Offsets and Overdispersion

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Poisson rates

- The meaning of λ often requires additional thought
- When we employ a Poisson model, what we are modeling is the rate of events
- We need to be careful about specifying what we are estimating: a rate per what?
- For example, if we are modeling motor vehicle crashes, we may be estimating a rate per 1,000 population, a rate per 1,000 licensed drivers, a rate per 1,000 registered motor vehicles, or a rate per 100,000 miles traveled

British doctor study

- A kind of rate that is particularly common in epidemiological studies is a rate per person-years of follow-up
- For example, consider the classic study by Doll *et al.* in which all British male doctors were sent a questionnaire about their age and whether they smoked tobacco
- The doctors were then followed up for a number of years to see whether or not they had died from coronary heart disease

Offsets

- Suppose, then, that we wish to model $\lambda(\mathbf{x})$, the rate per 1,000 person-years of follow-up, given the explanatory variables `Age` and `Smoking`
- Now,

$$\mathrm{E}(Y_i) = t_i \lambda_i,$$

where t_i denotes the person-years of follow-up for observation i

- This implies that

$$\begin{aligned} \log(\mu_i) &= \log(t_i) + \log(\lambda_i) \\ &= \log(t_i) + \eta_i; \end{aligned}$$

thus, the usual relationship between μ_i and the linear predictor is *offset* by the amount $\log(t_i)$

Including offsets in R/SAS

- Both `R` and SAS allow you to specify an offset
- In SAS, one simply adds the option `OFFSET=` to the model statement
- Similarly, in `R`, one specifies the `offset=` option in the `glm` function
- Note: In SAS, one must compute the offset in a separate `DATA` step, while in `R`, one can submit code such as `offset=log(PersonYears/1000)`

Estimating linear combinations

- We can then estimate the rate per 1,000 person-years of follow-up for any category we choose using either the `ESTIMATE` statement in SAS or the `predict` function in `R`
- For example, with SAS's default coding of class variables, the following statement estimates the rate of CHD deaths for smokers aged 45–54:

```
ESTIMATE '45-54 smokers' Intercept 1
                         Age 0 1 0 0 0
                         Smoking 0 1;
```

- In `R`, we can set up a data frame consisting of all the linear combinations we are interested in, and then submit

```
predict(fit,df,type="response")
```

- Note: In SAS, the offset is set to zero; in `R`, you specify the offset variable

Estimated rates

- The estimated rates from our Poisson regression model:

	Smokers	Non-smokers
35–44	0.52	0.36
45–54	2.29	1.60
55–64	7.17	5.03
65–74	14.78	10.37
75–84	20.97	14.71

- Note that, by fitting a model with no interaction between age and smoking, we enforce that the rate ratio (RR) between smokers and non-smokers are the same in each age group $(0.52/0.36 = \cdots = 20.97/14.71 = 1.43)$

Interaction

- If we allow an interaction, we obtain

	Smokers	Non-smokers	RR
35–44	0.61	0.11	5.5
45–54	2.40	1.12	2.1
55–64	7.20	4.90	1.5
65–74	14.69	10.83	1.4
75–84	19.18	21.20	0.9

- Poisson regression is an adequate tool for analyzing cohort studies; however, if one has detailed individual-level data, one can apply the more sophisticated approaches that have been developed in the field of *survival analysis*

Overdispersion

- One of the defining characteristics of Poisson regression is its lack of a scale parameter: $\mathrm{E}(Y) = \mathrm{Var}(Y)$, and no parameter is available to adjust that relationship
- In practice, when working with Poisson regression, it is often the case that the variability of y_i about $\hat{\lambda}_i$ is larger than what $\hat{\lambda}_i$ predicts
- This implies that there is more variability around the model's fitted values than is consistent with the Poisson distribution

Overdispersion (cont'd)

- The term for this phenomenon is *overdispersion*
- Data for which this phenomenon manifests itself are often called "overdispersed", although as we will see, it is perhaps better to refer to the model as overdispersed, not the data
- There are two common approaches to correcting for overdispersion:
  - Quasi-likelihood
  - Negative binomial regression

Tinkering with the score

- Recall that the score arising from a Poisson regression model is

$$\frac{\partial \ell}{\partial \theta} = \sum_i \{y_i - \hat{\lambda}_i\}$$

  where $\theta = \log(\lambda)$, the canonical parameter
- Note, of course, that there is no scale parameter, which would show up in the denominator on the right hand side
- Now suppose we add one:

$$\frac{\partial \ell}{\partial \theta} = \sum_i \frac{y_i - \hat{\lambda}_i}{\phi}$$

