Today

- HW 2
- `http://www.zoology.ubc.ca/~schluter/zoo502stats/Rtips.models.html`
- Examples §10.4
- thoughts on Shaghayegh's study
- thoughts on "speaking up" study from last week

Calcium data: Example 10.1 and 10.9

10.1 · Introduction

Table 10.1 Calcium uptake (nmoles/mg) of cells suspended in a solution of radioactive calcium, as a function of time suspended (minutes) (Rawlings, 1988, p. 403).

Time (minutes)	Calcium uptake (nmoles/mg)		
0.45	0.34170	−0.00438	0.82531
1.30	1.77967	0.95384	0.64080
2.40	1.75136	1.27497	1.17332
4.00	3.12273	2.60958	2.57429
6.10	3.17881	3.00782	2.67061
8.05	3.05959	3.94321	3.43726
11.15	4.80735	3.35583	2.78309
13.15	5.13825	4.70274	4.25702
15.00	3.60407	4.15029	3.42484

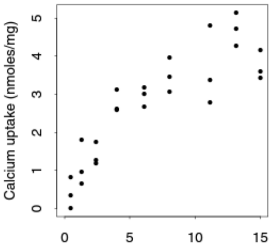


Figure 10.1 Calcium uptake (nmoles/mg) of cells suspended in a solution of radioactive calcium, as a function of time suspended (minutes).

... calcium data

§10.3 μ_j

- model
  $E(y_j) = \beta_0\{1-\exp(-x_j/\beta_1)\}, \quad y_j = E(y_j)+\epsilon_j,\ \epsilon_j \sim N(0,\sigma^2)$
- fitting:

$$\min_{\beta_0,\beta_1} \sum_{j=1}^{n} (y_j - \eta_j)^2$$

$\eta_j \neq x_j^T\beta$

§10.2

- use `nls` or `nlm`; requires starting values
-
```
> library(SMPracticals); data(calcium)
> fit = nls(cal ~ b0*(1-exp(-time/b1)), data = calcium, start = list(b0=5,b1=5))
> summary(fit)
Formula: cal ~ b0 * (1 - exp(-time/b1))

Parameters:
   Estimate Std. Error t value Pr(>|t|)
b0   4.3094     0.3029  14.226 1.73e-13 ***
b1   4.7967     0.9047   5.302 1.71e-05 ***
---
Signif. codes:  0 Ô***Õ 0.001 Ô**Õ 0.01 Ô*Õ 0.05 Ô.Õ 0.1 Ô Õ 1

Residual standard error: 0.5464 on 25 degrees of freedom

Number of iterations to convergence: 3
Achieved convergence tolerance: 9.55e-07
```

... calcium data

$\beta_0(1-e^{-x/\beta_1}) = \beta_0(1-e^{-\gamma x})$

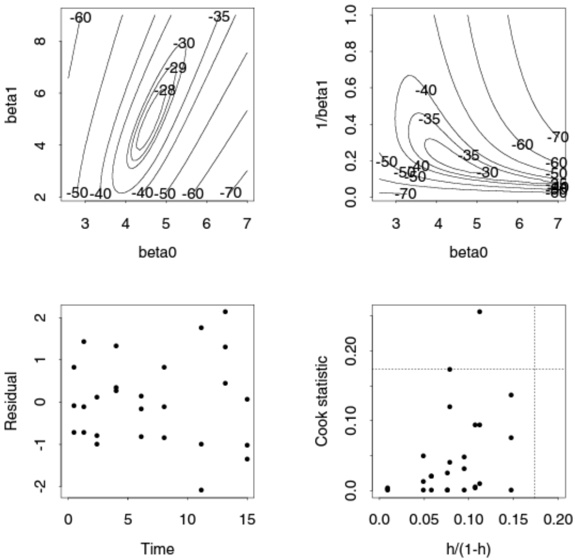


Figure 10.4 Fit of a nonlinear model to the calcium data. Upper left: contours for $\ell_p(\beta_0, \beta_1)$. Upper right: contours for $\ell_p(\beta_0, \gamma_1)$, where $\gamma_1 = 1/\beta_1$. Lower left: standardized residuals plotted against time. Lower right: plot of Cook statistics against $h/(1-h)$, where h is leverage.

