Count outcomes

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Key ideas

- Many data take the form of counts
 - Calls to a call center
 - Number of flu cases in an area
 - Number of cars that cross a bridge
- Data may also be in the form of rates
 - Percent of children passing a test
 - Percent of hits to a website from a country
- · Linear regression with transformation is an option

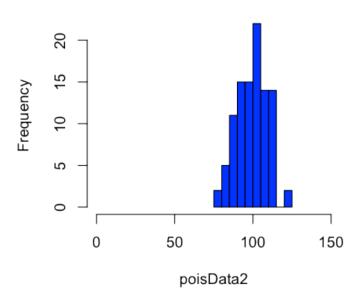
Poisson distribution

```
set.seed(3433); par(mfrow=c(1,2))
poisData2 <- rpois(100,lambda=100); poisData1 <- rpois(100,lambda=50)
hist(poisData1,col="blue",xlim=c(0,150)); hist(poisData2,col="blue",xlim=c(0,150))</pre>
```

Histogram of poisData1

Freduency 0 2 10 15 20 25 30 100 150 poisData1

Histogram of poisData2



Poisson distribution

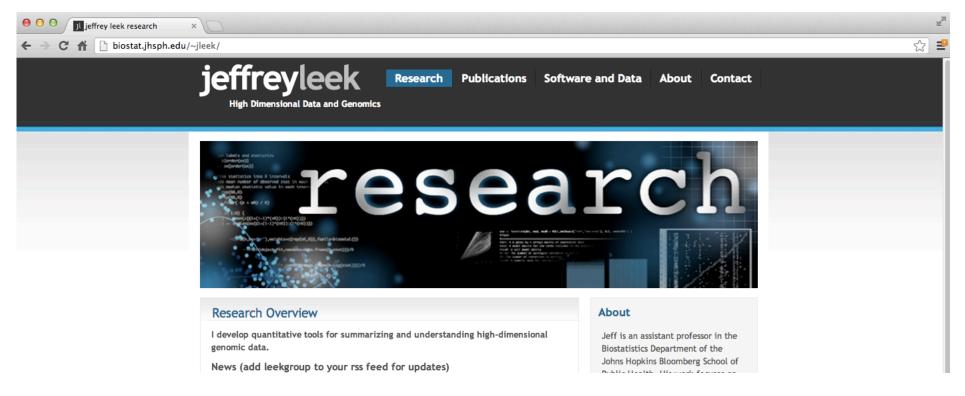
c(mean(poisData1), var(poisData1))

[1] 49.85 49.38

c(mean(poisData2),var(poisData2))

[1] 100.12 95.26

Example: Leek Group Website Traffic



http://biostat.jhsph.edu/~jleek/

Website data

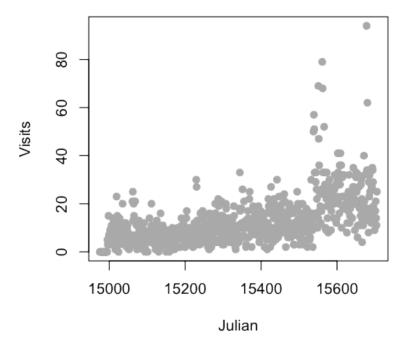
```
download.file("https://dl.dropbox.com/u/7710864/data/gaData.rda",destfile="./data/gaData.rda",metho
load("./data/gaData.rda")
gaData$julian <- julian(gaData$date)
head(gaData)</pre>
```

```
date visits simplystats julian
1 2011-01-01
                 0
                             0 14975
2 2011-01-02
                             0 14976
3 2011-01-03
                             0 14977
4 2011-01-04
                             0 14978
5 2011-01-05
                             0 14979
                 0
6 2011-01-06
                 0
                             0 14980
```

http://skardhamar.github.com/rga/

Plot data

plot(gaData\$julian,gaData\$visits,pch=19,col="darkgrey",xlab="Julian",ylab="Visits")



Linear regression

$$NH_i = b_0 + b_1 J D_i + e_i$$

 NH_i - number of hits to the website

 JD_i - day of the year (Julian day)

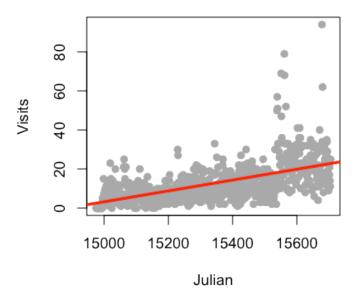
 b_0 - number of hits on Julian day 0 (1970-01-01)

 b_1 - increase in number of hits per unit day

 e_i - variation due to everything we didn't measure

Linear regression line

```
plot(gaData$julian,gaData$visits,pch=19,col="darkgrey",xlab="Julian",ylab="Visits")
lm1 <- lm(gaData$visits ~ gaData$julian)
abline(lm1,col="red",lwd=3)</pre>
```