Implications of our tinkering

- Recall that $\text{Var}(Y) = \phi V(\mu)$; thus, we now have a parameter that allows the variance to be larger or smaller than the mean by a multiplicative factor ϕ
- This will not change $\widehat{\boldsymbol{\beta}}$, of course
- However, it will affect inference, since

$$\widehat{\boldsymbol{\beta}} \dot{\sim} \text{N}\left(\boldsymbol{\beta}, \phi(\mathbf{X}^T\mathbf{W}\mathbf{X})^{-1}\right)$$

Quasi-likelihood

- So what distribution is this, that gives rise to this score?
- There isn't one (at least, not one for which you can write down the distribution in closed form)
- This approach, where you modify the score directly and never actually specify a distribution, is known as *quasi-likelihood*

Quasi-likelihood: Estimation of scale

- Typically, the scale parameter ϕ is estimated using the method of moments estimator

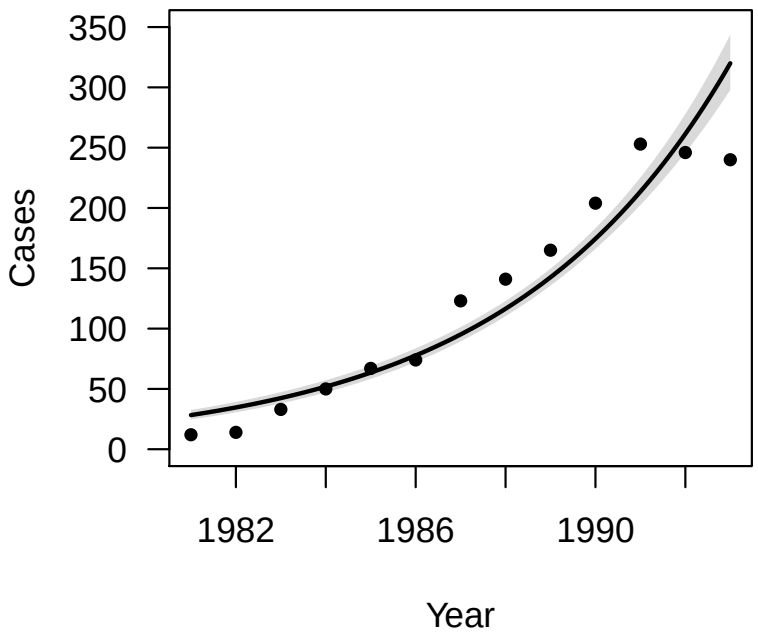
$$\hat{\phi} = \frac{X^2}{n-p}$$

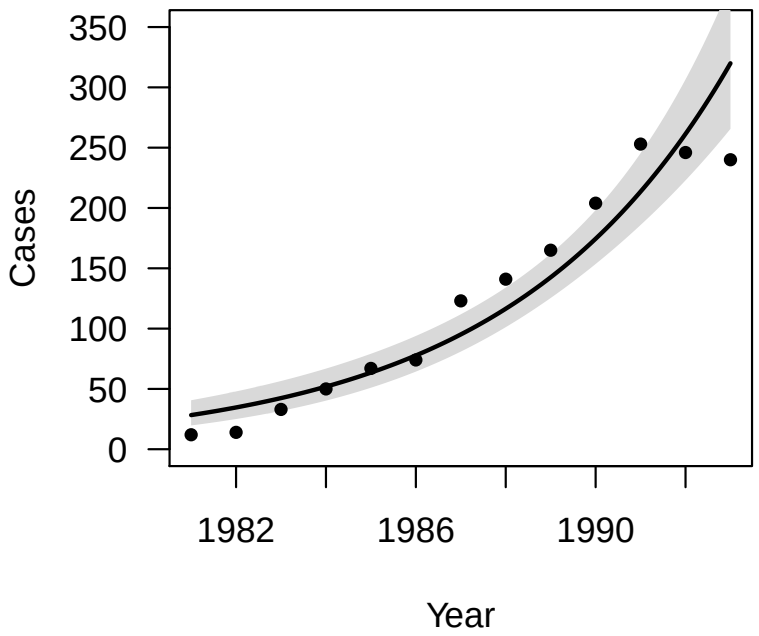
- To use this approach in `R`, one can specify `family=quasipoisson`; in SAS, one can add a `PSCALE` option to the model statement

