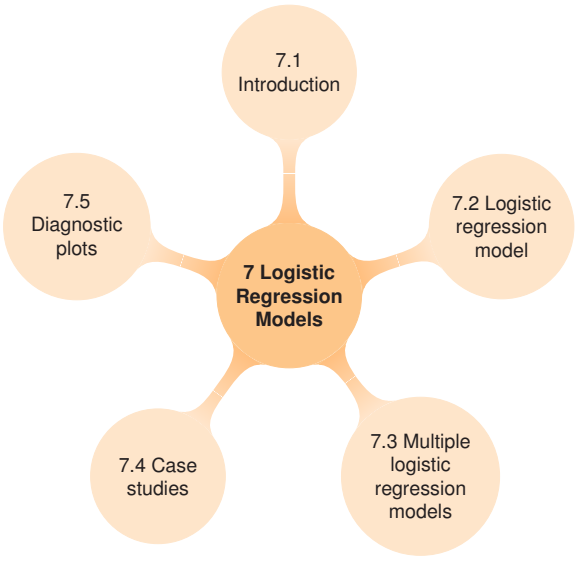


7

Logistic Regression Models

{ch:logistic}

This chapter introduces the modeling framework for categorical data in the simple situation where we have a categorical response variable, often binary, and one or more explanatory variables. A fitted model provides both statistical inference and prediction, accompanied by measures of uncertainty. Data visualization methods for discrete response data must often rely on smoothing techniques, including both direct, non-parametric smoothing and the implicit smoothing that results from a fitted parametric model. Diagnostic plots help us to detect influential observations which may distort our results.

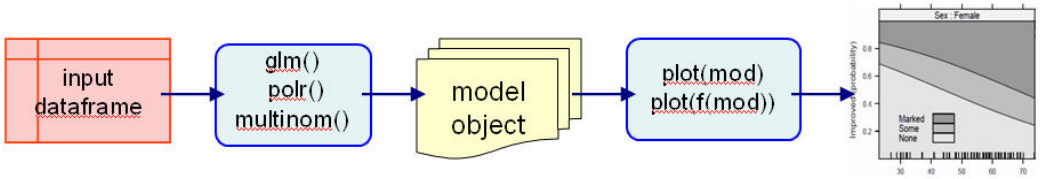
7.1 Introduction

{sec:logist-intro}

> All models are wrong, but some are useful
>
> George E. P. Box, (Box and Draper, 1987, p. 424)

Chapters 4–6 have been concerned primarily with simple, exploratory methods for studying the relations among categorical variables and with testing hypotheses about their associations through non-parametric tests and with overall goodness-of-fit statistics.

This chapter begins our study of model-based methods for the analysis of discrete data. These models differ from those we have examined earlier primarily in that they consider *explicitly* an assumed probability distribution for the observations, and make clear distinctions between the systematic component, which is explained by the model, and the random component, which is not. More importantly, the model-based approach allows a compact summary of categorical data in terms of a (hopefully) small number of parameters accompanied by measures of uncertainty (standard errors), and the ability to estimate predicted values over the range of explanatory variables.



{fig:goverview} **Figure 7.1:** Overview of fitting and graphing for model-based methods in R.

This model-fitting approach has several advantages: (a) Inferences for the model parameters include both hypothesis tests and confidence intervals. (b) The former help us to assess which explanatory variables affect the outcome; the size of the estimated parameters and the widths of their confidence intervals help us to assess the strength and importance of these effects. (c) There are a variety of methods for model selection, designed to help determine a favorable trade-off between goodness-of-fit and parsimony. (d) Finally, the predicted values obtained from the model effectively smooth the discrete responses, allow predictions for unobserved values of the explanatory variables, and provide important means to interpret the fitted relationship graphically.

Figure 7.1 provides a visual overview of the steps for fitting and graphing with model-based methods in R. (a) A modeling function such as `glm()` is applied to an input data frame. The result is a ***model object*** containing all the information from the fitting process. (b) As is standard in R, `print()` and `summary()` methods give, respectively, basic and detailed printed output. (c) Many modeling functions have `plot()` methods that produce different types of summary and diagnostic plots. (d) For visualizing the fitted model, most model methods provide a `predict()` method that can be used to plot the fitted values from the model over the ranges of the predictors. Such plots can be customized by the addition of points (showing the observations), lines, confidence bands, and so forth.

In this chapter we consider models for a ***binary response***, such as "success" or "failure", or the number of "successes" in a fixed number of "trials", where we might reasonably assume a binomial distribution for the random component. As we will see in Chapter 8, these methods extend readily to a ***polytomous response*** with more than two outcome categories, such as improvement in therapy, with categories "none," "some" and "marked.".

These models can be seen as simple extensions of familiar ANOVA and regression models for quantitative data. They are also important special cases of a more general approach, the ***generalized linear model*** that subsumes a wide variety of families of techniques within a single, unified framework. However, rather than starting at the top with the fully general version, this chapter details the important special cases of models for discrete outcomes, beginning with binary responses.

This chapter proceeds as follows: in Section 7.2 we introduce the simple logistic regression model for a binary response and a single quantitative predictor. This model extends directly to models for grouped, binomial data (Section 7.2.4) and to models with any number of regressors (Section 7.3), which can be quantitative, discrete factors and more general forms.

For interpreting and understanding the results of a fitted model, we emphasize plotting predicted probabilities and predicted log odds in various ways, for which effect plots (Section 7.3.3) are particularly useful for complex models.

Section 7.4 presents several case studies to highlight issues of data analysis, model building and visualization in the context of building and interpreting multiple logistic regression models. These focus on the combination of exploratory plots to see the data, modeling steps and graphs to interpret a given model. Individual observations sometimes exert great influence on a fitted model. Some measures of influence and diagnostic plots are illustrated in Section 7.5.

7.2 The logistic regression model

{sec:logist-model}

The logistic regression model describes the relationship between a discrete outcome variable, the "response", and a set of explanatory variables. The response variable is often ***dichotomous***, although extensions to the model permit multi-category, ***polytomous*** outcomes, discussed in Chapter 8. The explanatory variables may be continuous or (with factor variables) discrete.

For a binary response, Y, and a continuous explanatory variable, X, we may be interested in modeling the probability of a successful outcome, which we denote $\pi(x) \equiv \Pr(Y = 1 \,|\, X = x)$. That is, at a given value $X = x$, you can imagine that there is a binomial distribution of the responses, $\text{Bin}(\pi(x), n_x)$.

The simplest naive model, called the ***linear probability model***, supposes that this probability, $\pi(x)$ varies linearly with the value of x,

$$E(Y \,|\, x) = \pi(x) = \alpha + \beta x \ , \tag{7.1}$$

{eq:logit0}

where the notation $E(Y \,|\, x)$ indicates that the probability $\pi(x)$ represents the population conditional average of the 1s and 0s for all observations with a fixed value of x. For binary observations, this is simply the proportion of 1s.

Figure 7.2 illustrates the basic setup for modeling a binary outcome using the `Arthritis` data, and described more fully in Example 7.1–Example 7.3: The "Better" response represents a positive effect of some Arthritis medicament, given age. The 0/1 observations are shown as (jittered) points. The predicted values under the linear probability model (Eqn. (7.1)) are shown as the red lines in both panels. As you can see, this model cannot be right, because it predicts a probability less than 0 for small values of Age, and would also predict probabilities greater than 1 for larger values of Age.

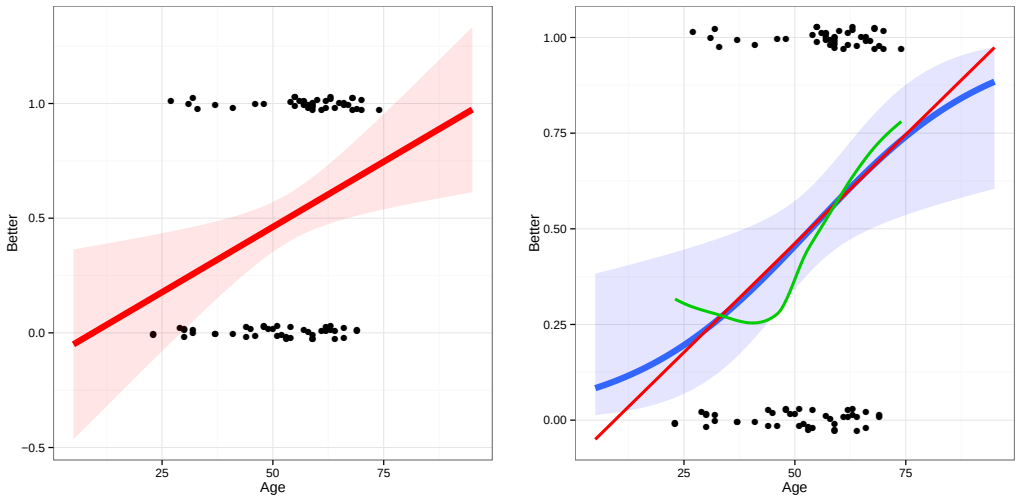


Figure 7.2: Arthritis treatment data, for the relationship of the binary response "Better" to Age, shown as jittered points. The left panel shows the predicted values and 95% confidence envelope under the linear probability model. The right panel shows the fitted logistic regression, together with the simple linear regression (red) and a non-parametric (loess) smoothed curve (green).

{fig:arthritis-age}

The linear probability model is also wrong because it assumes that the distribution of residuals, $Y_i - \hat{\pi}(x_i)$ is normal, with mean 0 and constant variance. However, because Y is dichotomous, the residuals are also dichotomous, and have variance $\pi(x_i)(1 - \pi(x_i))$, which is maximal for $\pi = 0.5$ and decreases as π goes toward 0 or 1.

One way around the difficulty of needing to constrain the predicted values to the interval [0, 1] is to re-specify the model so that a *transformation* of π has a linear relation to x, and that transformation keeps $\hat{\pi}$ between 0 and 1 for all x. This idea of modeling a transformation of the response that has desired statistical properties is one of the fundamental ones that led to the development of ***generalized linear model***s, which we treat more fully later in Chapter 11.

