Slide 1

Reference: Agresti, Section 7.1

Count data and Poisson distribution

- Many response variables have counts as their possible outcome.
- The standard distribution to model count data is the Poisson distribution, which has probability mass function

$$p(Y = y) = \frac{e^{-\mu}\mu^y}{y!}, \quad y = 0, 1, 2, \ldots, \quad \mu > 0.$$

$$E[Y] = Var(Y) = \mu.$$

- Thus, any factor that affects the mean will affect the variance (and vice versa). So the usual assumption of homoscedasticity is not appropriate.

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- The Poisson distribution with $\mu = n\pi$ can be derived as a limiting distribution of the binomial(n, π) as $n \to \infty$ and $\pi \to 0$.
- An alternative derivation is in terms of a stochastic process described somewhat informally as follows:
  - the probability of at least one event in a given time interval is proportional to the length of the interval;
  - the probability of two or more events in a very small time interval is negligible;
  - the number of events in disjoint time intervals are mutually independent.

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A useful property of the Poisson distribution is that the sum of independent Poisson random variables is also Poisson.

- Thus, we can analyze individual or grouped data with equivalent results.
- If $Y_{ij} \sim$ Poisson(μ_i) for $j = 1, 2, \ldots, n_i$, then the group total $Y_i \sim$ Poisson$(n_i\mu_i)$.
- We obtain exactly the same likelihood function if we work with the individual counts Y_{ij} or the group counts Y_i.

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Link function for count data

- Recall that $\eta_i = \log \mu_i$ is the canonical link for Poisson data

$$f(y_i) = \exp\left\{y_i \log \mu_i - \mu_i - \log(y_i!)\right\}.$$

- Thus, the log link is the canonical link for a Poisson GLM

$$\log \mu_i = \boldsymbol{x_i'\beta},$$

  which is often referred to as a **loglinear model**.
- β_j represents the expected change in the *log* of the mean per unit change in x_j.
- Exponentiating, we obtain a multiplicative model for the mean:

$$\mu_i = \exp(\boldsymbol{x_i'\beta}).$$

  So increasing x_j by one unit multiplies the mean by a factor $\exp(\beta_j)$.

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Maximum likelihood estimation

- The log-likelihood function for n independent Poisson observations is

$$\log L(\boldsymbol{\beta}) = \sum_{i=1}^{n} (y_i \log \mu_i - \mu_i),$$

  where $\mu_i = \exp(\boldsymbol{x_i'\beta})$.

- The score functions are given by

$$\frac{\partial \log L}{\partial \boldsymbol{\beta}} = \boldsymbol{X'(y-\mu)},$$

- So the ML estimates satisfy the estimating equations

$$\boldsymbol{X'y} = \boldsymbol{X'\hat{\mu}},$$

- Recall that this estimating equation arises more generally in any GLM with canonical link.

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Model fitting

- In general, we use the IRWLS algorithm or Fisher scoring (same as Newton-Raphson) procedure for estimation.

- Recall that one iteration of the algorithm is

$$\boldsymbol{\beta}^{(t)} = (\boldsymbol{X'W^{(t)}X})^{-1}\boldsymbol{X'W^{(t)}z^{(t)}},$$

  where the diagonal matrix $\boldsymbol{W}$ of iterative weights is

$$\boldsymbol{W} = \text{ Diag}\left[Var(Y_i)\left(\frac{\partial \eta_i}{\partial \mu_i}\right)^2\right]^{-1} = \text{Diag}(\mu_i)$$

  and the working dependent variate $\boldsymbol{z}$ is

$$\boldsymbol{z}^{(t)} = \boldsymbol{\eta}^{(t)} + \left(\frac{\partial \boldsymbol{\eta}^{(t)}}{\partial \boldsymbol{\mu}^{(t)}}\right)(\boldsymbol{y} - \boldsymbol{\mu^{(t)}}).$$

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Quantities of interest

After convergence, we should save and examine the following:

- $Var(\hat{\boldsymbol{\beta}}) = (\boldsymbol{X'WX})^{-1}$
- the Pearson residuals and the Pearson goodness-of-fit statistic

$$\mathcal{X}^2 = \sum_{i=1}^{N} \left(\frac{y_i - \hat{\mu}_i}{\sqrt{\hat{\mu}_i}} \right)^2$$

