

STATISTICS 538, Lecture #6

Overdispersion

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

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

Yields large deviance.

Standard errors too small if problem ignored?

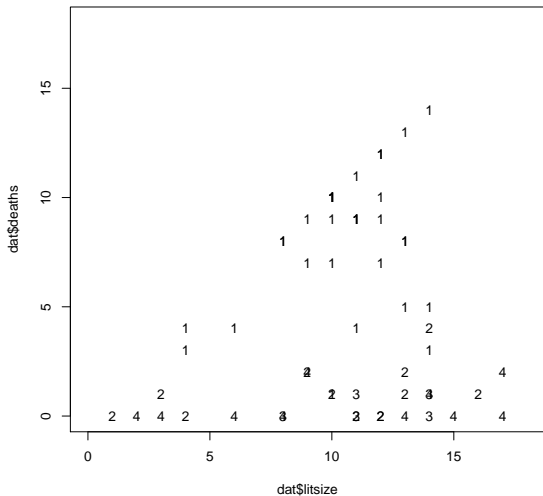
Example

```
### 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
###                2:iron supplement days 7 and 10
###                3:iron supplement days 0 and 7
###                4:iron supplement weekly

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

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

```
plot(litsize, deaths, pch=as.character(as.numeric(trtmnt)))
```



Quasi-likelihood

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.

Back to rats data

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

	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

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	***
trtnone	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	

(Dispersion parameter for quasibinomial family taken to be 2.864945)

Residual deviance: 173.45 on 54 degrees of freedom

AIC: NA

Comfortable doing inference without a real model?

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

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

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

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

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**.

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)
```

	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

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

(Dispersion parameter for quasipoisson family taken to be 2.016572)

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

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

Residual deviance: 92.740 on 77 degrees of freedom

AIC: 362.31

Theta: 3.11
Std. Err.: 1.06