A particularly convenient choice of the transformation gives the ***linear logistic regression model*** (or ***linear logit model***[1]) which posits a linear relation between the ***log odds*** (or ***logit***) of this probability and x,

{eq:logit1}
$$\text{logit}[\pi(x)] \equiv \log\left(\frac{\pi(x)}{1-\pi(x)}\right) = \alpha + \beta x \ . \tag{7.2}$$

When $\beta > 0$, $\pi(x)$ and the log odds increase as X increases; when $\beta < 0$ they decrease with X.

This model can also be expressed as a model for the probabilities $\pi(x)$ in terms of the *inverse* of the logit transformation used in Eqn. (7.2),

{eq:logit1a}
$$\pi(x) = \text{logit}^{-1}[\pi(x)] = \frac{1}{1+\exp[-(\alpha+\beta x)]} \tag{7.3}$$

This transformation uses the cumulative distribution function of the logistic distribution, $\Lambda(p) = \frac{1}{1+exp(-p)}$, giving rise to the term *logistic regression*.[2]

From Eqn. (7.2) we see that the odds of a success response can be expressed as

{eq:logit2}
$$\text{odds}(Y=1) \equiv \frac{\pi(x)}{1-\pi(x)} = \exp(\alpha+\beta x) = e^{\alpha}(e^{\beta})^{x} \ , \tag{7.4}$$

which is a multiplicative model for the odds. So, under the logistic model,

- β is the change in the log odds associated with a unit increase in x. The odds are multiplied by e^{β} for each unit increase in x.
- α is log odds at $x = 0$; e^{α} is the odds of a favorable response at this x-value (which may not have a reasonable interpretation if $X = 0$ is far from the range of the data).

It is easy to explore the relationships among probabilities, odds and log odds using R as we show below, using the function `fractions()` in MASS (Ripley, 2015a) to print the odds corresponding to probability `p` as a fraction.

```
> library(MASS)
> p <- c(.05, .10, .25, .50, .75, .90, .95)
> odds <- p / (1 - p)
> data.frame(p,
+            odds = as.character(fractions(odds)),
+            logit = log(odds))

     p odds   logit
1 0.05 1/19 -2.9444
2 0.10  1/9 -2.1972
3 0.25  1/3 -1.0986
4 0.50    1  0.0000
5 0.75    3  1.0986
6 0.90    9  2.1972
7 0.95   19  2.9444
```

[1] Some writers use the term *logit model* to refer to those using only categorical predictors; we use the terms logistic regression and logit regression interchangeably.

[2] Any other cumulative probability transformation serves the purpose of constraining the probabilities to the interval [0, 1]. The cumulative normal transformation $\pi(x) = \Phi(\alpha + \beta x)$ gives the ***linear probit regression*** model. We don't treat probit models here because: (a) The logistic and probit models give results so similar that it is hard to distinguish them in practice; (b) The logistic model is simpler to interpret as a linear model for the log odds or a multiplicative model for the odds.

Thus, a probability of $\pi = 0.25$ represents an odds of 1 to 3, or 1/3, while a probability of $\pi = 0.75$ represents an odds of 3 to 1, or 3. The logits are symmetric around 0, so $\text{logit}(.25) = -\text{logit}(.75)$.

Another simple way to interpret the parameter β in the logistic regression model is to consider the relationship between the probability $\pi(x)$ and x. From Eqn. (7.3) it can be shown that the fitted curve (the blue line in Figure 7.2) has slope equal to $\beta\pi(1-\pi)$. This has a maximum value of $\beta/4$ when $\pi = \frac{1}{2}$, so taking $\beta/4$ gives a quick estimate of the maximum effect of x on the probability scale.

In Figure 7.2 and other plots later in this chapter we try to show the binary responses (as jittered points or a rug plot) to help you appreciate how the fitted logistic curve arises from their distribution across the range a predictor. For didactic purposes this can be seen more readily by plotting the conditional distributions of $f(x \mid y), y \in \{0, 1\}$ as a histogram, boxplot or density plot. The function `logi.hist.plot()` in the popbio (Stubben *et al.*, 2012) package is a nice implementation of this idea (de la Cruz Rot, 2005). The call below produces Figure 7.3, and it is easy to see how increasing age produces a greater probability of a Better response.

```
> with(Arthritis,
+      logi.hist.plot(Age, Improved > "None", type = "hist", counts = TRUE,
+                     ylabel = "Probability (Better)", xlab = "Age",
+                     col.cur = "blue", col.hist = "lightblue", col.box = "lightblue")
+   )
```

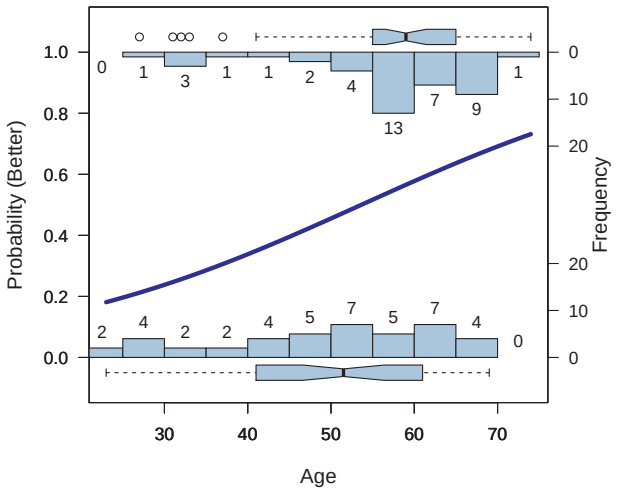


Figure 7.3: Plot of the Arthritis treatment data, showing the conditional distributions of the 0/1 observations of the Better response by histograms and boxplots. {fig:arth-logi-hist}

7.2.1 Fitting a logistic regression model

{sec:logist-fitting}

Logistic regression models are the special case of generalized linear models fit in R using `glm()` for a binary response using `family=binomial`. We first illustrate how simple models can be fit and interpreted.

{ex:arthrit6}

EXAMPLE 7.1: Arthritis treatment

In Chapter 4 we examined the data on treatment for rheumatoid arthritis in relation to two categorical predictors, sex of patient and treatment. In addition, the `Arthritis` data gives the age

of each patient in this study, and we focus here on the relationship between `Age` and the outcome, `Improved`. This response variable has three categories (none, some, or marked improvement), but for now we consider whether the patient showed any improvement at all, defining the event `Better` to be some or marked improvement.

```
> data("Arthritis", package = "vcd")
> Arthritis$Better <- as.numeric(Arthritis$Improved > "None")
```

The logistic regression model is fit using `glm()` as shown below, specifying `family=binomial` for a binary response.

```
> arth.logistic <- glm(Better ~ Age, data = Arthritis, family = binomial)
```

As usual for R modeling functions, the `print()` method for "glm" objects gives brief printed output, while the `summary()` method is more verbose, and includes standard errors and hypothesis tests for the model coefficients. To save some space, it is convenient to use the generic function `coeftest()` from the lmtest (Hothorn *et al.*, 2014) package. Then, we can use this instead of the more detailed `summary()`:

```
> library(lmtest)
> coeftest(arth.logistic)


z test of coefficients:

            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -2.6421     1.0732   -2.46    0.014 *
Age           0.0492     0.0194    2.54    0.011 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

In the output above, the parameter estimates are $\alpha = -2.642$, and $\beta = 0.0492$. So, the estimated odds of a better response are multiplied by $e^{\beta} = \exp(0.0492) = 1.05$ for each one year increase in age. Equivalently, you can think of this as a 5% increase per year (using $100(e^{\beta} - 1)$ to convert). Over 10 years, the odds are multiplied by $\exp(10 \times 0.0492) = 1.64$, a 64% increase, a substantial effect in the range for these data. You can do these calculations in R using the `coef()` method for the "glm" object.

```
> exp(coef(arth.logistic))

(Intercept)         Age
   0.071214    1.050482

> exp(10 * coef(arth.logistic)["Age"])

   Age
1.6364
```

For comparison with the logistic model, we could fit the linear probability model Eqn. (7.1) using either `lm()` or `glm()` with the default `family=gaussian` argument.

```
> arth.lm <- glm(Better ~ Age, data = Arthritis)
> coef(arth.lm)

(Intercept)         Age
  -0.107170    0.011379
```

The coefficient for age can be interpreted to indicate that the probability of a better response

increases by 0.011 for each one year increase in age. You can compare this with the $\beta/4$ rule of thumb, that gives 0.0492/4 = 0.0123. Even though the linear probability model is inappropriate theoretically, you can see in Figure 7.2 (the black line) that it gives similar predicted probabilities to those of the logistic model between age 25–75, where most of the data points are located.

△

7.2.2 Model tests for simple logistic regression

{sec:logist-tests}

There are two main types of hypothesis tests one might want to perform for a logistic regression model. We postpone general discussion of this topic until Section 7.3, but introduce the main ideas here using the analysis of the `Arthritis` data.

- The most basic test answers the question "How much better is the fitted model, $\text{logit}(\pi) = \alpha + \beta x$ than the null model $\text{logit}(\pi) = \alpha$ that includes only the regression intercept?" One answer to this question is given by the (Wald) test of the coefficient for age testing the hypothesis $H_0 : \beta = 0$ that appeared in the output from `summary(arth.logistic)` shown above. The more direct test compares the deviance[3] of the fitted model to the deviance of the null model, and can be obtained using the `anova()` function:

```
> anova(arth.logistic, test = "Chisq")

Analysis of Deviance Table

Model: binomial, link: logit

Response: Better

Terms added sequentially (first to last)


