# Intermediate Analytics

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**ALY 6015**

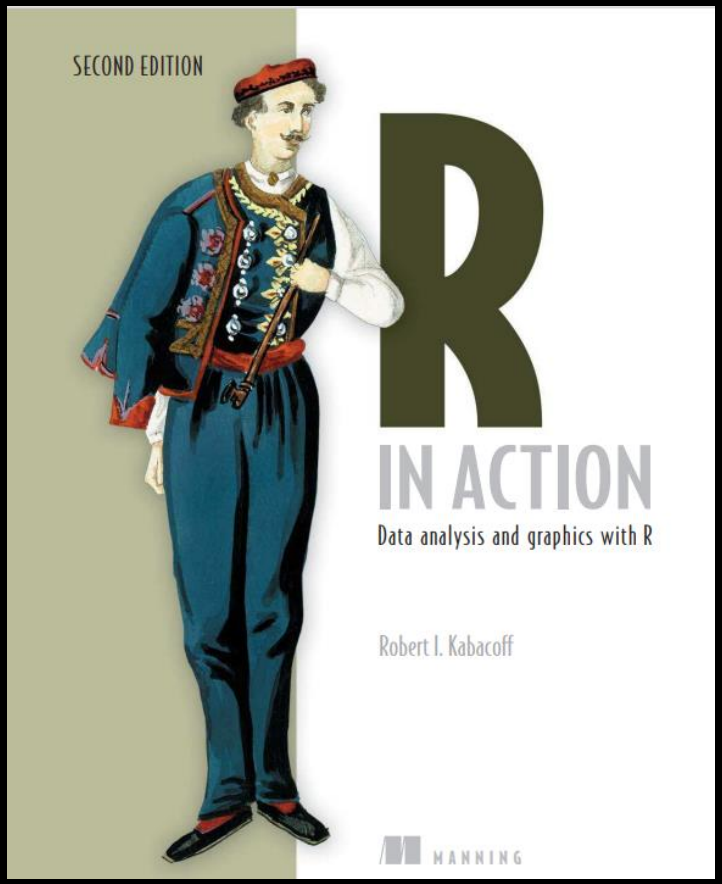
# *Generalized Linear Models*

Slides are mainly borrowed from the textbook:

- ***R in Action, 2nd Edition, R. Kabacoff, Manning***

# You will learn in this course:

- Formulating a generalized linear model
- Predicting categorical outcomes
- Modeling count data



# Introduction

In chapters 8 (Regression) and 9 (ANOVA), we explored linear models that can be used to predict a normally distributed response variable from a set of continuous and/or categorical predictor variables. **But there are many situations in which it's unreasonable to assume that the dependent variable is normally distributed (or even continuous)**. For example:

- ✓ The outcome variable may be categorical. Binary variables (for example, yes/ no, passed/failed, lived/died) and polytomous variables (for example, poor/good/excellent, republican/democrat/independent) clearly aren't normally distributed.
- ✓ The outcome variable may be a count (for example, the number of traffic accidents in a week, the number of drinks per day). Such variables take on a limited number of values and are never negative. Additionally, their mean and variance are often related (which isn't true for normally distributed variables).

# Introduction

In this chapter, we'll start with a brief overview of **generalized linear models** and the ***glm*()** function used to estimate them. Then we'll focus on two popular models in this framework: **Logistic regression (where the dependent variable is categorical) and Poisson regression (where the dependent variable is a count variable)**. To motivate the discussion, you'll apply generalized linear models to two research questions that aren't easily addressed with standard linear models:

- What personal, demographic, and relationship variables predict marital infidelity? In this case, the outcome variable is binary (affair/no affair).
- What impact does a drug treatment for seizures have on the number of seizures experienced over an eight-week period? In this case, the outcome variable is a count (number of seizures).

You'll apply logistic regression to address the first question and Poison regression to address the second. Along the way, we'll consider extensions of each technique.

# Generalized linear models and the glm() function

A wide range of popular data-analytic methods is subsumed within the framework of the generalized linear model. In this section, we'll briefly explore some of the theories behind this approach.

Let's say that you want to model the relationship between a response variable $Y$ and a set of $p$ predictor variables $X_1$ ...$X_p$. In the standard linear model, you assume that $Y$ is normally distributed and that the form of the relationship is:

$$\mu_Y = \beta_0 + \sum_{j=1}^{p} \beta_j X_j$$

# Generalized linear models and the glm() function

Note that you've made no distributional assumptions about the predictor variables, $X_j$. Unlike $Y$, there's no requirement that they are normally distributed. In fact, they're often categorical (for example, ANOVA designs). Additionally, nonlinear functions of the predictors are allowed. You often include such predictors as $X_2$ or $X_1 \times X_2$. What is important is that the equation is linear in the parameters ($\beta 0$, $\beta 1$,... $\beta p$). In generalized linear models, you fit models of the form:

$$g(\mu_Y) = \beta_0 + \sum_{j=1}^{p} \beta_j X_j$$

# The glm() function

Generalized linear models typically fit in *R* through the *glm*() function (although other specialized functions are available). The form of the function is similar to *lm*() but includes additional parameters. The basic format of the function is

```
glm(formula, family=family(link=function), data=)
```

where the probability distribution (*family*) and corresponding default link function (*function*) are given in table 13.1.