... calcium data

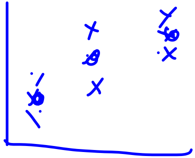
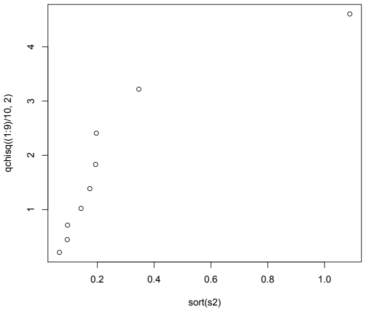
$$\frac{MSS_{model}/\sigma^2}{MSE/\sigma^2}$$

- there are 3 observations at each time point
- can fit a model with a different parameter for each time: $E(y_j) = \eta_j + \epsilon_j$
- the nonlinear model is nested within this; constrains η_j as above $y_{ij} = \mu + \alpha_i + \epsilon_{ij}$
- `anova(lm(cal ~ factor(time), data = calcium))`
- `Analysis of Variance Table`

$$y_{ij} = \beta_0(1-e^{-x_j/\beta_1}) + \epsilon_{ij}$$

```
Response: cal
              Df Sum Sq Mean Sq F value    Pr(>F)
factor(time)   8 48.437  6.0546  22.720 6.688e-08 ***
Residuals     18  4.797  0.2665
```

- ```
  > deviance(fit) # 7.464514 (mistake in Davison)
  > sum(residuals(fit)^2) # 7.464514
  > (7.464514 - 4.797)/(25 - 18) # 0.3811
  > .3811/.2665
  [1] 1.429919  ## Davison has 1.53
  > > pf(1.430,7,18)
  [1] 0.7461687
  ```


  ```

... calcium data

- checking constant variance assumption
- estimates of σ^2 at each time, each with 2 degrees of freedom
- ```
  > s2 = with(calcium, tapply(cal, factor(time),var))
  > s2
        0.45        1.3        2.4          4        6.1       8.05
  0.17367258 0.34616902 0.09523507 0.09422579 0.06686923 0.19656739
       11.15      13.15         15
  1.08876166 0.19415027 0.14279290
  > plot(sort(s2),qchisq((1:9)/10,2))
  ```


  ```

Binary Data: Example 10.18

- `library(SMPracticals); data(nodal)` has 53 binary observations; one per patient
- x_i's are: `age`, `stage`, `grade`, `xray`, `acid`
- all dummy variables

```
> data(nodal)
> nodal[1:10,]
   m r aged stage grade xray acid
1  1 1    0     1     1    1    1
2  1 1    0     1     1    1    1
3  1 1    0     1     1    1    1
4  1 1    0     1     1    1    1
5  1 1    0     1     1    1    1
6  1 0    0     1     1    1    1
7  1 1    0     0     0    0    1
8  1 0    0     0     0    0    1
9  1 0    0     0     0    0    1
10 1 0    0     0     0    0    1
```

... example 10.18

- model

$$\log\left(\frac{p_i}{1-p_i}\right) = x_i^T\beta$$

- maximum likelihood fitting

```
binaryfit = glm(cbind(r, m-r)~.  , data =
nodal, family = binomial)
```

- choice of variables: `step(fit)` ←
- selects the model with `stage`, `xray`, and `acid`
- estimated coefficients: $-3.05, 1.65, 1.91, 1.64$

$$\begin{bmatrix} | & | \\ \text{succ} & \text{fail} \\ | & | \end{bmatrix}$$

?glm (family
binom)

... example 10.18

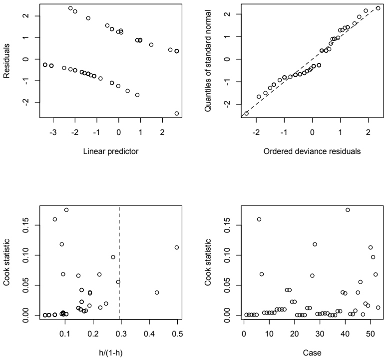
```
> summary(fit)

Call:
glm(formula = cbind(r, m - r) ~ ., family = binomial, data = nodal)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.3317  -0.6653  -0.2999   0.6386   2.1502

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -3.0794     0.9868  -3.121  0.00180 **
age1         -0.2917     0.7540  -0.387  0.69881
stage1        1.3729     0.7838   1.752  0.07986 .
grade1        0.8720     0.8156   1.069  0.28500
xray1         1.8008     0.8104   2.222  0.02628 *
acid1         1.6839     0.7915   2.128  0.03337 *
---
Signif. codes:  0 Ô***Õ 0.001 Ô**Õ 0.01 Ô*Õ 0.05 Ô.Õ 0.1 Ô Õ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 70.252  on 52  degrees of freedom
Residual deviance: 47.611  on 47  degrees of freedom
AIC: 59.611

Number of Fisher Scoring iterations: 5
```