     Df Deviance Resid. Df Resid. Dev Pr(>Chi)
NULL                    83        116
Age   1     7.29        82        109    0.007 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- A second question is "How bad is this model, compared to a model (the ***saturated model***) that fits the data perfectly?" This is a test of the size of the residual deviance, that is given by the function `LRstats()` in vcdExtra (Friendly, 2015).

```
> library(vcdExtra)
> LRstats(arth.logistic)

Likelihood summary table:
             AIC BIC LR Chisq Df Pr(>Chisq)
arth.logistic 113 118      109 82      0.024 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The summary of these tests is that linear logistic model Eqn. (7.2) fits significantly better than the null model, but that model also shows significant lack of fit.

[3]The deviance is basically defined as -2 times the log-likelihood ratio of some reduced model to the full model. Two nested models can thus be compared by computing the difference of the corresponding deviances. If the larger model has k more parameters than the reduced one, this difference follows a chi-squared distribution with k degrees of freedom.

7.2.3 Plotting a binary response

{sec:logist-plotting}

It is often difficult to understand how a binary response can give rise to a smooth, continuous relation between the predicted response, usually the probability of an event, and a continuous explanatory variable. Beyond this, plots of the data together with fitted models help you to interpret what these models imply.

We illustrate two approaches below using the `Arthritis` data shown in Figure 7.2, first using R base graphics, and then with the ggplot2 (Wickham and Chang, 2015) package that makes such graphs somewhat easier to do.

That plot, which was designed for didactic purposes, has the following features:

- It shows the *data*, that is, the 0/1 observations of the `Better` response in relation to age. To do this effectively and avoid over-plotting, the binary responses are jittered.
- It plots the predicted (fitted) logistic regression relationship on the scale of probability, together with a 95% confidence band.
- It also plots the predicted probabilities from the linear probability model.
- A smoothed, non-parametric regression curve for the binary observations is also added to the plot to give some indication of possible non-linearity in the relationship of Better to age.

{ex:arthrit7}

EXAMPLE 7.2: Arthritis treatment – Plotting logistic regression with base graphics

Here we explain how plots similar to Figure 7.2 can be constructed using R base graphics. We describe the steps needed to calculate predicted values and confidence bands and how to add these to a basic plot. These ideas are the basis for the higher-level and more convenient plotting methods illustrated later in this chapter (Section 7.3.2) The steps detailed below give the plot shown in Figure 7.4.

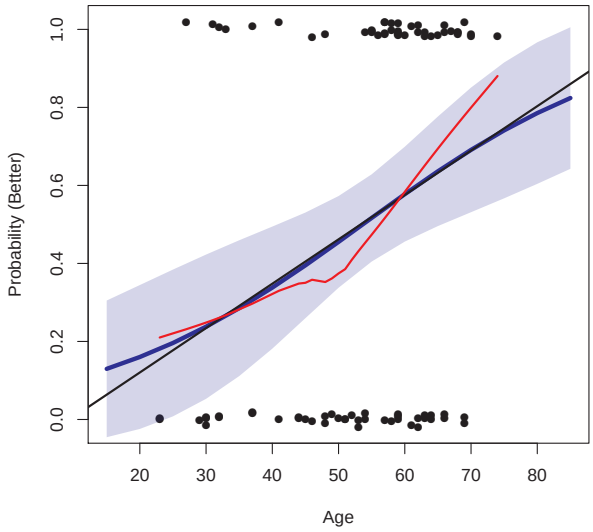


Figure 7.4: A version of plot of the Arthritis treatment data (Figure 7.2) produced with R base graphics, showing logistic, linear regression and lowess fits.

{fig:arthritis-age2}

First, we set up the basic plot of the jittered values of `Better` vs. `Age`, setting `xlim` to a larger range than that in the data, only to emphasize where the logistic and linear probability models diverge.

```
> plot(jitter(Better, .1) ~ Age, data = Arthritis,
+      xlim = c(15, 85), pch = 16,
+      ylab="Probability (Better)")
```

The fitted logistic curve can be obtained using the `predict()` method for the "glm" object `arth.logistic`. For this example, we wanted to get fitted values for the range of Age from 15–85, which is specified in the `newdata` argument.[4] The argument `type="response"` gives fitted values of the probabilities. (The default, `type="link"` would give predicted logits.) Standard errors of the fitted values are not calculated by default, so we set `se.fit=TRUE`.

```
> xvalues <- seq(15, 85, 5)
> pred.logistic <- predict(arth.logistic,
+                          newdata = data.frame(Age = xvalues),
+                          type = "response", se.fit = TRUE)
```

When `se.fit=TRUE`, the `predict()` function returns its result in a list, with components `fit` for the fitted values and `se.fit` for the standard errors. From these, we can calculate 95% pointwise prediction intervals using the standard normal approximation.

```
> upper <- pred.logistic$fit + 1.96 * pred.logistic$se.fit
> lower <- pred.logistic$fit - 1.96 * pred.logistic$se.fit
```

We can then plot the confidence band using `polygon()` and the fitted logistic curve using `lines`. A graphics trick is used here to use a transparent color for the confidence band using `rgb(r, g, b, alpha)`, where `alpha` is the transparency value.

```
> polygon(c(xvalues, rev(xvalues)),
+         c(upper, rev(lower)),
+         col = rgb(0, 0, 1, .2), border = NA)
> lines(xvalues, pred.logistic$fit, lwd=4 , col="blue")
```

This method, using `predict()` for calculations and `polygon()` and `lines()` for plotting can be used to display the predicted relationships and confidence bands under other models. Here, we simply used `abline()` to plot the fitted line for the linear probability model `arth.lm` and `lowess()` to calculate a smoothed, non-parametric curve.

```
> abline(arth.lm, lwd = 2)
> lines(lowess(Arthritis$Age, Arthritis$Better, f = .9), col = "red", lwd = 2)
```

△

{ex:arthrit8}

EXAMPLE 7.3: Arthritis treatment – Plotting logistic regression with ggplot2

Model-based plots such as Figure 7.2 are relatively more straight-forward to produce using ggplot2 . The basic steps here are to:

- set up the plot frame with `ggplot()` using Age and Better as (x, y) coordinates;
- use `geom_point()` to plot the observations, whose positions are jittered with `position_jitter()`;
- use `stat_smooth()` with `method = "glm"` and `family = binomial` to plot the predicted probability curve and confidence band. By default, `stat_smooth()` calculates and plots 95% confidence bands on the response (probability) scale.

[4] Omitting the `newdata` argument would give predicted values using the linear predictors in the data used for the fitted model. Some care needs to be taken if the predictor(s) contain missing values.

```
> library(ggplot2)
> # basic logistic regression plot
> gg <- ggplot(Arthritis, aes(x = Age, y = Better)) +
+   xlim(5, 95) +
+   geom_point(position = position_jitter(height = 0.02, width = 0)) +
+   stat_smooth(method = "glm", family = binomial,
+               alpha = 0.1, fill = "blue", size = 2.5, fullrange = TRUE)
```

Finally, we can add other smoothers to the plot, literally by using + to add these to the "ggplot" object.

```
> # add linear model and loess smoothers
> gg <- gg + stat_smooth(method = "lm", se = FALSE,
+                        size = 1.2, color = "black", fullrange = TRUE)
> gg <- gg + stat_smooth(method = "loess", se = FALSE,
+                        span = 0.95, colour = "red", size = 1.2)
> gg  # show the plot
```

△

7.2.4 Grouped binomial data

{sec:logist-grouped}

A related case occurs with grouped data, where rather than binary observations, $y_i \in \{0, 1\}$ in case form, the data is given in what is called ***events/trials form*** that records the number of successes, y_i that occurred in n_i trials associated with each setting of the explanatory variable(s) x_i.[5] Case form, with binary observations is the special case where $n_i = 1$.

Data in events/trials form often arises from contingency table data with a binary response. For example in the *UCBAdmissions* data, the response variable `Admit` with levels `"Admitted"`, `"Rejected"` could be treated in this way using the number of applicants as the number of trials.

As before, we can consider y_i/n_i to estimate the probability of success, π_i and the distribution of Y to be binomial, $\text{Bin}(\pi_i, n_i)$ at each x_i.

In practical applications, there are two main differences between the cases of ungrouped, case form data and grouped, event/trials form.

- In fitting models using `glm()`, the model formula, `response ~ terms`, can be given using a `response` consisting of a two-column matrix, whose columns contain the numbers of successes y_i and failures $n_i - y_i$. Alternatively, the `response` can be given as the proportion of successes, y_i/n_i, but then it is necessary to specify the number of trials as a `weight`.
- In plotting the fitted model on the scale of probability, you usually have to explicitly plot the fraction of successes, y_i/n_i.

{ex:nasa-temp}

EXAMPLE 7.4: Space shuttle disaster

In Example 1.2 and Example 1.10 we described the background behind the post-mortem examination of the evidence relating to the disastrous launch of the space shuttle *Challenger* on January 28, 1986. Here we consider a simple, but proper analysis of the data available at the time of launch. We also use this example to illustrate some details of the fitting and plotting of grouped binomial data. As well, we describe some of the possibilities for dealing with missing data.

The data set *SpaceShuttle* in vcd (Meyer *et al.*, 2015) contains data on the failures of the O-rings in 24 NASA launches preceding the launch of *Challenger*, as given by Dalal *et al.* (1989) and Tufte (1997), also analysed by Lavine (1991).

Each launch used two booster rockets with a total of six O-rings, and the data set records as

[5] Alternatively, the data may record the number of successes, y_i, and number of failures, $n_i - y_i$.

`nFailures` the number of these that were considered damaged after the rockets were recovered at sea. In one launch (flight # 4), the rocket was lost at sea, so the relevant response variables are missing.

In this example, we focus on the variable `nFailures` as a binomial with $n_i = 6$ trials. The missing data for flight 4 can be handled in several ways in the call to `glm()`

```
> data("SpaceShuttle", package = "vcd")
> shuttle.mod <- glm(cbind(nFailures, 6 - nFailures) ~ Temperature,
+           data = SpaceShuttle, na.action = na.exclude,
+           family = binomial)
```

Alternatively, we can add an explicit `trials` variable, represent the response as the proportion `nFailures/trials`, and use `weight = trials` to indicate the total number of observations.