# The glm() function

**Table 13.1** `glm()` parameters

| Family | Default link function |
|---|---|
| binomial | (link = "logit") |
| gaussian | (link = "identity") |
| gamma | (link = "inverse") |
| inverse.gaussian | (link = "1/mu^2") |
| poisson | (link = "log") |
| quasi | (link = "identity", variance = "constant") |
| quasibinomial | (link = "logit") |
| quasipoisson | (link = "log") |

# The glm() function

The *glm*() function allows you to fit a number of popular models, including *Logistic* regression, *Poisson* regression, and survival analysis (not considered here). You can demonstrate this for the first two models as follows:
Assume that you have a single response variable ($Y$), three predictor variables ($X_1$, $X_2$, $X_3$), and a data frame (*mydata*) containing the data. Logistic regression is applied to situations in which the response variable is dichotomous (0 or 1). The model assumes that $Y$ follows a binomial distribution and that you can fit a linear model of the form:

$$\log_e\left(\frac{\pi}{1-\pi}\right) = \beta_0 + \sum_{j=1}^{p}\beta_j X_j$$

where $\pi = \mu_Y$ is the conditional mean of Y (that is, the probability that Y = 1 given a set of X values), $(\pi/1-\pi)$ is the odds that Y = 1, and $\log(\pi/1-\pi)$ is the log odds, or *logit*.

# The glm() function

In this case, $\log(\pi/1-\pi)$ is the link function, the probability distribution is binomial, and the logistic regression model can be fit using

```
glm(Y~X1+X2+X3, family=binomial(link="logit"), data=mydata)
```

Logistic regression is described more fully in section 13.2.

Poisson regression is applied to situations in which the response variable is the number of events to occur in a given period of time. The Poisson regression model assumes that Y follows a Poisson distribution and that you can fit a linear model of the form

$$\log_e(\lambda) = \beta_0 + \sum_{j=1}^{p} \beta_j X_j$$

where $\lambda$ is the mean (and variance) of Y. In this case, the link function is $\log(\lambda)$, the probability distribution is Poisson, and the Poisson regression model can be fit using

```
glm(Y~X1+X2+X3, family=poisson(link="log"), data=mydata)
```

Poisson regression is described in section 13.3.

It's worth noting that the standard linear model is also a special case of the generalized linear model. If you let the link function $g(\mu_Y) = \mu_Y$ or the identity function and specify that the probability distribution is normal (Gaussian), then

```
glm(Y~X1+X2+X3, family=gaussian(link="identity"), data=mydata)
```

would produce the same results as

```
lm(Y~X1+X2+X3, data=mydata)
```

# Supporting Functions

**Table 13.2 Functions that support `glm()`**

| Function | Description |
|---|---|
| `summary()` | Displays detailed results for the fitted model |
| `coefficients()`, `coef()` | Lists the model parameters (intercept and slopes) for the fitted model |
| `confint()` | Provides confidence intervals for the model parameters (95% by default) |
| `residuals()` | Lists the residual values in a fitted model |
| `anova()` | Generates an ANOVA table comparing two fitted models |
| `plot()` | Generates diagnostic plots for evaluating the fit of a model |
| `predict()` | Uses a fitted model to predict response values for a new dataset |
| `deviance()` | Deviance for the fitted model |
| `df.residual()` | Residual degrees of freedom for the fitted model |

# Model fit and regression diagnostics

- ✓ The assessment of model adequacy is as important for generalized linear models as it is for standard (OLS) linear models.
- ✓ Unfortunately, there’s less agreement in the statistical community regarding appropriate assessment procedures.
- ✓ In general, you can use the techniques described in chapter 8, with the following caveats.
- ✓ When assessing model adequacy, you’ll typically want to plot predicted values expressed in the metric of the original response variable against residuals of the deviance type. For example, a common diagnostic plot would be:

# Model fit and regression diagnostics

```
plot(predict(model, type="response"),
     residuals(model, type= "deviance"))
```

where `model` is the object returned by the `glm()` function.