... example 10.18

```
> step(fit)
Start:  AIC=59.61
cbind(r, m - r) ~ age + stage + grade + xray + acid

        Df Deviance    AIC
- age    1   47.760 57.760
- grade  1   48.760 58.760
<none>       47.611 59.611
- stage  1   50.808 60.808
- acid   1   52.660 62.660
- xray   1   52.922 62.922

Step:  AIC=57.76
cbind(r, m - r) ~ stage + grade + xray + acid

        Df Deviance    AIC
- grade  1   49.180 57.180
<none>       47.760 57.760
- stage  1   50.817 58.817
- xray   1   53.162 61.162
- acid   1   53.526 61.526

Step:  AIC=57.18
cbind(r, m - r) ~ stage + xray + acid

        Df Deviance    AIC
<none>       49.180 57.180
- acid   1   54.463 60.463
- stage  1   54.788 60.788
- xray   1   55.915 61.915
```

... example 10.18

```
Call:  glm(formula = cbind(r, m - r) ~ stage + xray + acid, family = binomial, data = nodal)

Coefficients:
(Intercept)        stage1         xray1         acid1
     -3.052         1.645         1.912         1.638

Degrees of Freedom: 52 Total (i.e. Null);  49 Residual
Null Deviance:      70.25
Residual Deviance: 49.18   AIC: 57.18
```



- binary data
resid dev
doesn't check fit

- binomial maybe
$m_i > 5$

... example 10.18

aggregated data presented in textbook

Table 10.8 Data on nodal involvement (Brown, 1980).

m	*r*	age	stage	grade	xray	acid
6	5	0	1	1	1	1
6	1	0	0	0	0	1
4	0	1	1	1	0	0
4	2	1	1	0	0	1
4	0	0	0	0	0	0
3	2	0	1	1	0	1
3	1	1	1	0	0	0
3	0	1	0	0	0	1
3	0	1	0	0	0	0
2	0	1	0	0	1	0
2	1	0	1	0	0	1
2	1	0	0	1	0	0
1	1	1	1	1	1	1
1	1	1	1	0	1	1
1	1	1	0	1	1	1
1	1	1	0	0	1	1
1	0	1	0	1	0	0
1	1	0	1	1	1	0
1	0	0	1	1	0	0
1	1	0	1	0	1	0
1	1	0	0	1	0	1
1	0	0	0	0	1	1

... example 10.18

- In data set `nodal` several patients have the same value of the covariates
- these can be added up to make a binomial observation
- ```
   > nodal2[1:4,]
    m r age stage grade xray acid
  1 6 5   0     1     1    1    1
  2 6 1   0     0     0    0    1
  3 4 0   1     1     1    0    0
  4 4 2   1     1     0    0    1
  ```
- ```
  > fit2 = glm(cbind(r,m-r) ~ ., data = nodal2, family = binomial)
  > summary(fit2)  # stuff omitted
  Coefficients:
              Estimate Std. Error z value Pr(>|z|)
  (Intercept)  -3.0794     0.9868  -3.121  0.00180 **
  age          -0.2917     0.7540  -0.387  0.69881
  stage         1.3729     0.7838   1.752  0.07986 .
  grade         0.8720     0.8156   1.069  0.28500
  xray          1.8008     0.8104   2.222  0.02628 *
  acid          1.6839     0.7915   2.128  0.03337 *
  ---
  Signif. codes:  0 Ô***Õ 0.001 Ô**Õ 0.01 Ô*Õ 0.05 Ô.Õ 0.1 Ô Õ 1

  (Dispersion parameter for binomial family taken to be 1)

      Null deviance: 40.710  on 22  degrees of freedom
  Residual deviance: 18.069  on 17  degrees of freedom
  AIC: 41.693

  Number of Fisher Scoring iterations: 5
  ```

... example 10.18

```
> step(binomialfit)

Coefficients:
(Intercept)        stage          xray          acid
     -3.052        1.645         1.912         1.638

Degrees of Freedom: 22 Total (i.e. Null);  19 Residual
Null Deviance:       40.71
Residual Deviance: 19.64  AIC: 39.26
```

– same coefficient estimates; same estimated standard errors

– different residual deviance and different degrees of freedom

– MISTAKE in text on p. 491; residual scaled deviance is 49.180 on 49 df when fitting to all 53 observations; and cannot be used as a test of fit

– deviances in Table 10.9 are incorrect as well

`http://statwww.epfl.ch/davison/SM/` has corrected version

Parameter interpretation

link="logit"