```
> SpaceShuttle$trials <- 6
> shuttle.modw <- glm(nFailures / trials ~ Temperature, weight = trials,
+           data = SpaceShuttle, na.action = na.exclude,
+           family = binomial)
```

These two approaches give identical results for all practical purposes:

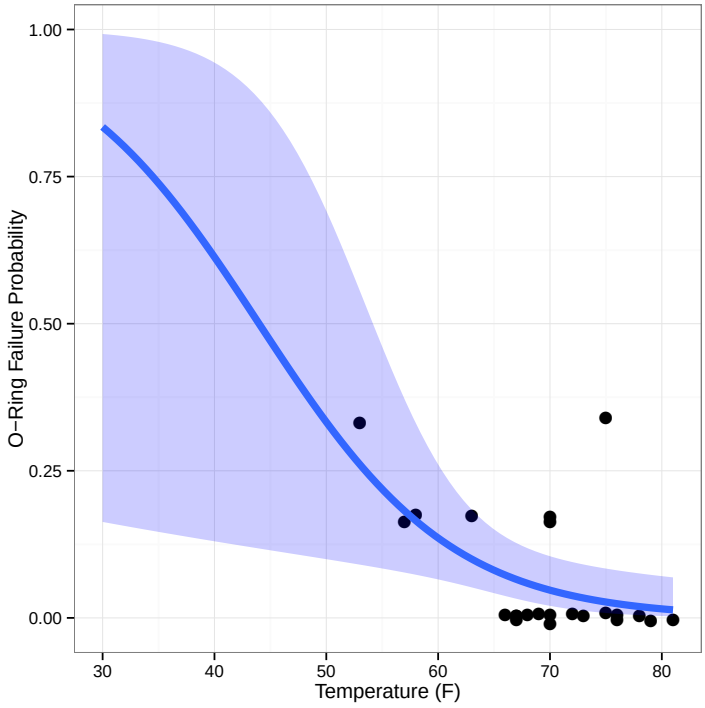
```
> all.equal(coef(shuttle.mod), coef(shuttle.modw))

[1] TRUE
```

As before, we can test whether temperature significantly improves prediction of failure probability using `anova()`:

```
> # testing, vs. null model
> anova(shuttle.mod, test = "Chisq")

Analysis of Deviance Table

Model: binomial, link: logit

Response: cbind(nFailures, 6 - nFailures)

Terms added sequentially (first to last)


            Df Deviance Resid. Df Resid. Dev Pr(>Chi)
NULL                           22       24.2
Temperature  1     6.14        21       18.1    0.013 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The code below gives a ggplot2 version in Figure 7.5 of the plot we showed earlier in Example 1.2 (Figure 1.2). The relevant details here are:

- We specify `y = nFailures / trials` to calculate the failure probabilities.
- Points are jittered in the call to `geom_point()` to prevent overplotting.
- In the call to `geom_smooth()`, we need to use `weight = trials`, just as in the call to `glm()` above.
- `fullrange = TRUE` makes the fitted regression curve and confidence band extend across the entire plot



{fig:nasa-temp-ggplot}

Figure 7.5: Space shuttle data, with fitted logistic regression model

```
> library(ggplot2)
> ggplot(SpaceShuttle, aes(x = Temperature, y = nFailures / trials)) +
+   xlim(30, 81) +
+   xlab("Temperature (F)") +
+   ylab("O-Ring Failure Probability") +
+   geom_point(position=position_jitter(width = 0, height = 0.01),
+              aes(size = 2)) +
+   theme(legend.position = "none") +
+   geom_smooth(method = "glm", family = binomial, fill = "blue",
+               aes(weight = trials), fullrange = TRUE, alpha = 0.2, size = 2)
```

△

7.3 Multiple logistic regression models

{sec:logist-mult}

As is the case in classical regression, generalizing the simple logistic regression to an arbitrary number of explanatory variables is quite straightforward. We let $\boldsymbol{x}_i = (x_{i1}, x_{i2}, \ldots, x_{ip})$ denote the vector of p explanatory variables for case or cluster i. Then the general logistic regression model can be expressed as

$$\begin{aligned} \text{logit}(\pi_i) \equiv \log \frac{\pi_i}{1-\pi_i} &= \alpha + \boldsymbol{x}_i^{\mathsf{T}} \boldsymbol{\beta} \\ &= \alpha + \beta_1 x_{i1} + \beta_2 x_{i2} + \cdots + \beta_p x_{ip} \ . \end{aligned} \tag{7.5}$$

Equivalently, we can represent this model in terms of probabilities as the logistic transformation of the ***linear predictor***, $\eta_i = \alpha + \boldsymbol{x}_i^\mathsf{T} \boldsymbol{\beta}$,

{eq:logistm1}

$$\begin{aligned} \pi_i = \Lambda(\eta_i) &= \Lambda(\alpha + \boldsymbol{x}_i^\mathsf{T} \boldsymbol{\beta}) \\ &= \frac{1}{1 + \exp(\alpha + \beta_1 x_{i1} + \beta_2 x_{i2} + \cdots + \beta_p x_{ip})} \; . \end{aligned} \tag{7.6}$$

The xs can include any of the following sorts of regressors, as in the general linear model:

- **quantitative** variables (e.g., age, income)
- **polynomial** powers of quantitative variables (e.g., age, age^2, age^3)
- **transformations** of quantitative variables (e.g., log salary)
- factors, represented as **dummy** variables for qualitative predictors (e.g., P_1, P_2, P_3 for four political party affiliations)
- **interaction** terms (e.g., sex $\times$ age, or age $\times$ income)

{ex:arthrit-mult}

EXAMPLE 7.5: Arthritis treatment

We continue with the analysis of the `Arthritis` data, fitting a model containing the main effects of `Age`, `Sex` and `Treatment`, with `Better` as the response. This model has the form

$$\text{logit}(\pi_i) = \alpha + \beta_1 x_{i1} + \beta_2 x_{i2} + \beta_3 x_{i3}$$

where x_1 is `Age` and x_2 and x_3 are the factors representing `Sex` and `Treatment`, respectively. Using the default (0/1) dummy coding that R uses ("treatment" contrasts against the lowest factor level),[6] they are defined as:

$$x_2 = \begin{cases} 0 & \text{if Female} \\ 1 & \text{if Male} \end{cases} \qquad x_3 = \begin{cases} 0 & \text{if Placebo} \\ 1 & \text{if Treatment} \end{cases}$$

In this model,

- α doesn't have a sensible interpretation here, but formally it would be the log odds of improvement for a person at age $x_1 = 0$ in the baseline or reference group with $x_2 = 0$ and $x_3 = 0$—females receiving the placebo. To make the intercept interpretable, we will fit the model centering age near the mean, by using $x_1 - 50$ as the first regressor.
- β_1 is the increment in log odds of improvement for each one-year increase in age.
- β_2 is the increment in log odds for male as compared to female. Therefore, e^{β_2} gives the odds of improvement for males relative to females.
- β_3 is the increment in log odds for being in the treated group. e^{β_3} gives the odds of improvement for the active treatment group relative to placebo.

We fit the model as follows. In `glm()` model formulas, "–" has a special meaning, so we use the identity function, `I(Age-50)` to center age.

```
> arth.logistic2 <- glm(Better ~ I(Age-50) + Sex + Treatment,
+                       data = Arthritis,
+                       family = binomial)
```

[6] For factor variables with the default treatment contrasts, you can change the reference level using `relevel()`. In this example, you could make male the baseline category using `Arthritis$Sex <- relevel(Arthritis$Sex, ref = "Male")`.

The parameters defined here are *incremental effects*. The intercept corresponds to a baseline group (50 year-old females given the placebo); the other parameters are incremental effects for the other groups compared to the baseline group. Thus, when α, β_1, β_2 and β_3 have been estimated, the fitted logits and predicted odds at `Age==50` are:

Sex	Treatment	Logit	Odds Improved
Female	Placebo	α	e^{α}
Female	Treated	$\alpha + \beta_3$	$e^{\alpha+\beta_3}$
Male	Placebo	$\alpha + \beta_2$	$e^{\alpha+\beta_2}$
Male	Treated	$\alpha + \beta_2 + \beta_3$	$e^{\alpha+\beta_2+\beta_3}$

We first focus on the interpretation of the coefficients estimated for this model shown below.

```
> coeftest(arth.logistic2)


z test of coefficients:

                 Estimate Std. Error z value Pr(>|z|)
(Intercept)       -0.5781     0.3674   -1.57    0.116
I(Age - 50)        0.0487     0.0207    2.36    0.018 *
SexMale           -1.4878     0.5948   -2.50    0.012 *
TreatmentTreated   1.7598     0.5365    3.28    0.001 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

To interpret these in terms of odds ratios and also find confidence intervals, just use `exp()` and `confint()`.

```
> exp(cbind(OddsRatio = coef(arth.logistic2),
+           confint(arth.logistic2)))

                 OddsRatio   2.5 %  97.5 %
(Intercept)         0.5609 0.26475  1.1323
I(Age - 50)         1.0500 1.01000  1.0963
SexMale             0.2259 0.06524  0.6891
TreatmentTreated    5.8113 2.11870 17.7266
```

Here,

- $\alpha = -0.578$: At age 50, females given the placebo have an odds of improvement of $\exp(-0.578) = 0.56$.
- $\beta_1 = 0.0487$: Each year of age multiplies the odds of improvement by $\exp(0.0487) = 1.05$, or a 5% increase.
- $\beta_2 = -1.49$: Males are only $\exp(-1.49) = 0.26$ times as likely to show improvement relative to females. (Or, females are $\exp(1.49) = 4.437$ times more likely than males to improve.)
- $\beta_3 = 1.76$: People given the active treatment are $\exp(1.76) = 5.8$ times more likely to show improvement compared to those given the placebo.

As you can see, the interpretation of coefficients in multiple logistic models is straightforward, though a bit cumbersome. This becomes more difficult in larger models, particularly when there are interactions. In these cases, you can understand (and explain) a fitted model more easily through plots of predicted values, either on the scale of response probability or on the logit scale of the linear predictor. We describe these methods in Section 7.3.1–Section 7.3.3 below.

△

7.3.1 Conditional plots

{sec:logist-condplots}

The simplest kind of plots display the data together with a representation of the fitted relationship (predicted values, confidence bands) separately for subsets of the data defined by one or more of the predictors. Such plots can show the predicted values for the response variable on the ordinate against one chosen predictor on the abscissa, and can use multiple curves and multiple panels to represent other predictors.

However, these plots are ***conditional plots***, meaning that the data shown in each panel and used in each fitted curve are limited to the subset of the observations defined by the curve and panel variables. As well, predictors that are not shown in a given plot are effectively ignored (or marginalized), as was the case in Figure 7.2 that showed only the effect of age in the `Arthritis` data.

{ex:arth-cond}

EXAMPLE 7.6: Arthritis treatment – conditional plots

For the `Arthritis` data, a basic conditional plot of `Better` vs. `Age`, showing the observations as jittered points (with `geom_point()`) and the fitted logistic curves (with `stat_smooth()` using `method="glm"`) can be produced with ggplot2 as shown below, giving Figure 7.6.