Linear vs. Poisson regression

Linear

$$NH_i = b_0 + b_1 JD_i + e_i$$

or

$$E[NH_i|JD_i, b_0, b_1] = b_0 + b_1JD_i$$

Poisson/log-linear

$$\log(E[NH_i|JD_i, b_0, b_1]) = b_0 + b_1 JD_i$$

or

$$E[NH_i|JD_i, b_0, b_1] = \exp(b_0 + b_1JD_i)$$

Multiplicative differences

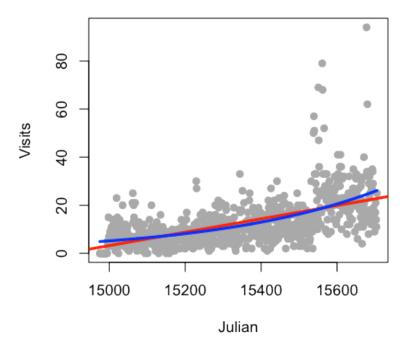
$$E[NH_i|JD_i, b_0, b_1] = \exp(b_0 + b_1JD_i)$$

$$E[NH_i|JD_i, b_0, b_1] = \exp(b_0) \exp(b_1JD_i)$$

If JD_i is increased by one unit, $E[NH_i|JD_i,b_0,b_1]$ is multiplied by $\exp(b_1)$

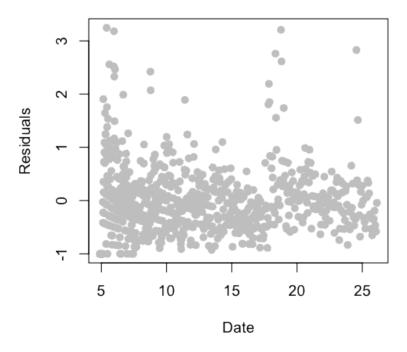
Poisson regression in R

```
plot(gaData$julian,gaData$visits,pch=19,col="darkgrey",xlab="Julian",ylab="Visits")
glm1 <- glm(gaData$visits ~ gaData$julian,family="poisson")
abline(lm1,col="red",lwd=3); lines(gaData$julian,glm1$fitted,col="blue",lwd=3)</pre>
```



Mean-variance relationship?

plot(glm1\$fitted,glm1\$residuals,pch=19,col="grey",ylab="Residuals",xlab="Date")



Model agnostic standard errors

```
library(sandwich)
confint.agnostic <- function (object, parm, level = 0.95, ...)
{
    cf <- coef(object); pnames <- names(cf)</pre>
    if (missing(parm))
        parm <- pnames
    else if (is.numeric(parm))
        parm <- pnames[parm]</pre>
    a <- (1 - level)/2; a <- c(a, 1 - a)
    pct <- stats:::format.perc(a, 3)</pre>
    fac <- qnorm(a)</pre>
    ci <- array(NA, dim = c(length(parm), 2L), dimnames = list(parm,
                                                                    pct))
    ses <- sqrt(diag(sandwich::vcovHC(object)))[parm]</pre>
    ci[] <- cf[parm] + ses %0% fac
    ci
```

http://stackoverflow.com/questions/3817182/vcovhc-and-confidence-interval

Estimating confidence intervals

```
confint(glm1)
```

```
2.5 % 97.5 %
(Intercept) -34.34658 -31.159716
gaData$julian 0.00219 0.002396
```

```
confint.agnostic(glm1)
```

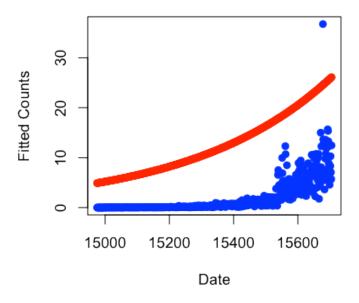
Rates

$$E[NHSS_i|JD_i, b_0, b_1]/NH_i = \exp(b_0 + b_1JD_i)$$

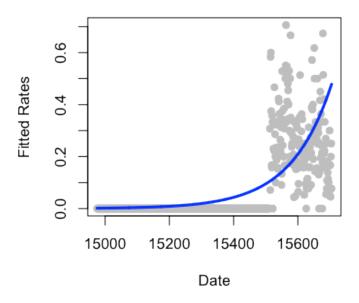
$$\log(E[NHSS_{i}|JD_{i}, b_{0}, b_{1}]) - \log(NH_{i}) = b_{0} + b_{1}JD_{i}$$

$$\log(E[NHSS_i|JD_i,b_0,b_1]) = \log(NH_i) + b_0 + b_1JD_i$$

Fitting rates in R



Fitting rates in R



More information

- Log-linear models and multiway tables
- · Wikipedia on Poisson regression, Wikipedia on overdispersion
- Regression models for count data in R
- pscl package the function zeroinfl fits zero inflated models.