- $$\log \frac{\Pr(Y=1 \mid x)}{\Pr(Y=0 \mid x)} = x^T\beta$$

log odds

- $$p(x) = \frac{\exp(x^T\beta)}{1+\exp(x^T\beta)}$$

- odds of 'success' increase by a factor of e^{β_j} for every 1-unit increase in x_j
- thus for Ex 10.8, odds of nodal involvement increase by $e^{1.91}$ when `acid =1` relative to `acid = 0`
- all other variables held fixed
- "fitted odds when all explanatory variables take their lower levels are $e^{-3.05} = 0.047$"
- corresponds to $\Pr(Y=1 \mid 0,0,0) = 0.045$ ("no such cases in the data" is incorrect)

acid, stage, xray

Dichotomizing continuous data (§10.4.1)

- suppose $Z_j = x_j^T\gamma + \sigma\epsilon_j, \quad j = 1, \ldots, n; \quad \epsilon_j \sim f(\cdot)$
- $Y_j = 1$ if $Z_j > 0;$ otherwise 0
- $$\Pr(Y_j = 1) = 1 - F(-x_j^T\gamma/\sigma) = 1 - F(-x_j^T\beta) = F(x_j^T\beta), \text{if} \ldots$$
- examples (Table 10.7)

logistic	$F(u) = e^u/(1+e^u)$	logit	$log\{p/(1-p)\} = x^T\beta$
normal	$F(u) = \Phi(u)$	probit	$\Phi^{-1}(p) = x^T\beta$
log-Weibull	$F(u) = 1 - \exp(-e^u)$	log-log	$-\log\{-\log(p)\} = x^T\beta$
Gumbel	$F(u) = \exp\{-e^{-u}\}$	c-log-log	$\log\{-\log(1-p)\} = x^T\beta$

- Example 10.17 considers how much information is lost in going from Z to Y
- in special case where $x_j = -1, -0.9, \ldots, 0.9, 1,$
  $z_j = 0.5 + 2x_j + \epsilon_j, \quad \epsilon_j \sim N(0, 1)$
  $y_j = 1(z_j > 0)$

2×2 table §10.4.2

- special case of binary regression, with one covariate taking values 0, 1
- $\Pr(Y_j = 1 \mid x_j = 0) = \dfrac{\exp(\beta_0)}{1 + \exp(\beta_0)} = \pi_0$
- $\Pr(Y_j = 1 \mid x_j = 1) = \dfrac{\exp(\beta_0 + \beta_1)}{1 + \exp(\beta_0 + \beta_1)} = \pi_1$
- in text: $\psi \leftarrow \beta_1, \lambda \leftarrow \beta_0, T \leftarrow x$

- $Y = 1$ is the event of interest – death, cure, heart attack, ...
- $x = 1$ is the factor of interest – treatment, smoking status, exposure, ... (Davison calls these 'cases')
- it is more usual to call the units with $Y = 1$ the cases (dead, sick, recovered, ...), and $Y = 0$ the controls (alive, well, not recovered ...)

Dichotomizing continuous data (§10.4.1)

- suppose $Z_j = x_j^T\gamma + \sigma\epsilon_j, \quad j = 1, \dots, n; \quad \epsilon_j \sim f(\cdot)$
- $Y_j = 1$ if $Z_j > 0$; otherwise 0
- $$\Pr(Y_j = 1) = 1 - F(-x_j^T\gamma/\sigma) = 1 - F(-x_j^T\beta) = F(x_j^T\beta), \text{if } \dots$$
- examples (Table 10.7)

logistic	$F(u) = e^u/(1+e^u)$	logit	$log\{p/(1-p)\} = x^T\beta$
normal	$F(u) = \Phi(u)$	probit	$\Phi^{-1}(p) = x^T\beta$
log-Weibull	$F(u) = 1 - \exp(-e^u)$	log-log	$-\log\{-\log(p)\} = x^T\beta$
Gumbel	$F(u) = \exp\{-e^{-u}\}$	c-log-log	$\log\{-\log(1-p)\} = x^T\beta$

- Example 10.17 considers how much information is lost in going from Z to Y
- in special case where $x_j = -1, -0.9, \dots, 0.9, 1,$
  $z_j = 0.5 + 2x_j + \epsilon_j, \quad \epsilon_j \sim N(0, 1)$
  $y_j = 1(z_j > 0)$

... example 10.17

- $x_j = -1, -0.9, \ldots, 0.9, 1,$
  $z_j = 0.5 + 2x_j + \epsilon_j, \quad \epsilon_j \sim N(0,1), \quad y_j = 1(z_j > 0)$
- $\hat\beta_Z$ is least squares estimator from original data
- $\text{cov}(\hat\beta_Z) = (X^TX)^{-1} = \begin{pmatrix} n & \sum x_i \\ \sum x_i & \sum x_i^2 \end{pmatrix}^{-1}$
- $\text{var}(\hat\beta_{1Z}) = 1/\sum(x_i - \bar x)^2$ smaller

