Lecture 9. GLM for Non-negative Continuous Response

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Examples of Non-negative Continuous Responses

Drug study

Clotting times of blood against plasma type and concentration.

Insurance study

claim amounts against policy holder age, car type and vehicle age

This Lecture

- Model options
- Gamma regression
- Inverse-Gaussian regression

Model options

- Exponential family

  Gamma, inverse Gaussian

- Several links are commonly used

name	$g(\mu)$	$\mu \geq 0$	canonical link
log	$\ln(\mu)$	yes	
inverse	μ^{-1}	no	for Gamma distribution
inverse-quadratic	μ^{-2}	yes	for inverse-Gaussian distribution

Gamma Regression

Recall

- When Y is a non-negative continuous random variable, we can choose the systematic and random components as follows.

$$\begin{aligned} \text{(systematic)} \quad & \mathbb{E}(Y \mid \mathbf{x}) = \exp(\beta^\top \mathbf{x}) \\ \text{(random)} \quad & Y \mid \mathbf{x} \text{ is Gamma distributed.} \end{aligned}$$

- We further assume the variance of the Gamma distribution is μ^2/ν (ν treated as known), thus

$$Y \mid \mathbf{x} \sim \Gamma(\mu = \exp(\beta^\top \mathbf{x}), \text{var} = \mu^2/\nu),$$

where $\Gamma(\mu = a, \text{var} = b)$ denotes a Gamma distribution with mean a and variance b.

Parameter interpretation

- Using log-link, $\mu = \exp(\mathbf{x}^\top \beta)$.
- One unit increase in x_i changes the mean by a factor of $\exp(\beta_i)$.
- No such simple interpretation for inverse link and inverse quadratic link.

Fisher scoring

- Consider the case of log link

$$Y \mid \mathbf{x} \sim \Gamma(\mu = \exp(\beta^\top \mathbf{x}), \mathrm{var} = \mu^2/\nu),$$

- Let $\mu_i = \exp(\mathbf{x}_i^\top \beta)$.
- The gradient and the Fisher information are

$$\nabla \ell(\beta) = \sum_i \frac{\nu(y_i - \mu_i)}{\mu_i} \mathbf{x}_i,$$
$$I(\beta) = \sum_i \nu \mathbf{x}_i^\top \mathbf{x}_i,$$

- Fisher scoring updates β to

$$\beta' = \beta + I(\beta)^{-1} \nabla \ell(\beta).$$

Note that ν actually has no effect on the update.

- Let $\mathbf{X}$ be the design matrix,

$$\boldsymbol{\mu} = (\mu_1, \ldots, \mu_n),$$
$$A = \mathrm{diag}(\nu(y_1 - \mu_1), \ldots, \nu(y_n - \mu_n)),$$

- In matrix notation, the gradient and the Fisher information are

$$\nabla \ell(\beta) = \mathbf{X}^\top A(\mathbf{y} - \boldsymbol{\mu}),$$
$$I(\beta) = \nu \mathbf{X}^\top \mathbf{X}.$$

Example

Data

id	conc	time	lot	id	conc	time	lot
1	5	118	1	10	5	69	2
2	10	58	1	11	10	35	2
3	15	42	1	12	15	26	2
4	20	35	1	13	20	21	2
5	30	27	1	14	30	18	2
6	40	25	1	15	40	16	2
7	60	21	1	16	60	13	2
8	80	19	1	17	80	12	2
9	100	18	1	18	100	12	2

- Blood clotting times in seconds under different plasma concentration and two lots of thromboplastin.
- Normal plasma diluted to nine different concentrations.
- Two lots of thromboplastin.

Gamma: inverse link (canonical)

```
> fit.gam.inv = glm(time ~ lot * log(conc), data=clot, family=Gamma)
> summary(fit.gam.inv)
Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
(Intercept)    -0.0165544  0.0008655 -19.127 1.97e-11 ***
lot2           -0.0073541  0.0016780  -4.383 0.000625 ***
log(conc)       0.0153431  0.0003872  39.626 8.85e-16 ***
lot2:log(conc)  0.0082561  0.0007353  11.228 2.18e-08 ***
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1

(Dispersion parameter for Gamma family taken to be 0.002129707)
```

$$\mu = \begin{cases} (-0.0165544 + 0.0153431 * log(conc))^{-1}, & \text{if lot=1.} \\ (-0.0073744 + 0.0082575 * log(conc))^{-1}, & \text{if lot=2.} \end{cases}$$

Gamma: inverse quadratic link

```
> fit.gam.invquad = glm(time ~ lot * log(conc), data=clot,
    family=Gamma(link='1/mu^2'))
> summary(fit.gam.invquad)
Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
(Intercept)    -1.004e-03  1.470e-04  -6.831 8.18e-06 ***
lot2           -1.486e-03  4.056e-04  -3.664 0.002551 **
log(conc)       6.649e-04  8.795e-05   7.560 2.63e-06 ***
lot2:log(conc)  1.002e-03  2.403e-04   4.171 0.000941 ***
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1

(Dispersion parameter for Gamma family taken to be 0.03015227)
```

Gamma: log-link

```
> fit.gam.log = glm(time ~ lot * log(conc), data=clot,
    family=Gamma(link='log'))
> summary(fit.gam.log)
Coefficients:
               Estimate Std. Error t value Pr(>|t|)
(Intercept)     5.50323    0.18794  29.282 5.83e-14 ***
lot2           -0.58447    0.26578  -2.199   0.0452 *
log(conc)      -0.60192    0.05462 -11.020 2.77e-08 ***
lot2:log(conc)  0.03448    0.07725   0.446   0.6621
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1

(Dispersion parameter for Gamma family taken to be 0.02375284)
```

- The lot factor does not show strong effect when we use log link.
- This is qualitatively different from the cases for the inverse link and inverse quadratic link.

```
> logLik(fit.gam.inv)
'log Lik.' -26.59759 (df=5)
> logLik(fit.gam.invquad)
'log Lik.' -50.13667 (df=5)
> logLik(fit.gam.log)
'log Lik.' -47.98692 (df=5)
```

Gamma regression with inverse link has the best fit (much better than the other two).

