

UG Reinis data

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Reinis Data

Data collected at the beginning of a 15 year follow-up study of probable risk factors for coronary thrombosis. Data are from all men employed in a car factory ($N = 1841$).

A table with 6 discrete variables. A: smoking, B: strenuous mental work, C: strenuous physical work, D: systolic blood pressure, E: ratio of lipoproteins, F: Family anamnesis of coronary heart disease.

```
library("readr")
data_reinis <- read_rds("data_reinis.rds")
colnames(data_reinis) <- c('A', 'B', 'C', 'D', 'E', 'F')
tab_reinis <- table(data_reinis)
head(as.data.frame(tab_reinis))
```

	A	B	C	D	E	F	Freq
1	y	y	y	y	y	y	44
2	n	y	y	y	y	y	40
3	y	n	y	y	y	y	112
4	n	n	y	y	y	y	67
5	y	y	n	y	y	y	129
6	n	y	n	y	y	y	145

Test of conditional independence

A conditional independence $F \perp\!\!\!\perp D \mid BECA$ is expected. Let's test this hypothesis

```
ci.test("F", "D", c("B", "E", "C", "A"), data = data_reinis)
```

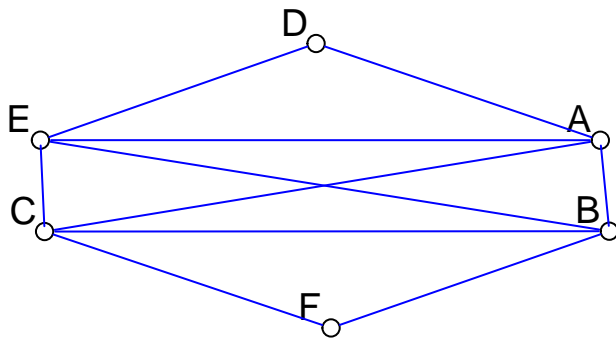
Mutual Information (disc.)

```
data: F ~ D | B + E + C + A
mi = 18.345, df = 16, p-value = 0.3041
alternative hypothesis: true value is greater than 0
```

The statistic `mi` is the same of the deviance. Apparently the conditional independence is not rejected.

The previous CI is implied for example by the following graph

```
G <- UG(~ F*C*B + B*E*C*A + E*A*D)
drawGraph(G, layout = layout_nicely)
```



Fit the graph

```
m_red <- glm(Freq ~ F*C*B + B*E*C*A + E*A*D,
             family = poisson,
             data = as.data.frame(tab_reinis))
summary(m_red)
```

