	1	1	0	0	0
	1	1	–1	1	1	–1	0	0	0
	1	–1	1	1	–1	1	0	0	0
	1	–1	–1	1	–1	–1	0	0	0
	–1	1	1	–1	1	1	0	0	0
	–1	1	–1	–1	1	–1	0	0	0
	–1	–1	1	–1	–1	1	0	0	0
	–1	–1	–1	–1	–1	–1	0	0	0
block 2	1	1	NA	1	1	1	0	0	1
				1	1	–1	0	0	1
	1	–1	NA	1	–1	1	0	0	1
				1	–1	–1	0	0	1
	–1	1	NA	–1	1	1	0	0	1
				–1	1	–1	0	0	1
	–1	–1	NA	–1	–1	1	0	0	1
				–1	–1	–1	0	0	1
block 3		⋮			⋮			⋮	

r_{jk} is 1 if comparison (jk) is missing

How many blocks? $\binom{3}{0} + \binom{3}{1} + \binom{3}{2} + \binom{3}{3} = 1 + 3 + 3 + 1 = 8 \quad (2^{\#comp})$

$\ell = 2^{\#comp}$ complete patterns in each block $\quad (\#resp.categories^{\#comp})$

total number of patterns in complete data is therefore $2^{2^{\#comp}} = 64$

number of all observable patterns is $3^{\#comp} = 27$

Modelling missing values

now we model the complete data

- pattern models including NA's have two parts:
- outcome model: which we modelled so far by

$f(y;\lambda)$ probabilities of outcome model

λs are related to y

$\exp\eta_y$ ... expected numbers in a cell (depend on λ parameters)

- nonresponse model:

$q(r|y;\psi)$ probabilities of nonresponse model

ψs are related to r (and y)

$\exp\eta_{r|y}$... expected numbers in a cell (depend on ψ parameters)

- the joint cell probability for the y and r patterns is

$$P\{y, r; \lambda, \psi\} = f(y)\, q(r|y)$$

Modelling missing values (cont'd)

relate the observed data with complete data

cell probabilities for observed data (incomplete data):

$$P\{y_{12}, y_{13}, y_{23}; \lambda, \psi\} = f(y_{12}, y_{13}, y_{23}; \lambda)\, q(0,0,0 \mid y_{12}, y_{13}, y_{23}; \psi)$$
$$P\{y_{12}, y_{13}, \text{NA}; \lambda, \psi\} = \sum_{y_{23}} f(y_{12}, y_{13}, y_{23}; \lambda)\, q(0,0,1 \mid y_{12}, y_{13}, y_{23}; \psi)$$
$$P\{y_{12}, \text{NA}, y_{23}; \lambda, \psi\} = \sum_{y_{13}} f(y_{12}, y_{13}, y_{23}; \lambda)\, q(0,1,0 \mid y_{12}, y_{13}, y_{23}; \psi)$$
$$\vdots$$

example $P\{y_{12}, y_{13}, \text{NA}; \lambda, \psi\}$:

$$P\{y_{12}, y_{13}, \text{NA}; \lambda, \psi\} = f(y_{12}, y_{13}, 1; \lambda) + f(y_{12}, y_{13}, -1; \lambda) \times q(0,0,1 \mid y_{12}, y_{13}, y_{23}; \psi)$$

- composite link approach

Missing data mechanisms (Rubin, 1976)

let $y_{complete} = (y_{obs}, y_{mis})$ and r_{jk} is NA indicator (if NA: $r_{jk} = 1$)

Missing completely at random (MCAR): $q(r;\,\psi)$
if the conditional distribution $q(r|y;\psi)$ is independent of y, i.e.
$q(r|y;\psi) = q(r;\,\psi)$

Missing at random (MAR): $q(r|\,y_{obs};\,\psi)$
if the conditional distribution depends on
the observed, but not on the missing values
$q(r|y;\psi) = q(r|y_{obs};\psi)$

Missing not at random (MNAR): $q(r|\,y_{obs}, y_{mis};\,\psi)$
if the conditional distribution depends on both
the observed and the missing values,
$q(r|y;\psi) = q(r|y_{obs}, y_{mis};\psi)$