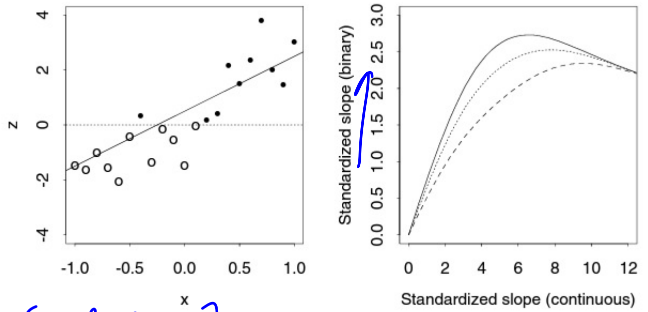
- $\hat\beta_Y$ is the estimator from dichotomized data
- $\text{cov}(\hat\beta_Y) \doteq (X^TWX)^{-1}, \quad W = \text{diag}(w_j)$ (p.488)
- $w_j = \dfrac{\phi^2(\beta_0 + \beta_1 x_j)}{\Phi(-\beta_0 - \beta_1 x_j)\Phi(\beta_0 + \beta_1 x_j)}$
- $\text{cov}(\hat\beta_Y) \doteq \begin{pmatrix} \sum w_j & \sum w_j x_j \\ \sum w_j x_j & \sum w_j x_j^2 \end{pmatrix}^{-1}$
- $\text{var}(\hat\beta_{1Y}) = (X^TWX)^{-1}_{(2,2)}$ bigger

... example 10.17

- Figure 10.6 (right) plots $\beta_1 / \left(\sqrt{\sum (x_j - \bar{x})^2}\right)^{-1}$ on the x-axis, and $\beta_1 / \sqrt{(X'WX)_{(2,2)}}$ on the y-axis
- trying to compare v_Z and v_Y, as well as indicate behaviour of $\beta_{1Y} / \sqrt{v_Y}$ as $\beta_1 \to \infty$

Vcov

Figure 10.6 Efficiency loss due to reducing continuous variables to binary ones. Left panel: simulated data. Blobs above the dotted line are counted as successes, with zeros below it as failures; the solid line is $0.5 + 2x$. Right panel: Comparison of asymptotic t statistics when continuous data are dichotomized, for normal error distribution, when $\beta_0 = 0.5, 1, 1.5$ (solid, dots, dashes).



? V_Y vs V_Z as a f of β_1 ?

2×2 table §10.4.2

$\log \frac{p}{1-p} = \beta_0 + \beta_1 x$

- special case of binary regression, with one covariate taking values 0, 1
- $\Pr(Y_j = 1 \mid x_j = 0) = \dfrac{\exp(\beta_0)}{1 + \exp(\beta_0)} = \pi_0$
- $\Pr(Y_j = 1 \mid x_j = 1) = \dfrac{\exp(\beta_0 + \beta_1)}{1 + \exp(\beta_0 + \beta_1)} = \pi_1$
- in text: $\psi \leftarrow \beta_1, \lambda \leftarrow \beta_0, T \leftarrow x$
- $Y = 1$ is the event of interest – death, cure, heart attack, ...
- $x = 1$ is the factor of interest – treatment, smoking status, exposure, ... (Davison calls these 'cases')
- it is more usual to call the units with $Y = 1$ the cases (dead, sick, recovered, ...), and $Y = 0$ the controls (alive, well, not recovered ...)

2×2 **table** §**10.4.2**

- special case of binary regression, with one covariate taking values 0, 1
- $\Pr(Y_j = 1 \mid x_j = 0) = \dfrac{\exp(\beta_0)}{1 + \exp(\beta_0)} = \pi_0$
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- in text: $\psi \leftarrow \beta_1, \lambda \leftarrow \beta_0, T \leftarrow x$

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Prospective and retrospective sampling C &D §3.6

Table 3.6 *Distribution of a binary explanatory variable, z, and response variable, y, in (a) population study, (b) prospective or cohort study, (c) retrospective or case-control study*

(a) Population

	$y=0$	$y=1$
$z=0$	π_{00}	π_{01}
$z=1$	π_{10}	π_{11}

(b) Prospective study

	$y=0$	$y=1$
$z=0$	$\pi_{00}/(\pi_{00}+\pi_{01})$	$\pi_{01}/(\pi_{00}+\pi_{01})$
$z=1$	$\pi_{10}/(\pi_{10}+\pi_{11})$	$\pi_{11}/(\pi_{10}+\pi_{11})$

