The loglinear - logit connection

```r
> d=factor(rep(c("White","Black"),2))
> v=factor(rep(c("White","Black"),each=2))
> yes=c(53,11,0,4);no=c(414,37,16,139)

Treat P as the response for logit models.

1. Model equivalent to (DP,VP,DV) is

\[ \log \left( \frac{P}{P = 1 | D = i, V = j} \right) = \alpha + \beta^D_i + \beta^V_j \]

```r
> fit.logit=glm(cbind(yes,no)~d+v, family=binomial(link=logit))
> summary(fit.logit)

Call:
glm(formula = cbind(yes, no) ~ d + v, family = binomial(link = logit))

Deviance Residuals:

<p>| | | | |</p>
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<tbody>
<tr>
<td>1</td>
<td>0.02660</td>
<td>-0.06232</td>
<td>-0.60535</td>
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Coefficients:

|                | Estimate | Std. Error | z value | Pr(>|z|) |
|----------------|----------|------------|---------|----------|
| (Intercept)    | -3.5961  | 0.5069     | -7.094  | 1.30e-12 *** |
| dWhite         | -0.8678  | 0.3671     | -2.364  | 0.0181 *  |
| vWhite         | 2.4044   | 0.6006     | 4.003   | 6.25e-05 *** |

---

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 22.26591 on 3 degrees of freedom
Residual deviance: 0.37984 on 1 degrees of freedom
AIC: 19.3

Number of Fisher Scoring iterations: 4

The \( G^2 = 0.4 \) with

\[
\text{df} = 8 - 7(\text{loglinear}) = 4 - 3(\text{logit}) = 1
\]

(8 poisson cell counts or 4 binomial logits) is the same as before. In addition, the standardized residuals are the same (due to standardization). However, the non-standardized residuals differ due to the different denominator \( V(Y_{ij}) \) due to different models.

```r
> std.pearson.dv=rstandard(fit.logit,type="pearson") # Pearson residuals
> predict.dv=fitted(fit.logit) # estimated proportion of yes verdicts
> sample= yes/(yes + no) # sample proportions
> cbind(sample, predict.dv, std.pearson.dv)
```
Controlling for defendant’s race, the odds of receiving the death penalty is estimated to be \( \exp(2.404) = 11.1 \) times as high when victims were black. A 95% CI for \( \theta(D|V_P) \) is \( \exp(2.404 \pm 1.96(0.600)) \equiv (3.4, 35.9) \). A more reliable CI (due to a zero cell count) is LR CI.

```r
> exp(confint(fit.logit, "vWhite")) # LR CI
   2.5 %    97.5 %
3.694533 41.165583
```

2. Model equivalent to \((DV, PV)\) is

\[
\logit[P(P = 1|D = i, V = j)] = \alpha + \beta_j^V
\]

```r
> fit.v = update(fit.logit, ~ . - d)
> summary(fit.v)
```

Call:
`glm(formula = cbind(yes, no) ~ v, family = binomial(link = logit))`

Deviance Residuals:

```
1 2 3 4
-0.7154 2.0056 -0.9030 0.2112
```

Coefficients:

```
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  -3.6571     0.5064  -7.222 5.14e-13 ***
vWhite       1.7045     0.5237   3.255 0.00114 **
```

---

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 22.266 on 3 degrees of freedom
Residual deviance: 5.394 on 2 degrees of freedom
AIC: 22.314

Number of Fisher Scoring iterations: 4

```r
> std.pearson.v = rstandard(fit.v, type = "pearson") # Pearson residuals
> predict.v = fitted(fit.v) # estimated proportion of yes verdicts
> cbind(sample, predict.v, std.pearson.v)
```

```r
sample predict.v std.pearson.v
1 0.11349036 0.11310026 0.4447328
2 0.22916667 0.23296207 -0.4447328
3 0.00000000 0.01138621 -0.4447329
4 0.02797203 0.02669805 0.4447329
```
has $G^2 = 5.4$ and df= 8 – 6 (for loglinear), or $4 – 2$ (for logit).

> summary(dv_pv)

Call:
  glm(formula = count ~ D + V + P + D:V + V:P, family = poisson(link = log),
     data = death)

Deviance Residuals:
   1       2       3       4       5       6       7       8
  -0.6708  0.24846 -0.89724  0.10149  1.84218 -0.79292  0.20843 -0.03411

Coefficients:  
             Estimate Std. Error z value Pr(>|z|)  
(Intercept)  4.93737   0.08459   58.369  < 2e-16 ***
DWhite       -2.19026   0.26362  -8.309   < 2e-16 ***
VWhite       -1.19886   0.16812  -7.131  9.96e-13 ***
PYes         -3.65713   0.50641  -7.222  5.14e-13 ***
DWhite:VWhite 4.46538   0.30408  14.685   < 2e-16 ***
VWhite:PYes   1.70455   0.52373   3.255   0.00114 **
---  
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 1225.080  on 7 degrees of freedom  
Residual deviance:  5.394  on 2 degrees of freedom  
AIC: 55.434

Number of Fisher Scoring iterations: 4