The hat values, studentized residuals, and Cook's D statistics that R provides will be approximate values. Additionally, there's no general consensus on cutoff values for identifying problematic observations. Values have to be judged relative to each other. One approach is to create index plots for each statistic and look for unusually large values. For example, you could use the following code to create three diagnostic plots:

```
plot(hatvalues(model))
plot(rstudent(model))
plot(cooks.distance(model))
```

Alternatively, you could use the code

```
library(car)
influencePlot(model)
```

# Logistic Regression

**Logistic regression is useful when you're predicting a binary outcome from a set of continuous and/or categorical predictor variables**. To demonstrate this, let's explore the data on infidelity contained in the data frame *Affairs*, provided with the *AER* package. Be sure to download and install the package (using *install.packages("AER"))* before first use.

```
> data(Affairs, package="AER")
> summary(Affairs)
    affairs          gender         age          yearsmarried    children
 Min.   : 0.000   female:315   Min.   :17.50   Min.   : 0.125   no :171
 1st Qu.: 0.000   male  :286   1st Qu.:27.00   1st Qu.: 4.000   yes:430
 Median : 0.000                Median :32.00   Median : 7.000
 Mean   : 1.456                Mean   :32.49   Mean   : 8.178
 3rd Qu.: 0.000                3rd Qu.:37.00   3rd Qu.:15.000
 Max.   :12.000                Max.   :57.00   Max.   :15.000
 religiousness     education       occupation        rating
 Min.   :1.000   Min.   : 9.00   Min.   :1.000   Min.   :1.000
 1st Qu.:2.000   1st Qu.:14.00   1st Qu.:3.000   1st Qu.:3.000
 Median :3.000   Median :16.00   Median :5.000   Median :4.000
 Mean   :3.116   Mean   :16.17   Mean   :4.195   Mean   :3.932
 3rd Qu.:4.000   3rd Qu.:18.00   3rd Qu.:6.000   3rd Qu.:5.000
 Max.   :5.000   Max.   :20.00   Max.   :7.000   Max.   :5.000

> table(Affairs$affairs)
  0   1   2   3   7  12
451  34  17  19  42  38
```

# Logistic Regression

Although the *number* of indiscretions was recorded, your interest here is in the binary outcome (had an affair/didn't have an affair). You can transform affairs into a dichotomous factor called ynaffair with the following code.

```
> Affairs$ynaffair[Affairs$affairs  > 0] <- 1
> Affairs$ynaffair[Affairs$affairs == 0] <- 0
```

```
> Affairs$ynaffair <- factor(Affairs$ynaffair,
                             levels=c(0,1),
                             labels=c("No","Yes"))
> table(Affairs$ynaffair)
No Yes
451 150
```

# Logistic Regression

```
> fit.full <- glm(ynaffair ~ gender + age + yearsmarried + children +
                  religiousness + education + occupation +rating,
                  data=Affairs, family=binomial())
> summary(fit.full)

Call:
glm(formula = ynaffair ~ gender + age + yearsmarried + children +
    religiousness + education + occupation + rating, family = binomial(),
    data = Affairs)

Deviance Residuals:
   Min      1Q  Median      3Q     Max
-1.571  -0.750  -0.569  -0.254   2.519

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)    1.3773     0.8878    1.55  0.12081
gendermale     0.2803     0.2391    1.17  0.24108
age           -0.0443     0.0182   -2.43  0.01530 *
yearsmarried   0.0948     0.0322    2.94  0.00326 **
childrenyes    0.3977     0.2915    1.36  0.17251
religiousness -0.3247     0.0898   -3.62  0.00030 ***
education      0.0211     0.0505    0.42  0.67685
occupation     0.0309     0.0718    0.43  0.66663
rating        -0.4685     0.0909   -5.15  2.6e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 675.38  on 600  degrees of freedom
Residual deviance: 609.51  on 592  degrees of freedom
AIC: 627.5

Number of Fisher Scoring iterations: 4
```

# Logistic Regression

From the p-values for the regression coefficients (last column), you can see that gender, presence of children, education, and occupation may not make a significant contribution to the equation (you can't reject the hypothesis that the parameters are 0).

Let's fit a second equation without them and test whether this reduced model fits the data as well:

```
> fit.reduced <- glm(ynaffair ~ age + yearsmarried + religiousness +
                       rating, data=Affairs, family=binomial())
> summary(fit.reduced)
```

# Logistic Regression

```
Call:
glm(formula = ynaffair ~ age + yearsmarried + religiousness + rating,
    family = binomial(), data = Affairs)

Deviance Residuals:
   Min      1Q  Median      3Q     Max
-1.628  -0.755  -0.570  -0.262   2.400

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)    1.9308     0.6103    3.16  0.00156 **
age           -0.0353     0.0174   -2.03  0.04213 *
yearsmarried   0.1006     0.0292    3.44  0.00057 ***
religiousness -0.3290     0.0895   -3.68  0.00023 ***
rating        -0.4614     0.0888   -5.19  2.1e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 675.38  on 600  degrees of freedom
Residual deviance: 615.36  on 596  degrees of freedom
AIC: 625.4

Number of Fisher Scoring iterations: 4
```