(c) Retrospective study

	$y=0$	$y=1$
$z=0$	$\pi_{00}/(\pi_{00}+\pi_{10})$	$\pi_{01}/(\pi_{01}+\pi_{11})$
$z=1$	$\pi_{10}/(\pi_{00}+\pi_{10})$	$\pi_{11}/(\pi_{01}+\pi_{11})$

$\pi_{js} = \Pr(z=i, y=s)$, z explanatory, y response

... prospective and retrospective

y c
no

x sm
no

Population

	$y=0$	$y=1$
$x=0$	π_{00}	π_{01}
$x=1$	π_{10}	π_{11}

$\boxed{\beta_1}$

Prospective study

	$y=0$	$y=1$
$x=0$	$\pi_{00}/(\pi_{00}+\pi_{01})$	$\pi_{01}/(\pi_{00}+\pi_{01})$
$x=1$	$\pi_{10}/(\pi_{10}+\pi_{11})$	$\pi_{11}/(\pi_{10}+\pi_{11})$

fixed

Grim Reaper 16.9

Retrospective study

case - control

	$y=0$	$y=1$
$x=0$	$\pi_{00}/(\pi_{00}+\pi_{10})$	$\pi_{01}/(\pi_{01}+\pi_{11})$
$x=1$	$\pi_{10}/(\pi_{00}+\pi_{10})$	$\pi_{11}/(\pi_{01}+\pi_{11})$

odds ratio in 2nd and 3rd table the same

OR same in both

Contingency Tables: Example 10.19

	Smoker	Non-smoker	
dead	139 (24%)	230 (31%)	
alive	443	502	
total	582	732	1314

$$\frac{Pr(y=1 \mid x=1)}{Pr(y=0 \mid x=1)} \Big/ \frac{Pr(y=1 \mid x=0)}{Pr(y=0 \mid x=0)}$$

OR

see `grimreaper.R`:

```
>  summary(glm(cbind(alive,dead) ~ smoker, data = smoking, family = binomial))
Call:
glm(formula = cbind(alive, dead) ~ smoker, family = binomial,
    data = smoking)

Deviance Residuals:
    Min        1Q    Median       3Q      Max
-12.173   -5.776    1.869    5.674    9.052

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.78052    0.07962   9.803  < 2e-16 ***
smoker       0.37858    0.12566   3.013  0.00259 **
---
Signif. codes:  0 Ô***Õ 0.001 Ô**Õ 0.01 Ô*Õ 0.05 Ô.Õ 0.1 Ô Õ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 641.5  on 13  degrees of freedom
Residual deviance: 632.3  on 12  degrees of freedom
AIC: 683.29

Number of Fisher Scoring iterations: 4
```

... example 10.19

	Smoker	Non-smoker	
dead	139 (24%)	230 (31%)	
alive	443	502	
total	582	732	1314

```
 > anova(glm(cbind(alive,dead) ~ smoker, data = smoking, family = binomial))
Analysis of Deviance Table

Model: binomial, link: logit

Response: cbind(alive, dead)

Terms added sequentially (first to last)


       Df Deviance Resid. Df Resid. Dev
NULL                      13      641.5
smoker  1   9.2003        12      632.3
> with(smoking, xtabs(cbind(dead,alive) ~ smoker))

smoker dead alive
     0  230   502
     1  139   443
> summary(.Last.value)
Call: xtabs(formula = cbind(dead, alive) ~ smoker)
Number of cases in table: 1314
Number of factors: 2
Test for independence of all factors:
Chisq = 9.121, df = 1, p-value = 0.002527
```

... Example 10.19

	sm	non-sm	sm	non-sm	sm	non-sm	
d	2	1	3	5	14	7	
a	53	61	121	152	95	114	...
	55	62	124	157	109	121	
Age	18-24		25-34		35-44		...

```
> summary(glm(cbind(alive,dead) ~ smoker + factor(age), data = smoking, family = binomial))

Call:
glm(formula = cbind(alive, dead) ~ smoker + factor(age), family = binomial,
    data = smoking)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-0.68162  -0.19146  -0.00005   0.22836   0.72545

Coefficients:
                   Estimate Std. Error z value Pr(>|z|)
(Intercept)          3.8601     0.5939   6.500 8.05e-11 ***
smoker              -0.4274     0.1770  -2.414 0.015762 *
factor(age)25-34    -0.1201     0.6865  -0.175 0.861178
factor(age)35-44    -1.3411     0.6286  -2.134 0.032874 *
factor(age)45-54    -2.1134     0.6121  -3.453 0.000555 ***
factor(age)55-64    -3.1808     0.6006  -5.296 1.18e-07 ***
factor(age)65-74    -5.0880     0.6195  -8.213  < 2e-16 ***
factor(age)75+     -27.8073 11293.1437  -0.002 0.998035
---
Signif. codes:  0 Ô***Õ 0.001 Ô**Õ 0.01 Ô*Õ 0.05 Ô.Õ 0.1 Ô Õ 1

(Dispersion parameter for binomial family taken to be 1)
```