Quasi-likelihood: Belgian AIDS data

- For our Belgian AIDS data, $\hat{\phi} = 6.7$, implying that the variance was nearly 7 times larger than that implied by the Poisson distribution
- Again, the fit is the same
- However, our standard errors are $\sqrt{6.7} \approx 2.6$ times larger

Quasi-likelihood: Belgian AIDS data (cont'd)





Drawbacks of quasi-likelihood

- The quasi-Poisson approach is attractive for several reasons, but its big drawback is that lacks a log-likelihood
- This prevents you from using any of the likelihood-based tools we have discussed for GLMs: likelihood ratio tests, AIC/BIC, deviance explained, deviance residuals
- An alternative approach that allows all those maximum likelihood tools is based on the negative binomial distribution

The negative binomial distribution

- The negative binomial distribution has other uses in probability and statistics, but for our purposes we can think about it as arising from a two-stage hierarchical process:

$$Z \sim \text{Gamma}(\theta, \theta)$$
$$Y|Z \sim \text{Poisson}(\lambda Z)$$

- The marginal distribution of Y is then negative binomial, with

$$\text{E}(Y) = \lambda$$
$$\text{Var}(Y) = \lambda + \lambda^2/\theta$$

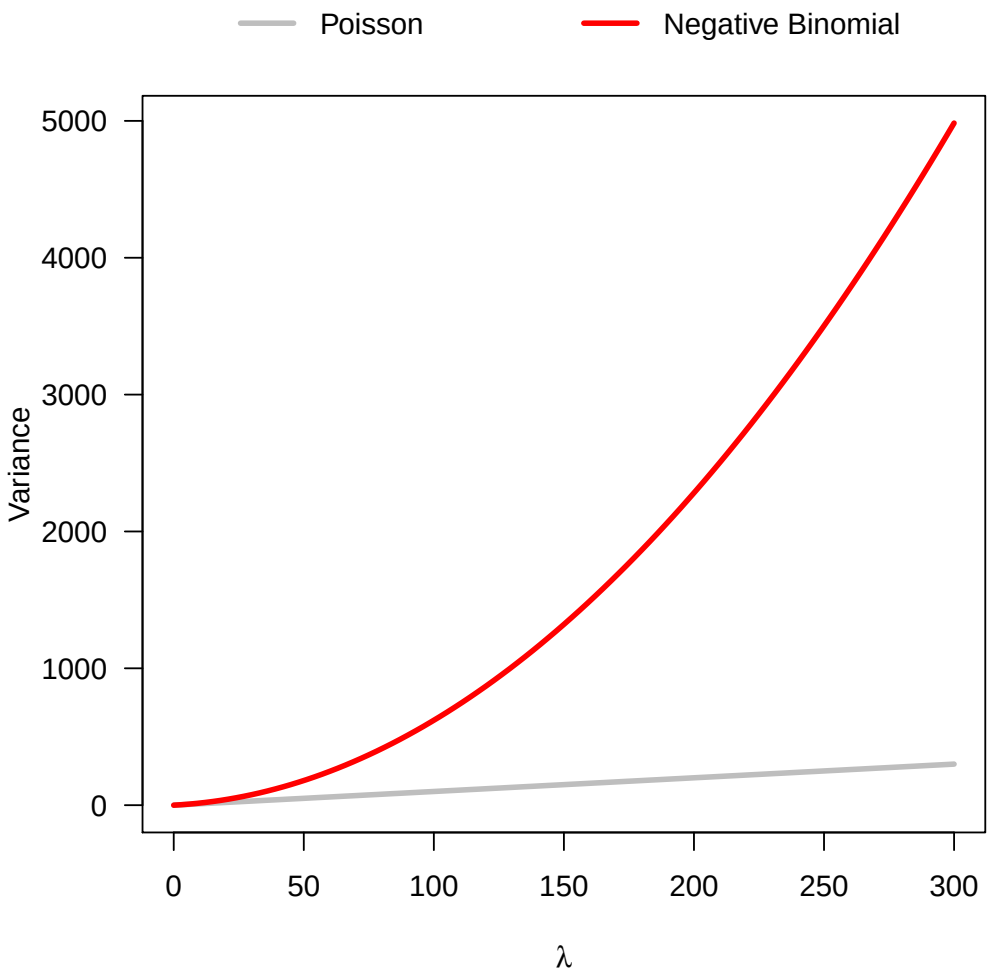
- Thus, like the Poisson distribution, the negative binomial has support only on the positive integers, but unlike the Poisson, its variance is larger than its mean