# Logistic Regression

Each regression coefficient in the reduced model is statistically significant ($p < .05$). Because the two models are nested (`fit.reduced` is a subset of `fit.full`), you can use the `anova()` function to compare them. For generalized linear models, you'll want a chi-square version of this test:

```
> anova(fit.reduced, fit.full, test="Chisq")
Analysis of Deviance Table

Model 1: ynaffair ~ age + yearsmarried + religiousness + rating
Model 2: ynaffair ~ gender + age + yearsmarried + children +
    religiousness + education + occupation + rating
  Resid. Df Resid. Dev Df Deviance P(>|Chi|)
1       596        615
2       592        610  4     5.85       0.21
```

The nonsignificant chi-square value ($p = 0.21$) suggests that the reduced model with four predictors fits as well as the full model with nine predictors, reinforcing your belief that gender, children, education, and occupation don't add significantly to the prediction above and beyond the other variables in the equation. Therefore, you can base your interpretations on the simpler model.

# Logistic Regression

***Interpreting the model parameters***

Let's look at the regression coefficients:

```
> coef(fit.reduced)
  (Intercept)           age  yearsmarried religiousness        rating
        1.931        -0.035         0.101        -0.329        -0.461
```

In logistic regression, the response being modeled is the *log(odds)* that Y = 1. The regression coefficients give the change in *log(odds)* in the response for a unit change in the predictor variable, holding all other predictor variables constant. Because *log(odds)* is difficult to interpret, you can exponentiate them to put the results on an odds scale:

```
> exp(coef(fit.reduced))
  (Intercept)           age  yearsmarried religiousness        rating
        6.895         0.965         1.106         0.720         0.630
```

# Assessing the impact of predictors on the probability of an outcome

For many of us, it's easier to think in terms of probabilities than odds. You can use the *predict*() function to observe the impact of varying the levels of a predictor variable on the probability of the outcome. The first step is to create an artificial dataset containing the values of the predictor variables you're interested in. Then you can use this artificial dataset with the *predict*() function to predict the probabilities of the outcome event occurring for these values. Let's apply this strategy to assess the impact of marital ratings on the probability of having an extramarital affair. First, create an artificial dataset where age, years married, and religiousness are set to their means, and marital rating varies from 1 to 5:

```
> testdata <- data.frame(rating=c(1, 2, 3, 4, 5), age=mean(Affairs$age),
                         yearsmarried=mean(Affairs$yearsmarried),
                         religiousness=mean(Affairs$religiousness))
> testdata
  rating  age yearsmarried religiousness
1      1 32.5         8.18          3.12
2      2 32.5         8.18          3.12
3      3 32.5         8.18          3.12
4      4 32.5         8.18          3.12
5      5 32.5         8.18          3.12
```

# Assessing the impact of predictors on the probability of an outcome

Next, use the test dataset and prediction equation to obtain probabilities:

```
> testdata$prob <- predict(fit.reduced, newdata=testdata, type="response")
  testdata
  rating  age yearsmarried religiousness  prob
1      1 32.5          8.18           3.12 0.530
2      2 32.5          8.18           3.12 0.416
3      3 32.5          8.18           3.12 0.310
4      4 32.5          8.18           3.12 0.220
5      5 32.5          8.18           3.12 0.151
```

From these results, you see that the probability of an extramarital affair decreases from 0.53 when the marriage is rated *1=very unhappy* to 0.15 when the marriage is rated *5=very happy* (holding age, years married, and religiousness constant).

Now look at the impact of *age*:

# Assessing the impact of predictors on the probability of an outcome

Here, you see that as age increases from 17 to 57, the probability of an extramarital encounter decreases from 0.34 to 0.11, holding the other variables constant. Using this approach, you can explore the impact of each predictor variable on the outcome.

```
> testdata <- data.frame(rating=mean(Affairs$rating),
                         age=seq(17, 57, 10),
                         yearsmarried=mean(Affairs$yearsmarried),
                         religiousness=mean(Affairs$religiousness))
> testdata
  rating age yearsmarried religiousness
1   3.93  17         8.18           3.12
2   3.93  27         8.18           3.12
3   3.93  37         8.18           3.12
4   3.93  47         8.18           3.12
5   3.93  57         8.18           3.12

> testdata$prob <- predict(fit.reduced, newdata=testdata, type="response")
> testdata
  rating age yearsmarried religiousness  prob
1   3.93  17         8.18           3.12 0.335
2   3.93  27         8.18           3.12 0.262
3   3.93  37         8.18           3.12 0.199
4   3.93  47         8.18           3.12 0.149
5   3.93  57         8.18           3.12 0.109
```

# Overdispersion

The expected variance for data drawn from a binomial distribution is $\sigma 2 = n\pi(1 - \pi)$, where $n$ is the number of observations and $\pi$ is the probability of belonging to the Y = 1 group. **Overdispersion** occurs when the observed variance of the response variable is larger than what would be expected from a binomial distribution. Overdispersion can lead to distorted test standard errors and inaccurate tests of significance. When overdispersion is present, you can still fit a logistic regression using the *glm*() function, but in this case, you should use the quasibinomial distribution rather than the binomial distribution.