Some models: $q(r\,|\,y;\,\psi)$

- under MCAR assumption: we use α to specify ψ

general model: one α for each comparison $q(r;\,\alpha_{jk})$

$$P\{R_{jk} = r_{jk}; \alpha_{ij}\} = \frac{e^{\alpha_{jk} r_{jk}}}{1+e^{\alpha_{jk}}} \qquad r_{jk} \in \{0,1\}$$

probability for a nonresponse for each comparison – α_{ij} can not be estimated

model 1: common α, i.e., $\alpha_{jk} = \alpha$ $q(r;\,\alpha)$

$$P\{R_{jk} = r_{jk}; \alpha\} = \frac{e^{\alpha \sum_{j<k} r_{jk}}}{1+e^{\alpha \sum_{j<k} r_{jk}}}$$

model 2: reparameterise α_{jk} with $\alpha_j + \alpha_k$ $q(r;\,\alpha_j)$

denominator is now: $\exp(\,\sum_{j=1}^{J} \alpha_j (\sum_{\nu=j+1}^{J} r_{j\nu} + \sum_{\nu=1}^{j-1} r_{\nu j})\,)$

Some models: $q(r\,|\,y;\,\psi)$

- under MNAR assumption: we use α and β to specify ψ
and include dependence on y

general model: one α and β for each comparison $q(r\,|\,y;\alpha_{jk}, \beta_{jk})$

$$P\{R_{jk} = r_{jk}|Y_{jk} = y_{jk}; \alpha_{jk}, \beta_{jk}\} = \frac{e^{(\alpha_{jk}+y_{jk}\beta_{jk})\,r_{jk}}}{1+e^{\alpha_{jk}+y_{jk}\beta_{jk}}}$$

βs are interaction parameters; linear dependent; can not be estimated

- our model: one α and β for each comparison $q(r\,|\,y;\alpha_j, \beta_j)$
reparameterise α_{jk} with $\alpha_j + \alpha_k$ and β_{jk} with $\beta_j + \beta_k$

Estimation:
linear predictors of outcome model η_y are extended to $\eta_y + \eta_{r|y}$
apart from that, the procedure remains the same as for the pure outcome model

The missing observations model in prefmod

some nonresponse models for missing observations are handled using further arguments in the pattern model functions

e.g.:

```
pattPC.fit(obj, nitems, formel = ~1, elim = ~1, resptype = "paircomp",
    obj.names = NULL, undec = FALSE, ia = FALSE,
    NItest = FALSE, NI = FALSE,
    MIScommon = FALSE,
    MISalpha = NULL, MISbeta = NULL, pr.it = FALSE)
```

`NItest` . . . separate estimation for complete and incomplete patterns
`NI` . . . large table (crossclassification with NA patterns)
`MIScommon` . . . fits a common parameter for NA indicators, i.e., $\alpha = \alpha_j = \alpha_k = \ldots$
`MISalpha` . . . specification to fit parameters for NA indicators using $\alpha_j + \alpha_k$
`MISbeta` . . . fits parameters for MNAR model using $\beta_j + \beta_k$

`MIScommon` , `MISalpha`, `MISbeta` not available for
`pattR.fit()` and `pattL.fit()` yet ♠

Missing values example: Attitudes towards foreigners

Survey at the Vienna University of Economics, 2010

98 students rated four extreme statements about hypothetical consequences of migration through a paired comparison experiment

1)	crimRate	Foreigners increase crime rates
2)	position	Foreigners take away training positions
3)	socBurd	Foreigners are a burden for the social welfare system
4)	culture	Foreigners threaten our culture

- the responses to the six comparisons are coded: $(1, 0, -1)$

1 if in a comparison (jk) item j was preferred

-1 if in a comparison (jk) item k was preferred

0 denotes an undecided response – "can not say "

NA is missing: if the answer was "refuse to say "

Data preparation

```
> load("../data/immig.RData")
> head(immig)
  V12 V13 V23 V14 V24 V34 SEX AGE      NAT
1  -1   0   1  -1   1  -1   2  21   Österr
2   1   1  -1   1   0   1   1  26   Österr
3   1   0  -1  NA  NA   1   2  22   Österr
4   1   1  -1   1  NA   1   2  21   Österr
5  NA  -1  NA  NA  NA   1   1  22 Slowakei
6  -1  -1   1   0   1   1   2  20   Österr
> immig<-immig[,1:6]
```

How many missings are in the 6 comparisons? Function: `checkMIS()`

```
> names <- c("crimRate", "position", "socBurd", "culture")
> checkMIS(immig, nitems = 4, verbose = TRUE, obj.names = names)
number of missing comparisons:
         crimRate position socBurd culture
crimRate        0       10      10      16
position       10        0      14      18
socBurd        10       14       0      17
culture        16       18      17       0
number of missing comparisons for objects:
 36 42 41 51
```