```
> library(ggplot2)
> gg <- ggplot(Arthritis, aes(Age, Better, color = Treatment)) +
+   xlim(5, 95) +
+   geom_point(position = position_jitter(height = 0.02, width = 0)) +
+   stat_smooth(method = "glm", family = binomial, alpha = 0.2,
+               aes(fill = Treatment), size = 2.5, fullrange = TRUE)
> gg   # show the plot
```

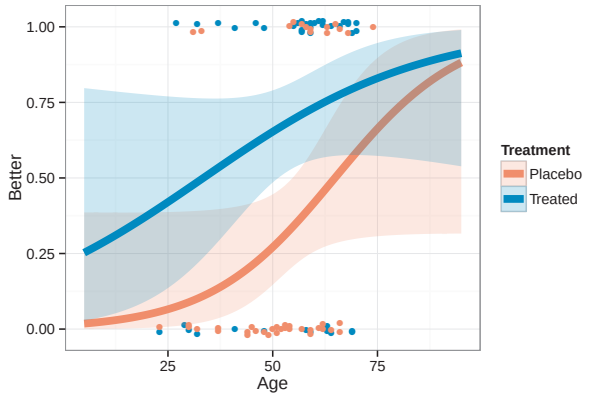


Figure 7.6: Conditional plot of Arthritis data showing separate points and fitted curves stratified by Treatment. A separate fitted curve is shown for the two treatment conditions, ignoring Sex.

{fig:arth-cond1}

In this call to `ggplot()`, specifying `color=Treatment` gives different point and line colors, but also automatically stratifies the fitted curves using the levels of this variable.

With such a plot, it is easy to add further stratifying variables in the data using ***facets*** to produce separate panels (functions `facet_wrap()` or `facet_grid()`, with different options to control the details). The following line further stratifies by `Sex`, producing Figure 7.7.

```
> gg + facet_wrap(~ Sex)
```

However, you can see from this plot how this method breaks down when the sample size is small in some of the groups defined by the stratifying factors. The panel for males shows a paradoxical

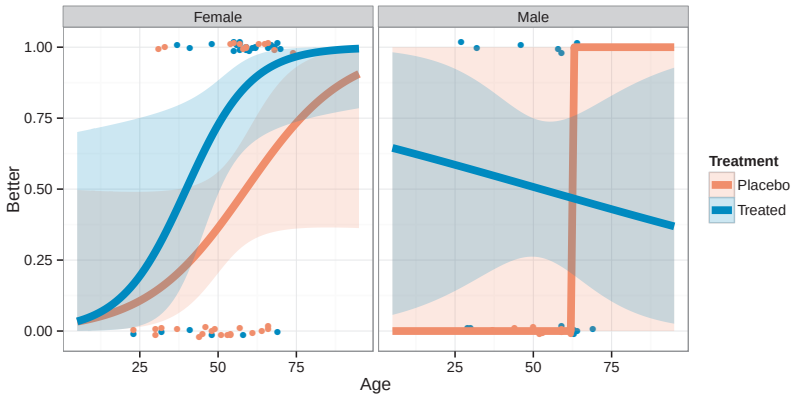


Figure 7.7: Conditional plot of Arthritis data, stratified by Treatment and Sex. The unusual patterns in the panel for Males signals a problem with this data. {fig:arth-cond2}

negative relation with age for the treated group and a step function for the placebo group. The explanation for this is shown in the two-way frequency table of the sex and treatment combinations:

```
> addmargins(xtabs(~Sex + Treatment, data = Arthritis), 2)

        Treatment
Sex      Placebo Treated Sum
  Female      32      27  59
  Male        11      14  25
```

Less than 1/3 of the sample were males, and of these only 11 were in the placebo group. `glm()` cannot estimate the fitted relationship against `Age` here— the slope coefficient is infinite, and the fitted probabilities are all either 0 or 1.[7]

△

7.3.2 Full-model plots

{sec:logist-fullplots}

For a model with two or more explanatory variables, *full-model plots* display the fitted response surface for all predictors together, rather than stratified by conditioning variables. Such plots show the predicted values for the response variable on the ordinate against one chosen predictor on the abscissa, and can use multiple curves and multiple panels to represent other predictors.

The programming steps used to plot a fitted logistic regression with base graphics and ggplot2 in the style of earlier examples (Example 7.2, 7.2 and 7.4) become more tedious with multiple predictors. The vcd package provides the function `binreg_plot()` designed to plot the predicted response surface for a binary outcome directly from a fitted model object. At the time of writing, this function does not yet handle multiple panels or facets, but separate plots for panel variables can be produced using the `subset` argument as illustrated in the next example. {ex:arth-full}

EXAMPLE 7.7: Arthritis treatment – full-model plots

This example shows how to plot the fitted main effects model using `binreg_plot()`. These plots can be shown either on the logit scale (with `type = "link"`) or the probability scale (`type = "response"`, the default).

[7] This is called ***complete separation***, and occurs whenever the responses have no overlap on the predictor variable(s) used in fitting the logistic regression model.

This plot method is designed to use a numeric predictor (`Age` here) as the horizontal axis, and show separate point symbols and curves for the levels of the combinations of factors (if any). A basic plot on the logit scale (not included here) showing both factors (`Sex`, `Treatment`) can be produced using:

```
> library(vcd)
> binreg_plot(arth.logistic2, type = "link")
```

With two or more factors, such plots are often easier to read when the main factor(s) to be compared appear (`Treatment` here) as lines or curves within a plot, and other factors (`Sex`) are shown in separate panels. Figure 7.8 does this in two plots, using the `subset` argument to select the appropriate data and predicted values for males and females. When this is done, it is important to include the same `xlim` and `ylim` arguments so that the scales of all plots are identical.

```
> binreg_plot(arth.logistic2, type = "link", subset = Sex == "Female",
+             main = "Female", xlim=c(25, 75), ylim = c(-3, 3))
> binreg_plot(arth.logistic2, type = "link", subset = Sex == "Male",
+             main = "Male", xlim=c(25, 75), ylim = c(-3, 3))
```

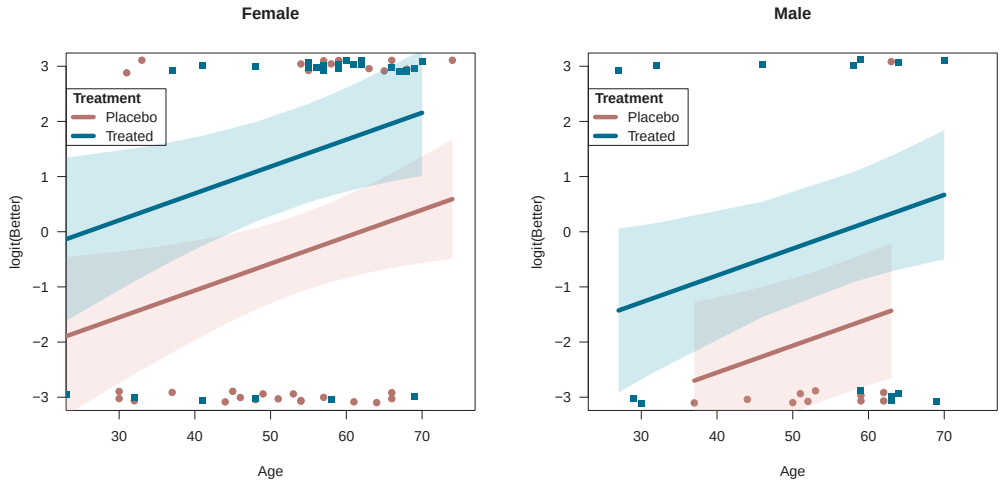


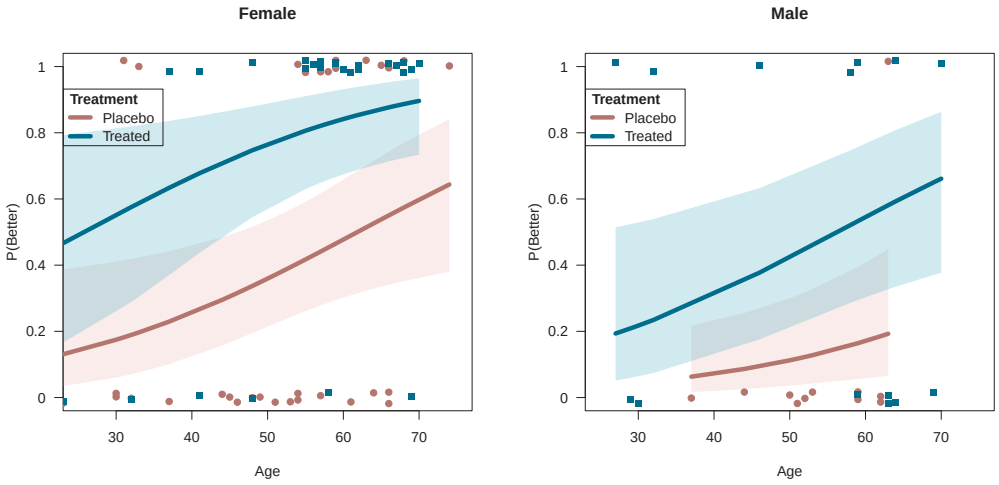
Figure 7.8: Full-model plot of Arthritis data, showing fitted logits by Treatment and Sex. {fig:arth-binreg1}

This plot method has several nice features:

- Plotting on the logit scale shows the additive, linear effects of all predictors (parallel lines for the combinations of `Sex` and `Treatment`).
- It provides a visual representation of the information contained in the table of coefficients.
- The choice to display `Treatment` within each panel makes it easier to judge the size of this effect, compared to the effect of `Sex` which must be judged across the panels.
- It shows the data as points, and the fitted lines and confidence bands are restricted to the range of the data in each. You can easily see the reason for the unusual pattern in the conditional plot for Males shown in Figure 7.7.
- It generalizes directly to any fitted model, because the predicted values are obtained from the model object. For example, you could easily add the interaction term `Age:Sex` and plot the result.

While plots on the logit scale have a simpler form, many people find it easier to think about such relationships in terms of probabilities, as we have done in earlier plots in this chapter. Figure 7.9 shows these plots using the default `type = "response"`.

