

STATISTICS 538, Lecture #6

Overdispersion

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Overdispersion: common phenomenon in situations where the obvious first-choice glm is binomial or Poisson

i.e. $E(Y|X) = g^{-1}(BX)$ o.k. Variance function

↑ inverse link

$Var(Y|X)$ bigger than $V(E(Y|X))$

Data may inherently be more variable than predicted by the model's mean-variance relationship.

Yields large deviance. ← flunk GOF test

Standard errors too small if problem ignored?

because pretending the data are better (less noisy) than they really are

Example

$Y_i \sim \text{Bin}(n_i, p_i) \quad i=1, \dots, 58$
deaths \uparrow litter size \leftarrow

logit(p_i) = $\beta_0 + \beta_1 I\{\text{grp}=2\} + \beta_2 I\{\text{grp}=3\} + \beta_3 I\{\text{grp}=4\}$

```
### data from Agresti book, www.stat.ufl.edu
### 58 pregnant female rats on iron-deficient diets
### mortality per litter in offspring
### treatment groups 1:none (31)
### 2:iron supplement days 7 and 10 (12)
### 3:iron supplement days 0 and 7 (5)
### 4:iron supplement weekly (10)
```

```
> dat <- read.table("rats.txt", header=F, row.names=1,
  col.names=c("", "trt", "litsize", "deaths") )
```

numeric coding of group in data file: 1, 2, 3, 4

```
> dat$trt <- factor(dat$trt,
  labels=c("none", "7/10", "0/7", "wkly"))
```

tell R
this is categorical

Quasi-likelihood

Recall $E(Y_i) = \mu_i$

$$\text{Var}(Y_i) = \phi v(\mu_i)$$

Bernoulli: $\phi = 1, v(\mu) = \mu(1-\mu)$

Poisson: $\phi = 1, v(\mu) = \mu$

Intuition: force the scaled deviance D/ϕ to be consistent with χ^2_{n-p}

Replace known dispersion ϕ with estimated $\hat{\phi} = (n-p)^{-1}D$.
(or a better estimator!)

Won't affect $\hat{\beta}$, but will boost standard errors by factor of $\sqrt{\hat{\phi}}$.

Recognition of additional uncertainty because of extra variability in data.

Why? recall exp. family structure

log-
like. $\rightarrow l(\beta) = \frac{1}{\phi} \times \text{function of } \beta$

$$l'(\beta) = \frac{1}{\phi} \times \dots$$

$$l''(\beta) = \frac{1}{\phi} \times \dots$$

Back to rats data

```
dat$trt <- relevel(dat$trt, ref="7/10")
fit1 <- glm( cbind(deaths,litsize-deaths)~trt,
            family=binomial, data=dat)
```

$e^{3.3} \approx 27$ huge multiplicative effect on odds of death

	Estimate	Std. Error	z value	Pr(> z)	
(Intercept)	-2.1785	0.3046	-7.153	8.51e-13	***
trtnone	3.3225	0.3308	10.043	< 2e-16	***
trt0/7	-1.1537	0.7814	-1.476	0.140	
trtwkly	-0.8071	0.5503	-1.467	0.142	

(Dispersion parameter for binomial family taken to be 1)
Residual deviance: 173.45 on 54 degrees of freedom
AIC: 252.92

f!unk!
GOF

Now with family=quasibinomial instead of family=binomial

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	-2.1785	0.5155	-4.226	9.23e-05	***
trtrnone	3.3225	0.5600	5.933	2.18e-07	***
trt0/7	-1.1537	1.3227	-0.872	0.387	
trtwkly	-0.8071	0.9315	-0.867	0.390	

Same as before

all inflated by a factor of $\sqrt{2.86}$

(Dispersion parameter for quasibinomial family taken to be 2.864945)

Residual deviance: 173.45 on 54 degrees of freedom

AIC: NA

using 'better' estimate than $\frac{D}{n-p} = \frac{173.45}{54}$

because quasi-likelihood isn't a real likelihood

Comfortable doing inference without a real model?