Various models to fit

How many missings in data?

```
> table(unlist(immig[,1:6]), useNA="always")
  -1    0    1 <NA>
 143  124  236   85
```

- complete cases CC – remove all patterns with missing values

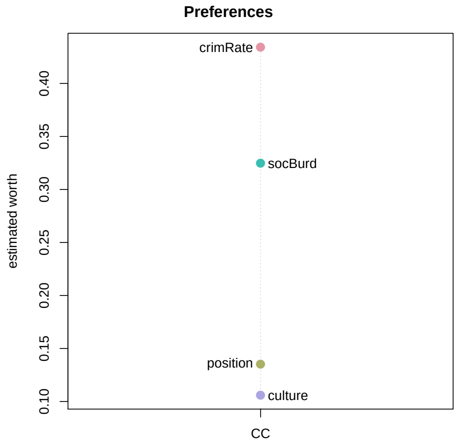
```
> cc <- complete.cases(immig)  # create index cc
> cc[1:5]
[1]  TRUE  TRUE FALSE FALSE FALSE
> # use only data where cc = TRUE i.e.  complete cases
> icompl <- immig[cc,]
```

- fit model for complete cases CC `icompl`

```
> mcc <-  pattPC.fit(icompl, nitems=4, undec=T)
> wcc <- patt.worth(mcc)
> rownames(wcc)<-c("crimRate","position","socBurd","culture")
> colnames(wcc)<-c("CC")
```



```
> plotworth(wcc, ylab = "estimated worth")
```



Pattern models including missing values

- two approaches to estimate outcome model $f(y;\lambda)$

MCAR – 1st approach:

• consider outcome model $f(y;\lambda)$ only – **no modelling of** $q(r|\alpha)$

(the parameters of the outcome model are the λs which include item parameters and may be undecided-term(s), interaction terms, subject covariates)

– possible as under MCAR outcome and nonresponse model are independent

– estimation of outcome model (using composite link) is based on the # of different missing patterns given in the data

– can use small table: only as many blocks as there are different observed missing patterns and no table for r_{jk} `default option: NI = F`

example:

```
> mn<-pattPC.fit(immig, nitems=4, undec=T)
```

deviance of `mn` is 537.5247

• this is the already known specification (and what is done by `prefmod` in case missing values are present in the data)

MCAR – 2nd approach:

estimate outcome model $f(y;\lambda)$ and nonresponse model $q(r;\alpha)$ simultanously – estimation based on big table
all possible blocks × # possible patterns = $2^{\#comp} \times \#resp.cat.^{\#comp}$

- no αs – reference model `option: NI = T`

```
> mn0 <- pattPC.fit(immig, nitems = 4, undec = T, NI = T)
```

deviance of `mn0` is 1353

- αs for each object

```
> mn2<-pattPC.fit(immig, nitems=4, undec=T, MISalpha=c(T,T,T,T))
```

deviance of `mn2` is 1018.533

- one α – same for all objects

```
> mn1<-pattPC.fit(immig, nitems=4, undec=T, MIScommon = T)
```

deviance of `mn1` is 1023.391

• in all MCAR models the λ-parameters for the objects are the same because under MCAR outcome model and nonresponse model are independent (no β)! (but not in complete cases - model)

MNAR models – including βs – always 2nd approach is used:

- αs and βs for each object

```
> mnbeta <- pattPC.fit(immig, nitems=4, undec=T, MISalpha=c(T,T,T,T),
+                      MISbeta=c(T,T,T,T))
```

deviance of `mnbeta` is 978.7235

• in MNAR models the λ-parameters might be different to MCAR models the inclusion of βs can affect the λs – the object parameters

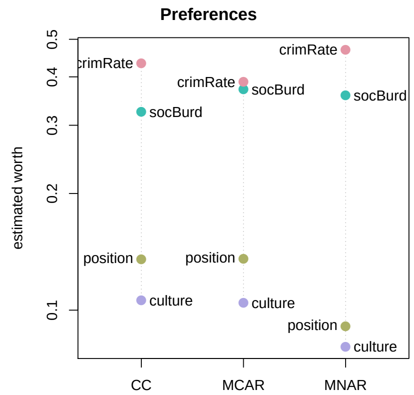
• are there not ignorable missing values?

we compare:
model with 4αs: `mn2` deviance is 1018.533 and
model with 4αs + 4βs : `mnbeta` deviance is 978.7235

```
> d <- (1018.533 - 978.7235)
> 1 - pchisq(d, 4)
[1] 4.74e-08
```

• there is a significant deviance change – we need β-parameters
• in this example missing values are not at random!