Negative binomial and exponential family

- Note, however, that the negative binomial distribution is not a member of the exponential family
- Thus, the theory and fitting procedures we have developed for GLMs do not directly apply here
- For example, there is no "canonical link"; however, it is customary to employ a log link to make negative binomial regression look like Poisson regression
- Regardless, `PROC GENMOD` in SAS allows the choice of `DIST=NB` for negative binomial models; in `R`, one must use the `glm.nb` function in the `MASS` package

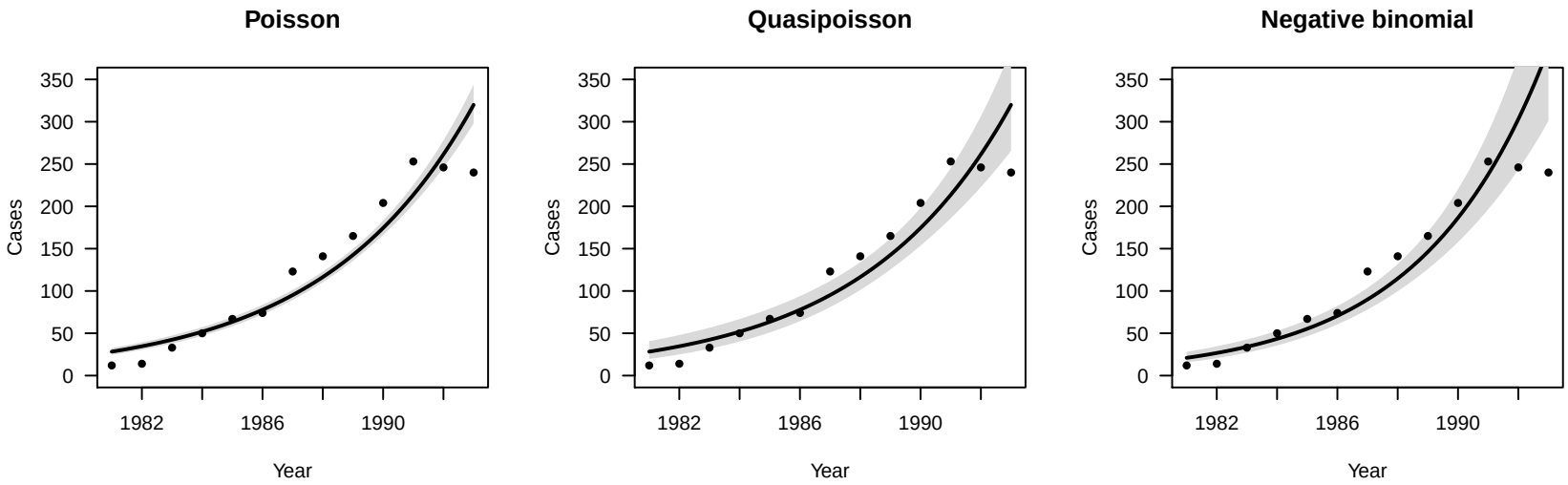
Negative binomial: Mean-variance relationship

For the Belgian AIDS data, $\hat{\theta} = 19.2$, implying the following mean-variance relationship:



Negative binomial: Estimate

This leads to the following:



Remarks

- Arguably, the negative binomial estimates are even worse than the Poisson estimates, and certainly drastically worse than the quadratic Poisson model
- However, its "goodness of fit" measures are much better
- This is why I remarked earlier that it's wrong to think of the *data* as overdispersed – if the data show more variability than the model can explain, the most likely explanation is a bad model
- The quadratic Poisson fit shows no overdispersion (the residuals are actually slightly "underdispersed")

Remarks (cont'd)

- Accounting for overdispersion *is* a good idea – if the model doesn't fit the data, this should be reflected with larger standard errors and wider confidence intervals
- However, many analysts have the view that quasi-Poisson or negative binomial regression automatically "fixes" the overdispersion problem
- This is a potentially dangerous misconception – surely, accurately modeling the mean is of greater priority than modeling the variance
- While quasi-Poisson and negative binomial approaches are useful, they are certainly no substitute for careful consideration of the systematic component of the model