$$Y = \begin{cases} 0 & \text{w.p. } \frac{1}{2} \\ n & \text{w.p. } \frac{1}{2} \end{cases} \quad \text{Var}(Y) = \frac{1}{2}(0 - n/2)^2 + \frac{1}{2}(n - n/2)^2 = \frac{n^2}{4} \\ = n^2 \times \frac{1}{2} \times (1 - \frac{1}{2})$$

Say Y is a random variable taking values in $\{0, \dots, n\}$ with mean np and variance $\phi np(1-p)$. Can show $\phi \leq n$.

Note that in the Rats data ex., $\hat{\phi} = 2.86$, while $n_i = 1, 2$ for some litters.

alternative to "quasi"

What about using real models with $v(\mu) > \mu(1-\mu)$ for "binomial" data, or $v(\mu) > \mu$ for "Poisson" data?

Negative-Binomial as alternative to Poisson

$\rightarrow \Pr(Y=y) = \binom{y+\alpha-1}{\alpha-1} p^\alpha (1-p)^y \rightarrow$ fix this up next time!

This family of distributions can be parameterized as $E(Y) = \mu$,
 $\text{Var}(Y) = \mu + \mu^2/\theta$.

So have a GLM, but with an unknown parameter in the variance function (does complicate fitting algorithm).

Connection to usual parameterization, $Y \sim$ number of failures in sequence of independent trials performed until α successes are seen, where p is success probability for each trial?

More relevant representation of NB distribution as a **mixture**.

$$\left. \begin{aligned} Y|Z &\sim \text{Poisson}(\mu Z) \\ Z &\sim \text{Gamma}(\text{mean } 1, \text{var } \frac{1}{\theta}) \end{aligned} \right\} \Rightarrow Y \text{ neg-bin}$$

check $E(Y) = E \bar{E}(Y|Z)$, $\text{Var}(Y) = E \text{Var}(Y|Z) + \text{Var} E(Y|Z)$

Simulate and fit some negative binomial data

```
set.seed(17)
n <- 80
x1 <- rnorm(n); x2 <- .8*x1 + sqrt(1-.8^2)*rnorm(n)
y <- rbinom(n, mu=exp(1 + 0.3*x1), size=3)
dat2 <- data.frame(y=y, x1=x1, x2=x2)

fit3 <- glm(y ~ . , family=poisson, data=dat2)
fit4 <- glm(y ~ . , family=quasipoisson, data=dat2)
library("MASS")
fit5 <- glm.nb(y ~ x1+x2, data=dat2)
```

two correlated predictors

log-link

β_0 β_1 θ

	Estimate	Std. Error	z value	Pr(> z)	
(Intercept)	1.15947	0.06349	18.262	<2e-16	***
x1	0.21035	0.09241	2.276	0.0228	*
x2	-0.01709	0.09490	-0.180	0.8571	

(Dispersion parameter for poisson family taken to be 1)
Residual deviance: 167.92 on 77 degrees of freedom
AIC: 382.47

*flunks
GOF*

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	1.15947	0.09016	12.860	<2e-16	***
x1	<u>0.21035</u>	<u>0.13123</u>	1.603	<u>0.113</u>	-sig. lost?
x2	-0.01709	0.13477	-0.127	0.899	

(Dispersion parameter for quasipoisson family taken to be 2.016572) = $\hat{\phi}$

Residual deviance: 167.92 on 77 degrees of freedom

AIC: NA

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.15885	0.08983	12.900	<2e-16 ***
x1	0.21493	0.13282	1.618	0.106
x2	-0.01731	0.13635	-0.127	0.899

very similar to quasi-lik., but

(Dispersion parameter for Negative Binomial(3.1055)
family taken to be 1)

Residual deviance: 92.740 on 77 degrees of freedom

AIC: 362.31

*comfort
of
real
model*

Theta: 3.11
Std. Err.: 1.06

*recall true
val. = 3*