One way to detect overdispersion is to compare the residual deviance with the residual degrees of freedom in your binomial model. If the ratio

$$\phi = \frac{Residual\ deviance}{Residual\ df}$$

is considerably larger than 1, you have evidence of overdispersion. Applying this to the `Affairs` example, you have

```
> deviance(fit.reduced)/df.residual(fit.reduced)
[1] 1.032
```

# Overdispersion

which is close to 1, suggesting no overdispersion.

You can also test for overdispersion. To do this, you fit the model twice, but in the first instance you use `family="binomial"` and in the second instance you use `family="quasibinomial"`. If the `glm()` object returned in the first case is called `fit` and the object returned in the second case is called `fit.od`, then

```
pchisq(summary(fit.od)$dispersion * fit$df.residual,
       fit$df.residual, lower = F)
```

provides the p-value for testing the null hypothesis $H_0$: $\phi = 1$ versus the alternative hypothesis $H_1$: $\phi \neq 1$. If p is small (say, less than 0.05), you'd reject the null hypothesis.

Applying this to the `Affairs` dataset, you have

```
> fit <- glm(ynaffair ~ age + yearsmarried + religiousness +
             rating, family = binomial(), data = Affairs)
> fit.od <- glm(ynaffair ~ age + yearsmarried + religiousness +
               rating, family = quasibinomial(), data = Affairs)
> pchisq(summary(fit.od)$dispersion * fit$df.residual,
         fit$df.residual, lower = F)

[1] 0.34
```

The resulting p-value (0.34) is clearly not significant ($p > 0.05$), strengthening your belief that overdispersion isn't a problem. We'll return to the issue of overdispersion when we discuss Poisson regression.

# Extensions

Several logistic regression extensions and variations are available in *R*:

- *Robust Logistic regression*—The *glmRob*() function in the *robust* package can be used to fit a robust generalized linear model, including robust logistic regression. Robust logistic regression can be helpful when fitting logistic regression models to *data containing outliers and influential observations*.
- *Multinomial Logistic regression*—If the response variable *has more than two unordered categories* (for example, married/widowed/divorced), you can fit a polytomous logistic regression using the *mlogit*() function in the *mlogit* package.
- *Ordinal Logistic regression*—If the response variable is *a set of ordered categories* (for example, credit risk as poor/good/excellent), you can fit an ordinal logistic regression using the *lrm*() function in the *rms* package.

# Poisson Regression

**Poisson regression is useful when you're predicting an outcome variable representing counts from a set of continuous and/or categorical predictor variables**.

To illustrate the fitting of a Poisson regression model, along with some issues that can come up in the analysis, we'll use the *Breslow seizure data* (Breslow, 1993) provided in the *robust* package. Specifically, we'll consider the impact of antiepileptic drug treatment on the number of seizures occurring over an eight-week period following the initiation of therapy. Be sure to install the *robust* package before continuing

Data were collected on the age and number of seizures reported by patients suffering from simple or complex partial seizures during an eight-week period before, and the eight-week period after, randomization into a drug or placebo condition. *SumY* (the number of seizures in the eight-week period post-randomization) is the response variable. Treatment condition (*Trt*), age in years (*Age*), and the number of seizures reported in the baseline eight-week period (*Base*) are the predictor variables. The baseline number of seizures and age are included because of their potential effect on the response variable. We're interested in whether or not evidence exists that the drug treatment decreases the number of seizures after accounting for these covariates.