```
> binreg_plot(arth.logistic2, subset = Sex == "Female",
+             main = "Female", xlim = c(25, 75))
> binreg_plot(arth.logistic2, subset = Sex == "Male",
+             main = "Male", xlim = c(25, 75))
```



{fig:arth-binreg2}

Figure 7.9: Full-model plot of Arthritis data, showing fitted probabilities by Treatment and Sex.

△

7.3.3 Effect plots

{sec:logist-effplots}

For more than two variables, full-model plots of the fitted response surface can be cumbersome, particularly when the model contains interactions or when the main substantive interest is focused on a given main effect or interaction, controlling for all other explanatory variables. The method of ***effect displays*** (tables and graphs), developed by John Fox (1987, 2003) and implemented in the effects (Fox *et al.*, 2015) package, is a useful solution to these problems.

The idea of effect plots is quite simple but very general and handles models of arbitrary complexity:[8] consider a particular subset of predictors (*focal predictors*) we wish to visualize in a given linear model or generalized linear model. The essence is to calculate fitted values (and standard errors) for the model terms involving these variables and all low-order relatives (e.g., main effects that are marginal to an interaction), as these variables are allowed to vary over their range.

All other variables are "controlled" by being fixed at typical values. For example a quantitative covariate could be fixed at its mean or median; a factor could be fixed at equal proportions of its levels or its proportions in the data. The result, when plotted, shows all effects of the focal predictors and their low-order relatives, but with all other variables not included controlled (or "adjusted for").

[8] Less general expression of these ideas include the use of ***adjusted means*** in analysis of covariance, and ***least squares means*** or ***population marginal means*** (Searle *et al.*, 1980) in analysis of variance; for example, see the lsmeans (Lenth and Hervé, 2015) package for classical linear models.

7.3.3.1 The score model matrix

More formally, assume we have fit a model with a linear predictor $\eta_i = \alpha + \boldsymbol{x}_i^\mathsf{T} \boldsymbol{\beta}$ (on the logit scale, for logistic regression). Letting $\beta_0 = \alpha$ and $\boldsymbol{x}_0 = \mathbf{1}$, we can rewrite this in matrix form as $\boldsymbol{\eta} = \boldsymbol{X}\boldsymbol{\beta}$ where $\boldsymbol{X}$ is the model matrix constructed by the modeling function, such as `glm()`. Fitting the model gives the estimated coefficients $\boldsymbol{b}$ and its estimated covariance matrix $\widehat{\boldsymbol{\mathcal{V}}}(\boldsymbol{b})$.

The `Effect()` function constructs an analogous *score model matrix*, $\boldsymbol{X}^*$, where the focal variables have been varied over their range, and all other variables represented as constant, typical values. Using this as input (the `newdata` argument) to the `predict()` function then gives the fitted values $\boldsymbol{\eta}^* = \boldsymbol{X}^* \boldsymbol{b}$. Standard errors used for confidence intervals are calculated by `predict()` (when `se.fit=TRUE`) as the square roots of $\text{diag}\,(\boldsymbol{X}^* \widehat{\boldsymbol{\mathcal{V}}(\boldsymbol{b})} \boldsymbol{X}^{*\mathsf{T}})$. Note that these ideas work not only for `glm()` models, but potentially for any modeling function that has a `predict()` and `vcov()` method.[9]

These results are calculated on the scale of the linear predictor $\boldsymbol{\eta}$ (logits, for logistic regression) when the `type` argument to `predict()` is `type="link"` or on the response scale (probabilities, here) when `type="response"`. The latter makes use of the inverse transformation, Eqn. (7.6).

There are two main calculation functions in the effects package:

- `Effect()` takes a character vector of the names of a subset of focal predictors and constructs the score matrix $\boldsymbol{X}^*$ by varying these over their ranges, while holding all other predictors constant at "typical" values. There are many options that control these calculations. For example, `xlevels` can be used to specify the values of the focal predictors; `typical` or `given.values` respectively can be used to specify either a function (`mean`, `median`) or a list of specific typical values used for the variables that are controlled. The result is an object of class "eff", for which there are `print()`, `summary()` and (most importantly) `plot()` methods. See `help(Effect)` for a complete description.

- `allEffects()` takes a model object, and calculates the effects for each high-order term in the model (including their low-order) relatives. Similar optional arguments control the details of the computation. The result is an object of class "efflist".

In addition, the plotting methods for "eff" and "efflist" objects offer numerous options to control the plot details, only a few of which are used in the examples below. For logistic regression models, they also solve the problem of the trade-off between plots on the logit scale, that have a simple representation in terms of additive effects, and plots on the probability scale that are usually simpler to understand. By default, the fitted model effects are plotted on the logit scale, but the response y axis is labeled with the corresponding probability values.

7.3.3.2 Partial residuals

We noted earlier that for discrete response data, it is usually important to display the *data* in some fashion, along with the fitted relationship. Conditional and full-model plots do this by jittering the binary values at 0 and 1 so you can see where the data exists.

The effects package takes this idea further, by allowing the display of ***partial residuals***. Letting $\boldsymbol{r}$ denote the vector of residuals for a given model (see Section 7.5.1 for details), the partial residuals $\boldsymbol{r}_j$ pertaining to predictor $\boldsymbol{x}_j$ are defined as

$$\boldsymbol{r}_j = \boldsymbol{r} + \widehat{\beta}_j \boldsymbol{x}_j$$

[9] For example, the effects package presently provides methods for models fit by `lm()` (including multivariate linear response models), `glm()`, `gls()`, multinomial (`multinom()` in the nnet (Ripley, 2015b) package) and proportional odds models (`polr()` in MASS), polytomous latent class models (poLCA (Linzer and Lewis., 2014) package), as well as a variety of multi-level and mixed-effects linear models fit with `lmer()` from the lme4 (Bates *et al.*, 2014) package, or with `lme()` from the nlme (Pinheiro *et al.*, 2015) package.

These are a natural extension of residuals in simple regression to the multiple regression setting, in that the slope of a simple regression of $\boldsymbol{r}$ on $\boldsymbol{x}$ is equal to the value of $\widehat{\beta}_j$ in the full multiple regression model.

{ex:arthrit-eff}

EXAMPLE 7.8: Arthritis treatment

Here we illustrate the use of the effects package with the simple main effects model which was fit in Example 7.5. `allEffects()` is used to calculate the predicted probabilities of the `Better` response for `Age` and the two factors, `Sex` and `Treatment`. Partial residuals (for quantitative predictors) must be requested in the call to `allEffects()` or `Effect()`.

```
> library(effects)
> arth.eff2 <- allEffects(arth.logistic2, partial.residuals = TRUE)
> names(arth.eff2)

[1] "I(Age-50)" "Sex"       "Treatment"
```

The result, `arth.eff2`, is a list containing the fitted values (response probabilities, by default) for each of the model terms. For example the main effect for `Sex` is shown below; the associated score `model.matrix` illustrates how `Sex` is varied over its range, while `Age-50` and `Treatment` are fixed at their average values in the data.

```
> arth.eff2[["Sex"]]


 Sex effect
Sex
 Female    Male
0.60932 0.26050

> arth.eff2[["Sex"]]$model.matrix

  (Intercept) I(Age - 50) SexMale TreatmentTreated
1           1      3.3571       0           0.4881
2           1      3.3571       1           0.4881
```

The default plot method for the "efflist" object produces one plot for each high-order term, which are just the main effects in this model. The call below produces Figure 7.10.

```
> plot(arth.eff2, rows = 1, cols = 3,
+      rescale.axis = FALSE, residuals.pch = 15)
```

You can quite easily also produce effect plots for several predictors jointly, or full-model plots by using all predictors in the model in a call to `Effect()`. For example, the

```
> arth.full <- Effect(c("Age", "Treatment", "Sex"), arth.logistic2)
```

Then plotting the result, with some options, gives the plot shown in Figure 7.11.

```
> plot(arth.full, multiline = TRUE, ci.style = "bands",
+      colors = c("red", "blue"), lwd = 3,
+      ticks = list(at = c(.05, .1, .25, .5, .75, .9, .95)),
+      key.args = list(x = .52, y = .92, columns = 1),
+      grid = TRUE)
```

Alternatively, we can plot these results directly on the scale of probabilities, as shown in Figure 7.12.

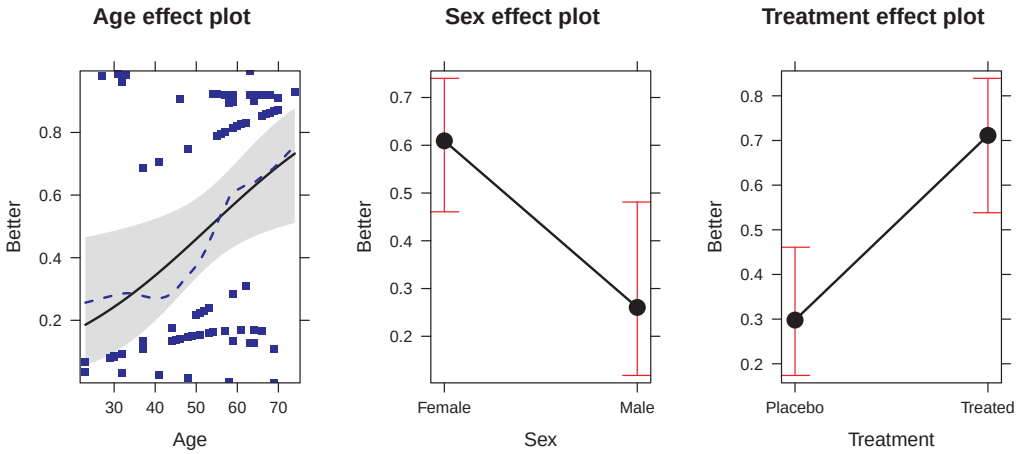


Figure 7.10: Plot of all effects in the main effects model for the Arthritis data. Partial residuals and their loess smooth are also shown for the continuous predictor, Age.

{fig:arth-effplot1}

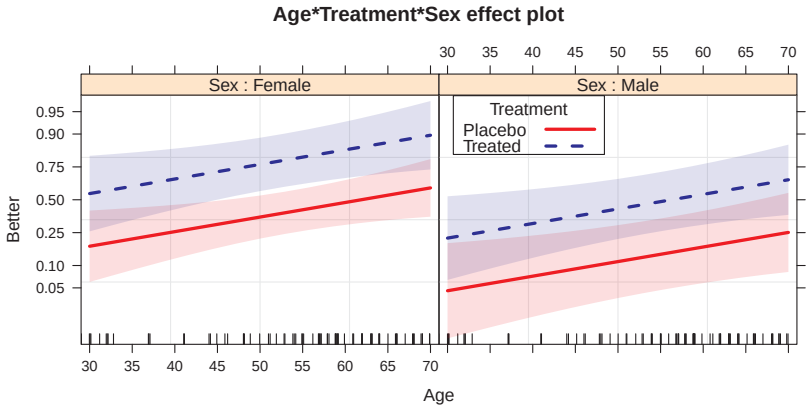


Figure 7.11: Full-model plot of the effects of all predictors in the main effects model for the Arthritis data, plotted on the logit scale.

{fig:arth-effplot2}