In the News

BONDS | FEBRUARY 7, 2012

Speaking Up Is Hard to Do: Researchers Explain Why

Article | Video | Comments (97)

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Robert Murphy, an online marketing representative in San Francisco, was invited to a business meeting with his boss and six colleagues a few weeks ago. He had attended previous meetings on the subject, and he prepared with additional research. He brought a thick sheaf of notes and contracts with him to the conference room.

Ever felt like an idiot in a meeting at work or clammed up at a cocktail party? New research from Virginia Tech shows that many people are actually less intelligent in

So what did he contribute to the discussion? Absolutely nothing.

"I just sat there like a lump, fixated on the fact that I was quiet," says Mr. Murphy, 31 years old.

Have you ever clammed up at a party or found yourself tongue-tied at a meeting for fear of saying something stupid—even

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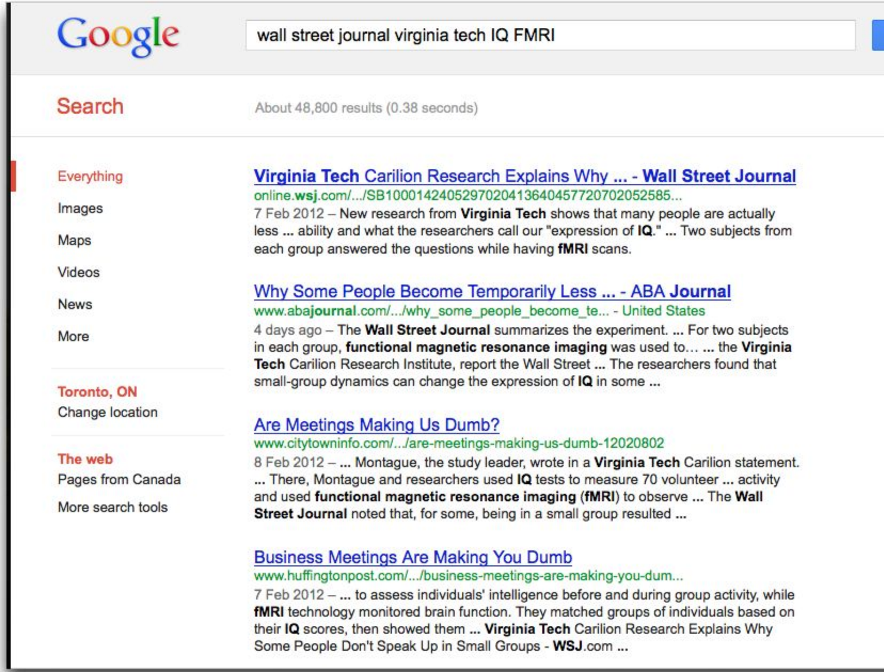
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[**Virginia Tech** Carilion Research Explains Why ... - **Wall Street Journal**]

online.**wsj**.com/.../SB10001424052970204136404577207020525853...

7 Feb 2012 – New research from **Virginia Tech** shows that many people are actually less ... ability and what the researchers call our "expression of **IQ**." ... Two subjects from each group answered the questions while having **fMRI** scans.

[Why Some People Become Temporarily Less ... - ABA **Journal**]

www.aba**journal**.com/.../why_some_people_become_te... - United States

4 days ago – The **Wall Street Journal** summarizes the experiment. ... For two subjects in each group, **functional magnetic resonance imaging** was used to... ... the **Virginia Tech** Carilion Research Institute, report the Wall Street ... The researchers found that small-group dynamics can change the expression of **IQ** in some ...

[Are Meetings Making Us Dumb?]

www.citytowninfo.com/.../are-meetings-making-us-dumb-12020802

8 Feb 2012 – ... Montague, the study leader, wrote in a **Virginia Tech** Carilion statement. ... There, Montague and researchers used **IQ** tests to measure 70 volunteer ... activity and used **functional magnetic resonance imaging** (**fMRI**) to observe ... The **Wall Street Journal** noted that, for some, being in a small group resulted ...