# Poisson Regression

First, let's look at summary statistics for the dataset:

```
> data(breslow.dat, package="robust")
> names(breslow.dat)
 [1] "ID"    "Y1"    "Y2"    "Y3"    "Y4"    "Base"  "Age"   "Trt"   "Ysum"
[10] "sumY"  "Age10" "Base4"
```

```
> summary(breslow.dat[c(6,7,8,10)])
      Base             Age               Trt          sumY
 Min.   :  6.0   Min.   :18.0   placebo  :28   Min.   :  0.0
 1st Qu.: 12.0   1st Qu.:23.0   progabide:31   1st Qu.: 11.5
 Median : 22.0   Median :28.0                  Median : 16.0
 Mean   : 31.2   Mean   :28.3                  Mean   : 33.1
 3rd Qu.: 41.0   3rd Qu.:32.0                  3rd Qu.: 36.0
 Max.   :151.0   Max.   :42.0                  Max.   :302.0
```

```
> breslow.dat
   ID  Y1  Y2 Y3 Y4 Base Age       Trt Ysum sumY Age10 Base4
1  104   5   3  3  3   11  31   placebo   14   14   3.1  2.75
2  106   3   5  3  3   11  30   placebo   14   14   3.0  2.75
3  107   2   4  0  5    6  25   placebo   11   11   2.5  1.50
4  114   4   4  1  4    8  36   placebo   13   13   3.6  2.00
5  116   7  18  9 21   66  22   placebo   55   55   2.2 16.50
6  118   5   2  8  7   27  29   placebo   22   22   2.9  6.75
7  123   6   4  0  2   12  31   placebo   12   12   3.1  3.00
8  126  40  20 23 12   52  42   placebo   95   95   4.2 13.00
9  130   5   6  6  5   23  37   placebo   22   22   3.7  5.75
10 135  14  13  6  0   10  28   placebo   33   33   2.8  2.50
11 141  26  12  6 22   52  36   placebo   66   66   3.6 13.00
12 145  12   6  8  4   33  24   placebo   30   30   2.4  8.25
13 201   4   4  6  2   18  23   placebo   16   16   2.3  4.50
14 202   7   9 12 14   42  36   placebo   42   42   3.6 10.50
15 205  16  24 10  9   87  26   placebo   59   59   2.6 21.75
16 206  11   0  0  5   50  26   placebo   16   16   2.6 12.50
17 210   0   0  3  3   18  28   placebo    6    6   2.8  4.50
18 213  37  29 28 29  111  31   placebo  123  123   3.1 27.75
19 215   3   5  2  5   18  32   placebo   15   15   3.2  4.50
20 217   3   0  6  7   20  21   placebo   16   16   2.1  5.00
21 219   3   4  3  4   12  29   placebo   14   14   2.9  3.00
22 220   3   4  3  4    9  21   placebo   14   14   2.1  2.25
23 222   2   3  3  5   17  32   placebo   13   13   3.2  4.25
24 226   8  12  2  8   28  25   placebo   30   30   2.5  7.00
25 227  18  24 76 25   55  30   placebo  143  143   3.0 13.75
26 230   2   1  2  1    9  40   placebo    6    6   4.0  2.25
27 234   3   1  4  2   10  19   placebo   10   10   1.9  2.50
28 238  13  15 13 12   47  22   placebo   53   53   2.2 11.75
```

# Poisson Regression

Note that although there are 12 variables in the dataset, we're limiting our attention to the 4 described earlier. Both the baseline and post-randomization number of seizures are highly skewed. Let's look at the response variable in more detail. The following code produces the graphs in figure 13.1:

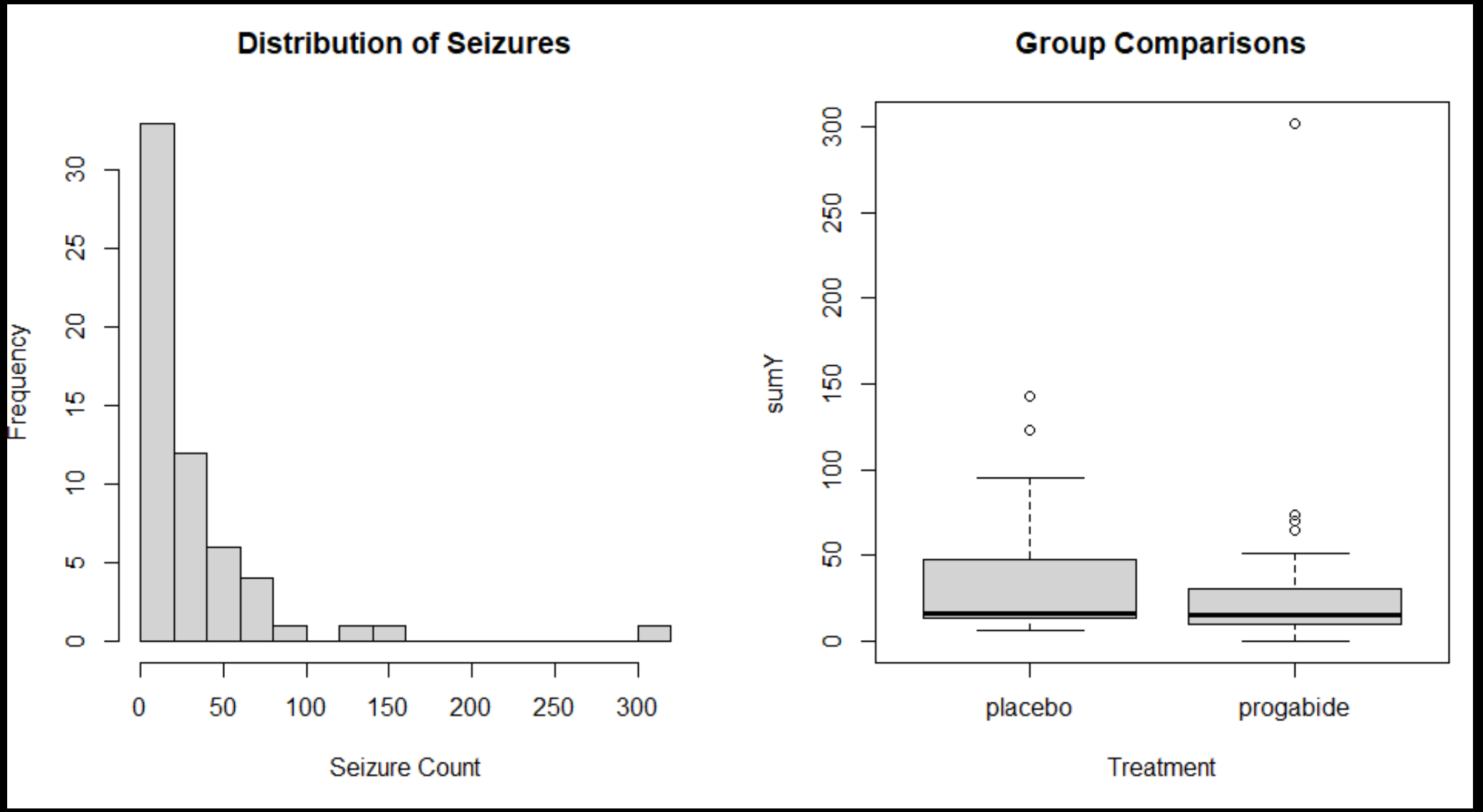
```
opar <- par(no.readonly=TRUE)
par(mfrow=c(1,2))
attach(breslow.dat)
hist(sumY, breaks=20, xlab="Seizure Count",
     main="Distribution of Seizures")
boxplot(sumY ~ Trt, xlab="Treatment", main="Group Comparisons")
par(opar)
```