```
> plot(arth.full, multiline = TRUE, ci.style = "bands",
+      rescale.axis = FALSE,
+      colors = c("red", "blue"), lwd = 3,
+      key.args = list(x = .52, y = .92, columns = 1),
+      grid = TRUE)
```

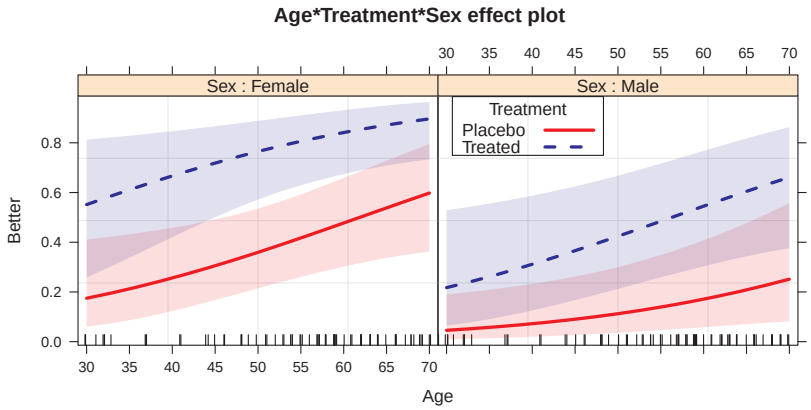


Figure 7.12: Full-model plot of the effects of all predictors in the main effects model for the Arthritis data, plotted on the probability scale.

{fig:arth-effplot3}

△

7.4 Case studies

{sec:logist-case}

The examples below take up some issues of data analysis, model building and visualization in the context of multiple logistic regression models. We focus on the combination of exploratory plots to see the data, modeling steps and graphs to interpret a given model.

7.4.1 Simple models: Group comparisons and effect plots

{sec:complex}
{ex:donner1}

EXAMPLE 7.9: Donner Party

In Chapter 1, Example 1.3, we described the background behind the sad story of the Donner Party, perhaps the most famous tragedy in the history of the westward settlement in the United States. In brief, the party was stranded on the eastern side of the Sierra Nevada mountains by heavy snow in late October, 1846, and by the time the last survivor was rescued in April, 1847, nearly half of the members had died from famine and exposure to extreme cold. Figure 1.3 showed that survival decreased strongly with age.

Here we consider a more detailed analysis of these data, which are contained in the data set `Donner` in vcdExtra . This data set lists 90 people in the Donner Party by name, together with age, sex, survived (0/1) and the date of death for those who died.[10]

[10] Most historical sources count the number in the Donner Party at 87 or 89. An exact accounting of the members of the Donner Party is difficult, because: (a) several people joined the party in mid-route, at Fort Bridger and in the Wasatch Mountains; (b) several rode ahead to search for supplies and one (Charles Stanton) brought two more with him (Luis and Salvador); (c) five people died before reaching the Sierra Nevada mountains. `Donner` incorporates updated information from Kristin Johnson's listing, `http://user.xmission.com/~octa/DonnerParty/Roster.htm`.

```
> data("Donner", package = "vcdExtra")    # load the data
> library(car)                           # for some() and Anova()
> some(Donner, 8)

                      family age    sex survived      death
Breen, Peter           Breen   3   Male        1       <NA>
Donner, Jacob         Donner  65   Male        0 1846-12-21
Foster, Jeremiah   MurFosPik   1   Male        0 1847-03-13
Graves, Nancy         Graves   9 Female        1       <NA>
McCutchen, Harriet McCutchen   1 Female        0 1847-02-02
Reed, James             Reed  46   Male        1       <NA>
Reinhardt, Joseph      Other  30   Male        0 1846-12-21
Wolfinger, Doris    FosdWolf  20 Female        1       <NA>
```

The main purpose of this example is to try to understand, through graphs and models, how survival was related to age and sex. However, first, we do some data preparation and exploration. The response variable, `survived` is a 0/1 integer, and it is more convenient for some purposes to make it a factor.

```
> Donner$survived <- factor(Donner$survived, labels = c("no", "yes"))
```

Some historical accounts (Grayson, 1990) link survival in the Donner Party to kinship or family groups, so we take a quick look at this factor here. The variable `family` reflects a recoding of the last names of individuals to reduce the number of factor levels. The main families in the Donner party were: Donner, Graves, Breen and Reed. The families of Murphy, Foster and Pike are grouped as `"MurFosPik"`, those of Fosdick and Wolfinger are coded as `"FosdWolf"`, and all others as `"Other"`.

```
> xtabs(~ family, data = Donner)

family
    Breen    Donner      Eddy  FosdWolf    Graves  Keseberg
        9        14         4         4        10         4
McCutchen MurFosPik     Other      Reed
        3        12        23         7
```

For the present purposes, we reduce these 10 family groups further, collapsing some of the small families into `"Other"`, and reordering the levels. Assigning new values to the `levels()` of a factor is a convenient trick for recoding factor variables.

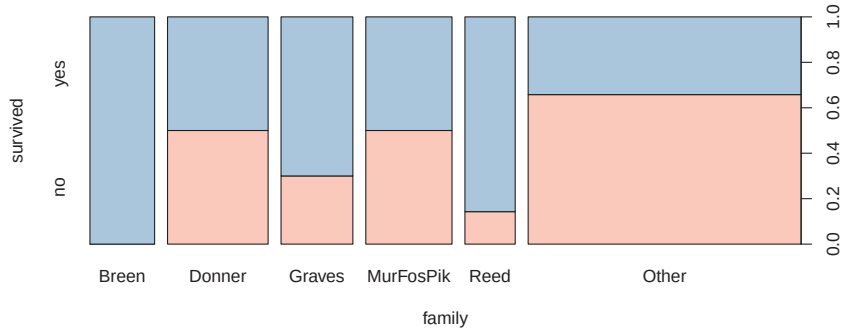
```
> # collapse small families into "Other"
> fam <- Donner$family
> levels(fam)[c(3, 4, 6, 7, 9)] <- "Other"
>
> # reorder, putting Other last
> fam = factor(fam,levels(fam)[c(1, 2, 4:6, 3)])
> Donner$family <- fam
> xtabs(~family, data=Donner)

family
    Breen    Donner    Graves MurFosPik      Reed     Other
        9        14        10        12         7        38
```

`xtabs()` then shows the counts of survival by these family groups:

```
> xtabs(~ survived + family, data = Donner)

        family
survived Breen Donner Graves MurFosPik Reed Other
     no      0      7      3         6    1    25
     yes     9      7      7         6    6    13
```

Plotting this distribution of survival by family with a formula gives a ***spineplot***, a special case of the mosaic plot, or a generalization of a stacked bar plot, shown in Figure 7.13. The widths of the bars are proportional to family size, and the shading highlights in light blue the proportion who survived in each family.

```
> plot(survived ~ family, data = Donner, col = c("pink", "lightblue"))
```



{fig:donner1-spineplot}

Figure 7.13: Spineplot of survival in the Donner Party by family.

A generalized pairs plot (Section 5.6.2), shown in Figure 7.14 gives a visual overview of the data. The diagonal panels here show the marginal distributions of the variables as bar plots, and highlight the skewed distribution of age and the greater number of males than females in the party. The boxplots and barcode plots for survived and age show that those who survived were generally younger than those who perished.

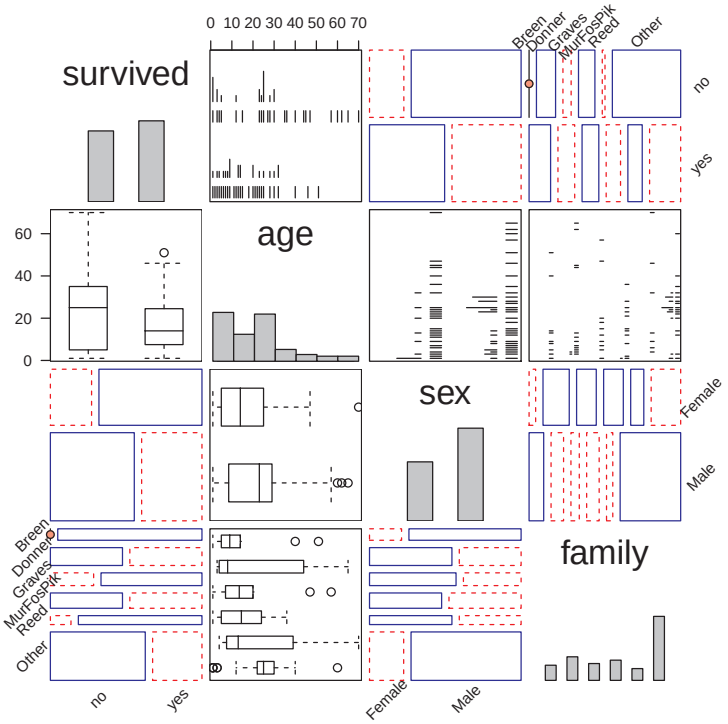
```
> library(gpairs)
> library(vcd)
> gpairs(Donner[,c(4, 2, 3, 1)],
+     diag.pars = list(fontsize = 20, hist.color = "gray"),
+     mosaic.pars = list(gp = shading_Friendly),
+     outer.rot = c(45, 45)
+ )
```

From an exploratory perspective, we now proceed to examine the relationship of survival to age and sex, beginning with the kind of conditional plots we illustrated earlier (in Example 7.6). Figure 7.15 shows a plot of `survived`, converted back to a 0/1 variable as required by `ggplot()`, together with the binary responses as points and the fitted logistic regressions separately for males and females.