Example (cont'd)



MNAR models – βs

- estimation problems if there are no missing values for certain objects

use option: checkMIS() in MISalpha and MISbeta

```
> nam <- c("crimRate","position","socBurd","culture")
> mnbetac <- pattPC.fit(immig, nitems=4, undec=T,
+                       MISalpha=checkMIS(immig,nitems=4),
+                       MISbeta=checkMIS(immig,nitems=4),
+                       obj.names=nam)
```

```
Deviance:  979
log likelihood:  -727

no of iterations:  35  (Code: 1 )

             estimate    se       z p-value
crimRate       0.8826 0.117   7.549  0.0000
position       0.0605 0.102   0.594  0.5525
socBurd        0.7463 0.109   6.819  0.0000
mis.alpha1    -1.1057 0.212  -5.213  0.0000
mis.alpha2    -1.0072 0.213  -4.736  0.0000
mis.alpha3    -1.4851 0.316  -4.693  0.0000
mis.alpha4    -0.4054 0.200  -2.024  0.0430
mis.beta1     -0.8243 0.252  -3.266  0.0011
mis.beta2     -0.4636 0.225  -2.059  0.0395
mis.beta3      1.6111 0.321   5.026  0.0000
mis.beta4     -0.7903 0.243  -3.256  0.0011
U             -0.2678 0.108  -2.487  0.0129
```


Interpretation of βs

According to the NMAR model:

example: odds for nonresponse in comparison (34) i.e. (socBurd, culture)

$\exp(2\beta_3 + 2\beta_4)$ gives the odds ratio of

the odds for NA if socBurd would have been chosen $y_{34} = 1$ to
the odds for NA if culture would have been chosen $y_{34} = -1$
to be the more likely consequence of migration

```
> exp(2 * 1.6111 + 2 * -0.7903)
[1] 5.16
```

- if someone would have chosen socBurd (compared to culture),

the odds for a nonresponse are 5.16 times higher

- The inclination not to respond in a given comparison (jk) depends on

the objects involved – it depends on

the response which would have been given

odds for all comparisons – $\exp(2\beta_i + 2\beta_j)$

consequences	if choosen			
	crimRate	position	socBurd	culture
crimRate1	–	13.14		25.26
position	0.08	–		12.28
socBurd	4.82	9.92	–	
culture	0.04	0.08	5.16	–

- if someone would have chosen position (compared to culture), the odds for a nonresponse are $\exp(2 * -0.4636 + 2 * -0.7903)$ =0.08 times lower but

- if someone would have chosen culture (compared to position), the odds for a nonresponse are $1/\exp(2 * -0.4636 + 2 * -0.7903) = 12.28$ times higher

- if someone would have chosen culture (compared to crimRate), the odds for a nonresponse are $1/\exp(2 * -0.8243 + 2 * -0.7903) = 25.26$ times higher

examine log odds: $(2\beta_i + 2\beta_j)$

```
> beta <- coef(mnbetac)[8:11]
> #  get sum of all combinations of 4 betas
> b<-outer(beta,beta, "+")
> # upper triangle is minus lower triangle on log scale
> b[upper.tri(b)]<- b[upper.tri(b)]*(-1)
> # need to multiply by 2
> b <- b*2
> # diagonal should be 0
> diag(b)<-0
> nam <- c("crime","pos","socB","culture")
> dimnames(b) <- list(nam, nam)
```

examine log odds: (cont'd)

```
> b
        crime   pos  socB culture
crime    0.00  2.58 -1.57    3.23
pos     -2.58  0.00 -2.30    2.51
socB     1.57  2.30  0.00   -1.64
culture -3.23 -2.51  1.64    0.00
> # sum of all columns (log odds for NA for item i versus all other items)
> colSums(b)
  crime     pos    socB culture
  -4.23    2.36   -2.23    4.10
```

- for items with positive log odds for NA (position, culture) compared to all others the λs decrease in MNAR model

- for items with negative log odds for NA (crime, socB) compared to all others the λs increase in MNAR model

examine odds: $\exp(2\beta_i + 2\beta_j)$

```
> odds <- exp(b)
> odds
         crime     pos  socB culture
crime   1.0000 13.1412 0.207  25.262
pos     0.0761  1.0000 0.101  12.278
socB    4.8241  9.9256 1.000   0.194
culture 0.0396  0.0814 5.163   1.000
> # sum of all columns (odds of NA for item i versus all other items)
> colSums(odds)
  crime     pos    socB culture
   5.94   24.15    6.47   38.73
```