You can clearly see the skewed nature of the dependent variable and the possible presence of outliers. At first glance, the number of seizures in the drug condition appears to be smaller and has a smaller variance. (You'd expect a smaller variance to accompany a smaller mean with Poisson distributed data.) Unlike standard OLS regression, this heterogeneity of variance isn't a problem in Poisson regression.

The next step is to fit the Poisson regression:

```
> fit <- glm(sumY ~ Base + Age + Trt, data=breslow.dat, family=poisson())
> summary(fit)
```

# Poisson Regression



# Poisson Regression

```
Call:
glm(formula = sumY ~ Base + Age + Trt, family = poisson(), data =
    breslow.dat)

Deviance Residuals:
   Min      1Q  Median      3Q     Max
-6.057  -2.043  -0.940   0.793  11.006

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  1.948826   0.135619   14.37  < 2e-16 ***
Base         0.022652   0.000509   44.48  < 2e-16 ***
Age          0.022740   0.004024    5.65  1.6e-08 ***
Trtprogabide -0.152701   0.047805   -3.19   0.0014 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 2122.73  on 58  degrees of freedom
Residual deviance:  559.44  on 55  degrees of freedom
AIC: 850.7

Number of Fisher Scoring iterations: 5
```

The output provides the deviances, regression parameters, and standard errors, and tests that these parameters are 0. Note that each of the predictor variables is significant at the $p < 0.05$ level.

# Interpreting the Model Parameters

The model coefficients are obtained using the `coef()` function or by examining the `Coefficients` table in the `summary()` function output:

```
> coef(fit)
 (Intercept)         Base          Age Trtprogabide
      1.9488       0.0227       0.0227      -0.1527
```

In a Poisson regression, the dependent variable being modeled is the log of the conditional mean $\log_e(\lambda)$. The regression parameter 0.0227 for Age indicates that a one-year increase in age is associated with a 0.03 increase in the log mean number of seizures, holding baseline seizures and treatment condition constant. The intercept is the log mean number of seizures when each of the predictors equals 0. Because you can't have a zero age and none of the participants had a zero number of baseline seizures, the intercept isn't meaningful in this case.

It's usually much easier to interpret the regression coefficients in the original scale of the dependent variable (number of seizures, rather than log number of seizures). To accomplish this, exponentiate the coefficients:

```
> exp(coef(fit))
 (Intercept)         Base          Age Trtprogabide
       7.020        1.023        1.023        0.858
```

# Interpreting the Model Parameters

- ✓ Now you see that a one-year increase in age multiplies the expected number of seizures by 1.023, holding the other variables constant. This means that increased age is associated with higher numbers of seizures.
- ✓ More important, a one-unit change in *Trt* (that is, moving from placebo to progabide) multiplies the expected number of seizures by 0.86. You'd expect a 20% decrease in the number of seizures for the drug group compared with the placebo group, holding the baseline number of seizures and age constant.
- ✓ It's important to remember that, like the exponentiated parameters in Logistic regression, the exponentiated parameters in the Poisson model have a multiplicative rather than an additive effect on the response variable.
- ✓ Also, as with Logistic regression, you must evaluate your model for overdispersion.