- the deviance residuals and the deviance statistic

$$G^2 = 2 \sum_{i=1}^{N} \left\{ y_i \log \frac{y_i}{\hat{\mu}_i} - (y_i - \hat{\mu}_i) \right\}$$

- the leverage values, i.e., the diagonal elements of

$$\boldsymbol{H} = \boldsymbol{W}^{1/2} \boldsymbol{X} (\boldsymbol{X'WX})^{-1} \boldsymbol{X'W}^{1/2}.$$

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Tests of hypotheses

- Likelihood ratio tests for log-linear models can easily be constructed, as we did for the other GLMs.
- In large samples, the difference in deviances between two nested models is approximately $\chi^2_{df_1 - df_2}$.
- One can also construct Wald tests and confidence intervals as we have done before, based on the asymptotic distribution

$$\hat{\boldsymbol{\beta}} \sim N\left(\boldsymbol{\beta}, (\boldsymbol{X'WX})^{-1}\right).$$

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Example

The data below reports fatalities in the Prussian army due to horse kicks from 1875 to 1894 across 14 army corps:

Year	75	76	77	78	79	80	81	82	83	84
Deaths	3	5	7	9	10	18	6	14	11	9
Year	85	86	87	88	89	90	91	92	93	94
Deaths	5	11	15	6	11	17	12	15	8	4

For illustration, we will look at the data by year to see if there appears to be any trend over time.

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```
year = 75:94
deaths = c(3, 5, 7, 9, 10, 18, 6, 14, 11, 9, 5, 11, 15, 6, 11, 17, 12, 15, 8, 4)
plot(year, log(deaths))
fit.loess = loess(log(deaths) ~ year)
lines(year, predict(fit.loess))
```

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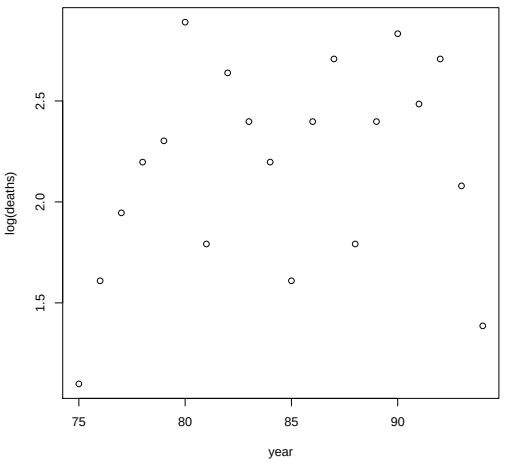
Scatter plot of log(death) versus year:



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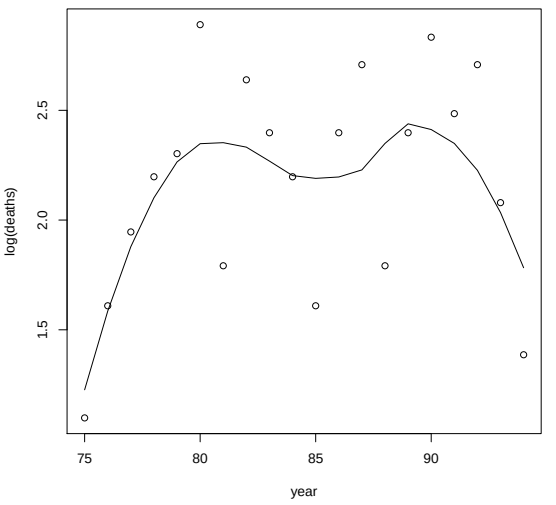
Apply `loess( )` to look for trends:



May need a 4th-degree polynomial to capture the trend over time.

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```
fit.poisson = glm(deaths ~ year, family=poisson)

> summary(fit.poisson)

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.69095    1.06056   0.651    0.515
year         0.01876    0.01243   1.509    0.131

    Null deviance: 38.503  on 19  degrees of freedom
Residual deviance: 36.216  on 18  degrees of freedom
AIC: 120.87

> 1-pchisq(36.216, 18)
[1] 0.006619696
```

The model does not fit the data well.