[Business Meetings Are Making You Dumb]

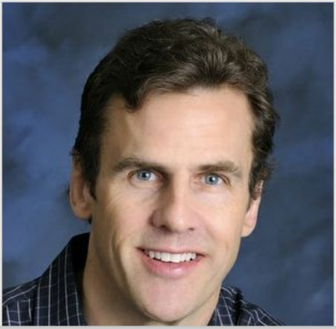
www.huffingtonpost.com/.../business-meetings-are-making-you-dum...

7 Feb 2012 – ... to assess individuals' intelligence before and during group activity, while **fMRI** technology monitored brain function. They matched groups of individuals based on their **IQ** scores, then showed them ... **Virginia Tech** Carilion Research Explains Why Some People Don't Speak Up in Small Groups - **WSJ**.com ...

Category: Research

Group settings can diminish expressions of intelligence, especially among women

ROANOKE, VA -- In the classic film *12 Angry Men*, Henry Fonda's character sways a jury with his quiet, persistent intelligence. But would he have succeeded if he had allowed himself to fall sway to the social dynamics of that jury?



Research led by scientists at the Virginia Tech Carilion Research Institute found that small-group dynamics -- such as jury deliberations, collective bargaining sessions, and cocktail parties -- can alter the expression of IQ in some susceptible people. "You may joke about how committee

Faculty profile

- Ken Kishida
- Read Montague

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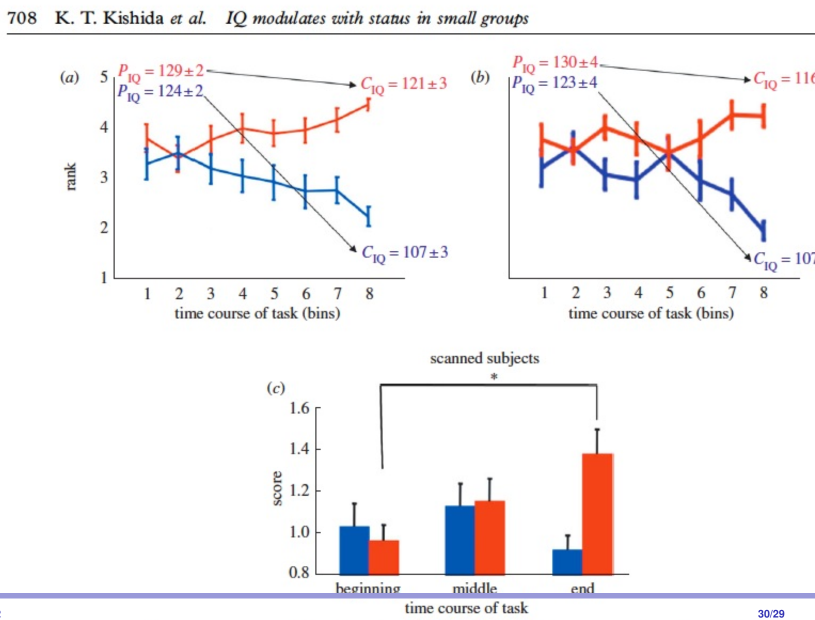
... speaking up


708 K. T. Kishida et al. IQ modulates with status in small groups
(a)
P_{IQ} = 129±2
P_{IQ} = 124±2
C_{IQ} = 121±3
C_{IQ} = 107±3
rank
time course of task (bins)
(b)
P_{IQ} = 130±4
P_{IQ} = 123±4
time course of task (bins)
scanned subjects
(c)
score
beginning
middle
end
time course of task

... speaking up

- claim: IQ score decreases in group 2 ("low performers") over time
- claim: this is caused by receiving information on how others in the group are doing
- methods: baseline IQ test (P_{IQ}); series of IQ task questions ("ranked group task")
- methods: during series of IQ questions, "Following every trial, the computer display showed each subject's personal rank privately and one randomly chosen subject's rank"
- control group ???
- analysis: "following the completion of the ranked group IQ task, we performed a median-based categorization of subjects into two analysis groups; we placed individuals with a final average rank greater than the median into one group, Group 1 and those with final average rank less than or equal to the median into a second group, Group 2"
- analysis: "we excluded an equal number of individuals with the highest and lowest P_{IQ} before the separation"
- analysis: "by design, these two groups did not differ in baseline IQ scores, but were categorically different based on their final rank"
- results: "the performance of Group 1 members remained relatively intact, a drop of 8 ± 4 points, which is significantly less than the drop expressed by group 2, $p = 0.04$"