# Overdispersion

There are several reasons why overdispersion may occur (Coxe et al., 2009):

- The omission of an important predictor variable can lead to overdispersion.
- Overdispersion can also be caused by a phenomenon known as **state dependence**. Within observations, each event in a count is assumed to be independent. For the seizure data, this would imply that for any patient, the probability of a seizure is independent of each other seizure. But this assumption is often untenable. For a given individual, the probability of having a first seizure is unlikely to be the same as the probability of having a 40th seizure, given that they've already had 39.
- In longitudinal studies, overdispersion can be caused by the clustering inherent in repeated measures data. We won't discuss longitudinal Poisson models here.

# Overdispersion

If overdispersion is present and you don't account for it in your model, you'll get standard errors and confidence intervals that are too small, and significance tests that are too liberal (that is, you'll find effects that aren't really there).

As with logistic regression, overdispersion is suggested if the ratio of the residual deviance to the residual degrees of freedom is much larger than 1. For the seizure data, the ratio is

```
> deviance(fit)/df.residual(fit)
[1] 10.17
```

which is clearly much larger than 1.

The qcc package provides a test for overdispersion in the Poisson case. (Be sure to download and install this package before first use.) You can test for overdispersion in the seizure data using the following code:

```
> library(qcc)
> qcc.overdispersion.test(breslow.dat$sumY, type="poisson")
```

```
Overdispersion test Obs.Var/Theor.Var Statistic p-value
       poisson data              62.9      3646       0
```

Not surprisingly, the significance test has a p-value less than 0.05, strongly suggesting the presence of overdispersion.

You can still fit a model to your data using the `glm()` function, by replacing `family="poisson"` with `family="quasipoisson"`. Doing so is analogous to the approach to logistic regression when overdispersion is present:

# Overdispersion

Notice that the parameter estimates in the *quasi-Poisson* approach are identical to those produced by the Poisson approach. The standard errors are much larger, though. In this case, the larger standard errors have led to p-values for *Trt* (and *Age*) that are greater than 0.05. When you take overdispersion into account, there's insufficient evidence to declare that the drug regimen reduces seizure counts more than receiving a placebo, after controlling for baseline seizure rate and age.

```
> fit.od <- glm(sumY ~ Base + Age + Trt, data=breslow.dat,
                family=quasipoisson())
> summary(fit.od)

Call:
glm(formula = sumY ~ Base + Age + Trt, family = quasipoisson(),
    data = breslow.dat)

Deviance Residuals:
   Min      1Q  Median      3Q     Max
-6.057  -2.043  -0.940   0.793  11.006

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)   1.94883    0.46509    4.19  0.00010 ***
Base          0.02265    0.00175   12.97  < 2e-16 ***
Age           0.02274    0.01380    1.65  0.10509
Trtprogabide -0.15270    0.16394   -0.93  0.35570
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for quasipoisson family taken to be 11.8)

    Null deviance: 2122.73  on 58  degrees of freedom
Residual deviance:  559.44  on 55  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 5
```

# Extensions

*R* provides several useful extensions to the basic Poisson regression model, including models that allow varying time periods, models that correct for too many zeros, and robust models that are useful when data includes outliers and influential observations. I'll describe each separately.

**POISSON REGRESSION WITH VARYING TIME PERIODS**

Our discussion of Poisson regression has been limited to response variables that measure a count over a fixed length of time (for example, number of seizures in an eight-week period, number of traffic accidents in the past year, or number of pro-social behaviors in a day). The length of time is constant across observations. But you can fit Poisson regression models that allow the time period to vary for each observation. In this case, the outcome variable is a rate.

To analyze rates, you must include a variable (for example, time) that records the length of time over which the count occurs for each observation. You then change the model from

$$\log_e(\lambda) = \beta_0 + \sum_{j=1}^{p} \beta_j X_j$$

to

$$\log_e\left(\frac{\lambda}{time}\right) = \beta_0 + \sum_{j=1}^{p} \beta_j X_j$$

or equivalently

$$\log_e(\lambda) = \log_e(time) + \beta_0 + \sum_{j=1}^{p} \beta_j X_j$$

# Extensions

To fit this new model, you use the `offset` option in the `glm()` function. For example, assume that the length of time that patients participated post-randomization in the Breslow study varied from 14 days to 60 days. You could use the rate of seizures as the dependent variable (assuming you had recorded time for each patient in days) and fit the model

```
fit <- glm(sumY ~ Base + Age + Trt, data=breslow.dat,
           offset= log(time), family=poisson)
```

where sumY is the number of seizures that occurred post-randomization for a patient during the time the patient was studied. In this case, you're assuming that rate doesn't vary over time (for example, 2 seizures in 4 days is equivalent to 10 seizures in 20 days).

# References


- **R in Action, R. Kabacoff, 2nd edition, Manning, ISBN 978-1-617-29138-8, Chapter 13.**