Call:

```
glm(formula = Freq ~ F * C * B + B * E * C * A + E * A * D, family = poisson,
     data = as.data.frame(tab_reinis))
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	3.76049	0.11497	32.708	< 2e-16 ***

Fn	-1.96308	0.18589	-10.560	< 2e-16	***
Cn	1.08271	0.12610	8.586	< 2e-16	***
Bn	0.89935	0.12894	6.975	3.06e-12	***
En	-0.52184	0.18076	-2.887	0.003891	**
An	-0.15948	0.17283	-0.923	0.356127	
Dn	-0.22841	0.08232	-2.775	0.005525	**
Fn:Cn	0.03573	0.21424	0.167	0.867559	
Fn:Bn	0.25384	0.21506	1.180	0.237867	
Cn:Bn	-3.34495	0.25075	-13.340	< 2e-16	***
Bn:En	0.14105	0.19736	0.715	0.474819	
Cn:En	-0.40269	0.20281	-1.986	0.047080	*
Bn:An	-0.29927	0.20126	-1.487	0.137011	
En:An	0.27564	0.26177	1.053	0.292347	
Cn:An	0.29101	0.18812	1.547	0.121872	
En:Dn	0.22290	0.13340	1.671	0.094738	.
An:Dn	-0.49731	0.12886	-3.859	0.000114	***
Fn:Cn:Bn	0.34909	0.32898	1.061	0.288629	
Cn:Bn:En	0.45540	0.37614	1.211	0.225999	
Bn:En:An	0.12678	0.29504	0.430	0.667409	
Cn:Bn:An	0.77717	0.33870	2.295	0.021757	*
Cn:En:An	0.08344	0.28944	0.288	0.773116	
En:An:Dn	0.32489	0.19311	1.682	0.092487	.
Cn:Bn:En:An	-0.42525	0.50350	-0.845	0.398340	

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

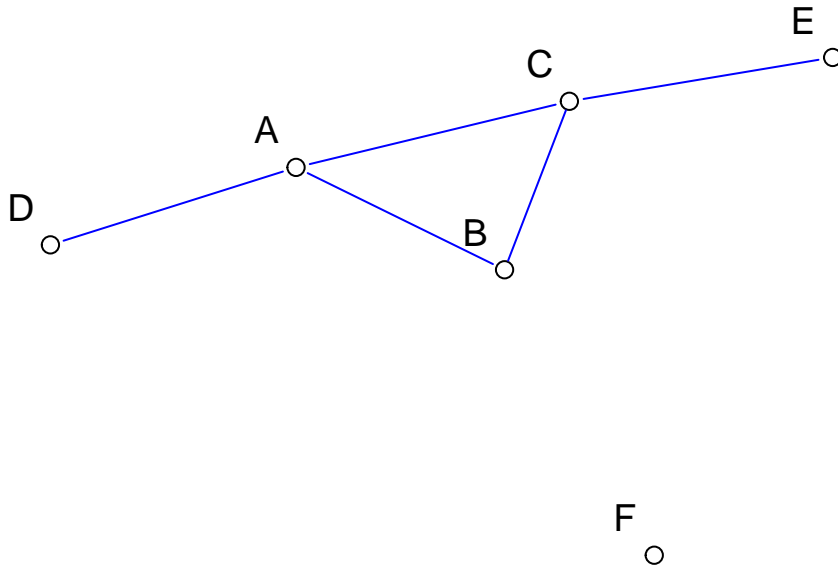
Null deviance: 2026.740 on 63 degrees of freedom
 Residual deviance: 42.298 on 40 degrees of freedom
 AIC: 379.95

Number of Fisher Scoring iterations: 4

The model shows some further possible reductions

The strongest terms correspond to CB, CE, AD and CBA. Therefore a suitable graph should be

```
GO <- UG(~ F + C*B*A + C*E + A*D)
drawGraph(GO, layout = layout_nicely)
```



Notice that surprisingly there is a complete independence of family anamnesis of CHD from the other variables.

Fitting this graphical model we get

```
m0 <- glm(Freq ~ F + C*B*A + C*E + A*D,
           family = poisson,
           data = as.data.frame(tab_reinis))
summary(m0)
```

Call:

```
glm(formula = Freq ~ F + C * B * A + C * E + A * D, family = poisson,
    data = as.data.frame(tab_reinis))
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	3.57204	0.09380	38.083	< 2e-16 ***
Fn	-1.80513	0.06692	-26.973	< 2e-16 ***
Cn	1.10930	0.10549	10.516	< 2e-16 ***
Bn	0.99274	0.09689	10.246	< 2e-16 ***
An	-0.04598	0.12910	-0.356	0.721691
En	-0.11880	0.06580	-1.805	0.071016 .
Dn	-0.14385	0.06468	-2.224	0.026156 *
Cn:Bn	-3.11567	0.18512	-16.831	< 2e-16 ***
Cn:An	0.28787	0.14175	2.031	0.042270 *

Bn:An	-0.21704	0.14614	-1.485	0.137519	
Cn:En	-0.38619	0.09482	-4.073	4.65e-05	***
An:Dn	-0.31399	0.09472	-3.315	0.000917	***
Cn:Bn:An	0.60616	0.24928	2.432	0.015030	*

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 2026.740 on 63 degrees of freedom
 Residual deviance: 96.812 on 51 degrees of freedom
 AIC: 412.46

Number of Fisher Scoring iterations: 4

The deviance however indicates a quite poor agreement with the hypothesis so this model is rejected.