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Let's include the effects of time as a fourth degree polynomial

```
yr2 = year^2; yr3 = year^3; yr4 = year^4;
fit.polynom = glm(deaths ~ year+yr2+yr3+yr4, family=poisson)

> summary(fit.polynom)
              Estimate Std. Error z value Pr(>|z|)
(Intercept) -1.921e+04  5.880e+03  -3.266  0.00109 **
year         9.096e+02  2.789e+02   3.262  0.00111 **
yr2         -1.613e+01  4.952e+00  -3.258  0.00112 **
yr3          1.270e-01  3.902e-02   3.254  0.00114 **
yr4         -3.743e-04  1.151e-04  -3.251  0.00115 **
---
    Null deviance: 38.503  on 19  degrees of freedom
Residual deviance: 17.669  on 15  degrees of freedom
AIC: 108.32
```

There seems to be a problem of collinearity.

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Let's center the variable year and refit the model:

```
yr = (year-mean(year)); yr2 = yr^2; yr3 = yr^3; yr4 = yr^4;
fit.center = glm(deaths ~ yr+yr2+yr3+yr4, family=poisson)

> summary(fit.center)
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  2.2142611  0.1365518  16.216  < 2e-16 ***
yr          -0.0006781  0.0315795  -0.021  0.98287
yr2          0.0222576  0.0091181   2.441  0.01465 *
yr3          0.0004726  0.0005855   0.807  0.41950
yr4         -0.0003743  0.0001151  -3.251  0.00115 **
---
    Null deviance: 38.503  on 19  degrees of freedom
Residual deviance: 17.669  on 15  degrees of freedom
AIC: 108.32
```

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```
> 1-pchisq(17.669, 15)
[1] 0.2804668
```

Let's do a few diagnostic plots:

```
resid.fit = residuals(fit.center, type="pearson")
plot(year, fit.center$fitted.values, ylab=expression(hat(mu)),
        main="Estimated Mean by Year")
plot(fit.center$fitted.values, resid.fit, xlab=expression(hat(eta)), ylab="residuals",
      main = "Pearson residuals versus linear predictor")
plot(fit.center$fitted.values, abs(resid.fit), xlab=expression(hat(eta)), ylab="|residuals|",
      main = "Absolute value of residuals versus linear predictor")
```

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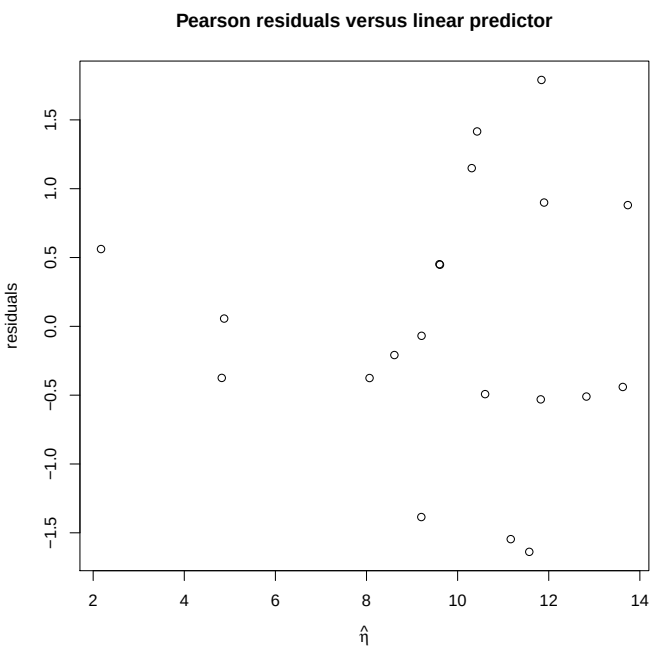

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- There's an increasing trend, suggesting that the variance function $Var(Y) = \mu$ may be wrong.
- It's possible that the overall size of the Prussian army varied over the twenty-year period, which could then cause the mean number of deaths to vary.
- Next, we talk about how to include a measure of size when it is available, i.e., consider rates rather than counts.

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Poisson regression for rates

- When events occur over some index of size (time or space) that varies among observations, it is more relevant to model the **rate** of events.
- When a response count Y_i has index (such as population size) equal to t_i, the sample rate of outcomes is Y_i/t_i.
- A log-linear model for the expected rate is given by

$$\log(\mu_i/t_i) = \sum_{j=1}^{p} \beta_j x_{ij} \quad \Rightarrow \quad \log \mu_i = \log t_i + \sum_{j=1}^{p} \beta_j x_{ij}.$$

- The adjustment term, $\log t_i$, is called an **offset**.
- The fit corresponds to using $\log t_i$ as a predictor and forcing its coefficient to equal 1.0.

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- The expected number of outcomes satisfies

$$\mu_i = t_i \exp\left(\sum_{j=1}^{p} \beta_j x_{ij}\right).$$

- A one-unit increase in the j-th element of $\boldsymbol{x}_i$ multiplies the incidence rate by $\exp(\beta_j)$.
- The mean is proportional to the index t_i, with proportionality constant depending on the value of the explanatory variable, x_i.
- For example, for a fixed value of x_i, doubling the population size t_i also doubles the expected number μ_i.

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Example

The data below reports the survival of patients after heart-valve replacement surgery (Agresti, p. 129, Table 4.5). A sample of 109 patients were classified by type of heart valve (aortic or mitral) and by age ($< 55, \geq 55$). Follow-up observations occurred until the patient died or the study ended, and covered lengths of time varying from 3 to 97 months.

Age	Type	Time at risk (months)	Deaths
Under 55	aortic	1,259	4
	mitral	2,082	1
55+	aortic	1,417	7
	mitral	1,647	9

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- We need to account for the fact that each group involves a different total time at risk (i.e., number of person-years).
- Thus, we model the *rate* of death

$$\log(\mu_i/t_i) = \boldsymbol{x}_i'\boldsymbol{\beta},$$

which is equivalent to

$$\eta_i = \log \mu_i = \log t_i + \boldsymbol{x}_i'\boldsymbol{\beta}.$$

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Let's first fit the saturated model with log-exposure as an offset:

```
heart = data.frame(Age=as.factor(rep(c("<55","55+"),rep(2,2))),
              Type=as.factor(rep(c("Aortic","Mitral"),2)),
              Deaths=c(4,1,7,9), Exposure=c(1259,2082,1417,1647))

heart.fit = glm(Deaths ~ Age*Type , offset = log(Exposure),
                         family=poisson, data=heart)
> summary(heart.fit)
                  Estimate Std. Error z value Pr(>|z|)
(Intercept)        -5.3104     0.3780 -14.050   <2e-16 ***
Age<55             -0.4414     0.6268  -0.704    0.481
TypeMitral          0.1009     0.5040   0.200    0.841
Age<55:TypeMitral  -1.9902     1.2264  -1.623    0.105
```

Make sure the offset is the logarithm of the exposure, not the exposure itself.

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Note that none of the regression coefficients are statistically significant, so they should not be interpreted. If we went ahead and did it nonetheless, we would state:

- When type = aortic, the death rate for the younger group is estimated to be 0.644 times that in the older group ($\exp(-0.44) = 0.644$).
- For the older group, the death rate for mitral valve replacement is 1.11 times that for aortic ($\exp(1.11) = 1.106$).
- For the younger group, the effect of mitral versus aortic replacement is $\beta_2 + \beta_3$, which is estimated to be $0.10009 - 1.9902 = -1.889$. Since $\exp(-1.889) = 0.15 = 1/6.67$, we estimate that among younger patients, the death rate for mitral valve replacement is 6 to 7 times lower than for aortic.

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Repeating the model-fitting for various sets of predictors, we obtain the following analysis-of-deviance table:

Model	G^2	*df*	*p*-value
Saturated**	0.00	0	–
Age+Type	3.223	1	0.073
Type	9.886	2	0.007
Age	3.790	2	0.150
Null	10.841	3	0.013

The model with Age is the best fit we get for these data.

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```
> summary(glm(Deaths ~ Age , offset = log(Exposure),
+                           family=poisson, data=heart))

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -5.2549     0.2500 -21.020   <2e-16 ***
Age<55       -1.2497     0.5123  -2.439   0.0147 *
---
    Null deviance: 10.8405  on 3  degrees of freedom
Residual deviance:  3.7897  on 2  degrees of freedom
AIC: 20.917
```

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Overdispersion

- Under the Poisson model

$$E[Y_i] = Var(Y_i) = \mu_i.$$

- Real data, however, often exhibit more variation than allowed by the Poisson model.
- One approach to deal with overdispersion is to change the response distribution to **negative binomial**, which is more dispersed than the Poisson.