Inverse Gaussian Regression

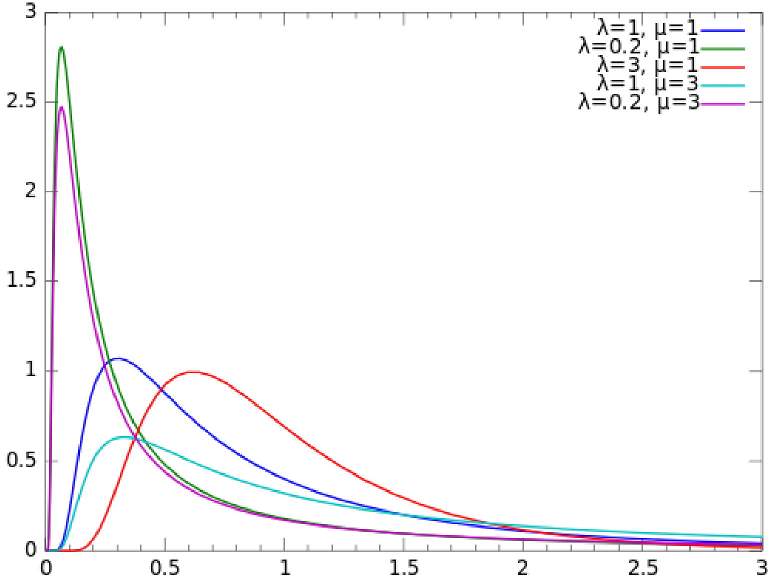
Inverse Gaussian distribution

- The PDF is given by

$$f(y \mid \mu, \lambda) = \left[\frac{\lambda}{2\pi y^3}\right]^{1/2} \exp\left\{\frac{-\lambda(y-\mu)^2}{2\mu^2 y}\right\},$$

  where μ is the mean and λ is the shape.
- The variance is cubic in the mean

$$\mathrm{var}(X) = \mu^3/\lambda.$$



PDF of inverse Gaussians.

Example (cont.)

Inverse Gaussian: inverse link

```
> fit.ig.inv = glm(time ~ lot * log(conc), data=clot,
    family=inverse.gaussian(link='inverse'))
> summary(fit.ig.inv)
Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
(Intercept)    -0.0177893  0.0012377 -14.373 8.95e-10 ***
lot2           -0.0073744  0.0020333  -3.627  0.00275 **
log(conc)       0.0158014  0.0004350  36.327 2.96e-15 ***
lot2:log(conc)  0.0082575  0.0007075  11.671 1.33e-08 ***
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1

(Dispersion parameter for inverse.gaussian family taken to be
    6.942317e-05)
```

Inverse Gaussian: inverse-quadratic link (canonical)

```
> fit.ig.invquad = glm(time ~ lot * log(conc), data=clot,
    family=inverse.gaussian)
> summary(fit.ig.invquad)
Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
(Intercept)    -1.108e-03  1.761e-04  -6.291 1.99e-05 ***
lot2           -1.617e-03  4.024e-04  -4.018 0.001269 **
log(conc)       7.219e-04  9.954e-05   7.253 4.21e-06 ***
lot2:log(conc)  1.071e-03  2.233e-04   4.797 0.000284 ***
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1

(Dispersion parameter for inverse.gaussian family taken to be
    0.001216639)
```

Inverse Gaussian: log link

```
> fit.ig.log = glm(time ~ lot * log(conc), data=clot,
    family=inverse.gaussian(link='log'))
> summary(fit.ig.log)
Coefficients:
               Estimate Std. Error t value Pr(>|t|)
(Intercept)     5.29038    0.23211  22.793 1.82e-12 ***
lot2           -0.56699    0.29495  -1.922   0.0752 .
log(conc)      -0.54163    0.06068  -8.925 3.75e-07 ***
lot2:log(conc)  0.02969    0.07725   0.384   0.7065
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1

(Dispersion parameter for inverse.gaussian family taken to be
    0.000758257)
```

```
> logLik(fit.ig.inv)
'log Lik.' -25.33805 (df=5)
> logLik(fit.ig.invquad)
'log Lik.' -50.26075 (df=5)
> logLik(fit.ig.log)
'log Lik.' -45.55859 (df=5)
```

Inverse Gaussian regression with inverse link has the best fit (much better than the other two).

Some Observations

- Link function plays an important role in fitting a good model.

  inverse link is the best for both Gamma and inverse Gaussian in our example

- When the same link is used, the coefficients are similar for different exponential families

  for each link, compare the coefficients for Gamma and inverse Gaussian in our example..

What You Need to Know

- Model options
- Gamma regression
- Inverse-Gaussian regression