```
> # basic plot: survived vs. age, colored by sex, with jittered points
> gg <- ggplot(Donner, aes(age, as.numeric(survived=="yes"), color = sex)) +
+   ylab("Survived") +
+   geom_point(position = position_jitter(height = 0.02, width = 0))
> # add conditional linear logistic regressions
> gg + stat_smooth(method = "glm", family = binomial, formula = y ~ x,
+                  alpha = 0.2, size = 2, aes(fill = sex))
```

It is easy to see that survival among women was greater than for men, perhaps narrowing the gap among the older people, but the data gets thin towards the upper range of age.

The curves plotted in Figure 7.15 assume a linear relationship between the log odds of survival



{fig:donner1-gpairs} **Figure 7.14:** Generalized pairs plot for the Donner data

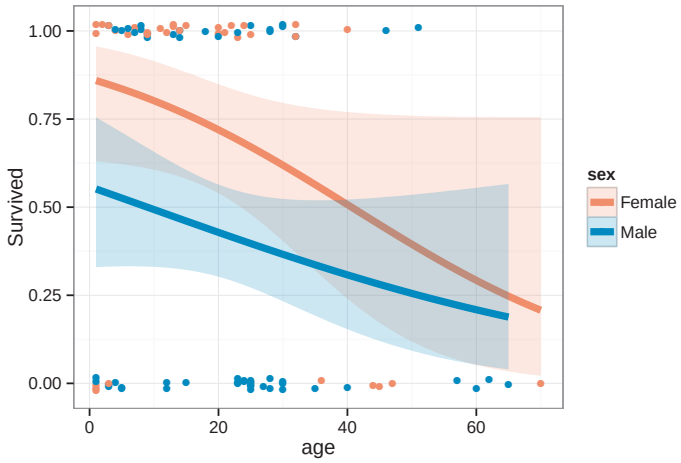


Figure 7.15: Conditional plot of the Donner data, showing the relationship of survival to age and sex. The smoothed curves and confidence bands show the result of fitting separate linear logistic regressions on age for males and females.

{fig:donner1-cond1}

and age (expressed as `formula = y ~ x` in the call to `stat_smooth()`). One simple way to check whether the relationship between survival and age is non-linear is to re-do this plot, but now allow a quadratic relationship with age, using `formula = y ~ poly(x,2)`. The result is shown in the left panel of Figure 7.16.

```
> # add conditional quadratic logistic regressions
> gg + stat_smooth(method = "glm", family = binomial, formula = y ~ poly(x,2),
+                  alpha = 0.2, size = 2, aes(fill = sex))
>
> # add loess smooth
> gg + stat_smooth(method = "loess", span=0.9, alpha = 0.2, size = 2,
+                  aes(fill = sex)) + coord_cartesian(ylim = c(-.05,1.05))
```

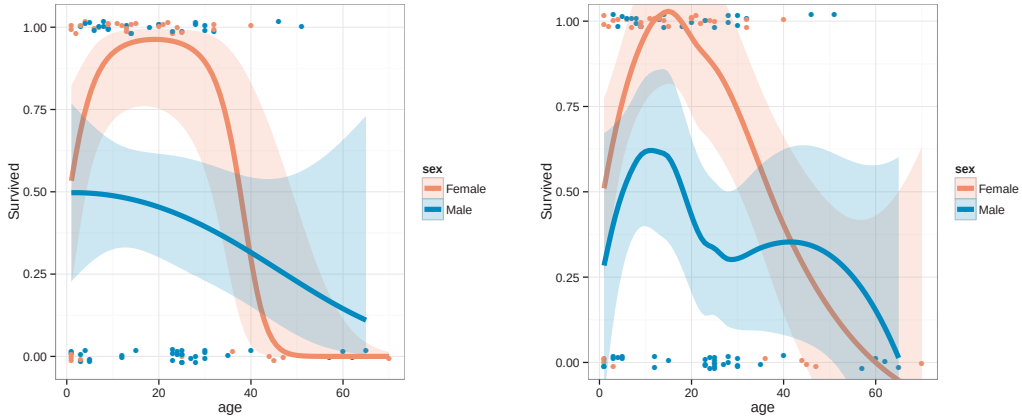


Figure 7.16: Conditional plots of the Donner data, showing the relationship of survival to age and sex. Left: The smoothed curves and confidence bands show the result of fitting separate quadratic logistic regressions on age for males and females. Right: Separate loess smooths are fit to the data for males and females

{fig:donner1-cond3}

This plot is quite surprising. It suggests quite different regimes relating to survival for men and women. Among men, survival probability decreases steadily with age, at least after age 20. For women, those in the age range 10–35 were very likely to have lived, while those over 40 were almost all predicted to perish.

Another simple technique is to fit a non-parametric loess smooth, as shown in the right panel of Figure 7.16.[11] The curve for females is similar to that of the quadratic fit in the left panel, but the curve for males suggests that survival also has a peak around the teenage years. One lesson to be drawn from these graphs is that a linear logistic regression, such as shown in Figure 7.16 may tell only part of the story, and, for a binary response it is not easy to discern whether the true relationship is linear. If it really is, all these graphs would look much more similar. As well, we usually obtain a more realistic smoothing of the data using full-model plots or effect plots.

The suggestions from these exploratory graphs can be used to define and test some models for survival in the Donner Party. The substantive questions of interest are:

- Is the relationship different for men and women? This is, is it necessary to allow for an interaction of age with sex, or separate fitted curves for men and women?

[11] A technical problem with the use of the loess smoother for binary data is that it can produce fitted values outside the [0–1] interval, as happens in the right panel of this figure. Kernel smoothers, such as the KernSmooth (Wand, 2015) package avoid this problem, but are not available through ggplot2 .

- Is the relationship between survival and age well-represented in a linear logistic regression model?

The first question is the easiest to deal with: we can simply fit a model allowing an interaction of age (or some function of age) and sex,

```
survived ~ age * sex
survived ~ f(age) * sex
```

and compare the goodness of fit with the analogous additive, main-effects models.

From a modeling perspective, there is a wide variety of approaches for testing for non-linear relationships. We only scratch the surface here, and only for a single quantitative predictor, x, such as age in this example. One simple approach, illustrated in Figure 7.16 is to allow a quadratic (or higher-power, e.g., cubic) function to describe the relationship between the log odds and x,

$$\begin{aligned} \text{logit}(\pi_i) &= \alpha + \beta_1 x_i + \beta_2 x_i^2 \\ \text{logit}(\pi_i) &= \alpha + \beta_1 x_i + \beta_2 x_i^2 + \beta_3 x_i^3 \\ &\dots \end{aligned}$$

In R, these model terms can be fit using `poly(x, 2)`, `poly(x, 3)` ..., which generate orthogonal polynomials for the powers of x. A simple way to test for non-linearity is a likelihood ratio test comparing the more complex model to the linear one. This method is often sufficient for a hypothesis test, and, if the relationship truly is linear, the fitted logits and probabilities will not differ greatly from what they would be under a linear model. A difficulty with this approach is that polynomial models are often unrealistic, particularly for data that approach an asymptote.

Another simple approach is to use a ***regression spline***, that fits the relationship with x in terms of a set of piecewise polynomials, usually cubic, joined at a collection of points, called *knots* so that the overall fitted relationship is smooth and continuous. See Fox (2008, §17.2) for a cogent, brief description of these methods.

One particularly convenient method is a ***natural spline***, implemented in the splines package in the `ns()` function. This method constrains the fitted cubic spline to be linear at lower and upper limits of x, and, for k knots, fits df $= k + 1$ parameters not counting the intercept. The k knots can be conveniently chosen as k cutpoints in the percentiles of the distribution of x. For example, with $k = 1$, the knot would be placed at the median, or 50th percentile; with $k = 3$, the knots would be placed at the quartiles of the distribution of x; $k = 0$ corresponds to no knots, i.e., a simple linear regression.

In the `ns()` function, you can specify the locations of knots or the number of knots with the `knots` argument, but it is conceptually simpler to specify the number of degrees of freedom used in the spline fit. Thus, `ns(x, 2)` and `poly(x, 2)` both specify a term in `x` of the same complexity, the former a natural spline with $k = 1$ knot and the later a quadratic function in `x`.

We illustrate these ideas in the remainder of this example, fitting a 2×2 collection of models to the *Donner* data corresponding to: (a) whether or not age and sex effects are additive; (b) whether the effect is linear on the logit scale or non-linear (quadratic, here). A brief summary of each model is given using the `Anova()` in the car (Fox and Weisberg, 2015) package, providing Type II tests of each effect. As usual, `summary()` would give more detailed output, including tests for individual coefficients. First, we fit the linear models, without and with an interaction term:

```
> donner.mod1 <- glm(survived ~ age + sex,
+                    data = Donner, family  =binomial)
> Anova(donner.mod1)

Analysis of Deviance Table (Type II tests)
```

```
Response: survived
    LR Chisq Df Pr(>Chisq)
age     5.52  1     0.0188 *
sex     6.73  1     0.0095 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> donner.mod2 <- glm(survived ~ age * sex,
+                    data = Donner, family = binomial)
> Anova(donner.mod2)

Analysis of Deviance Table (Type II tests)

Response: survived
        LR Chisq Df Pr(>Chisq)
age         5.52  1     0.0188 *
sex         6.73  1     0.0095 **
age:sex     0.40  1     0.5269
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The main effects of `age` and `sex` are both significant here, but the interaction term, `age:sex` is not in model `donner.mod2`. Note that the terms tested by `Anova()` in `donner.mod1` are a redundant subset of those in `donner.mod2`.

Next, we fit non-linear models, representing the linear and non-linear trends in age by `poly(age,2)`.[12] The `Anova()` results for terms in both models are contained in the output from `Anova(donner.mod4)`.

```
> donner.mod3 <- glm(survived ~ poly(age, 2) + sex,
+                    data = Donner, family = binomial)
> donner.mod4 <- glm(survived ~ poly(age, 2) * sex,
+                    data = Donner, family = binomial)
> Anova(donner.mod4)

Analysis of Deviance Table (Type II tests)

Response: survived
                LR Chisq Df Pr(>Chisq)
poly(age, 2)        9.91  2     0.0070 **
sex                 8.09  1     0.0044 **
poly(age, 2):sex    8.93  2     0.0115 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Now, in model `donner.mod4`, the interaction term `poly(age, 2):sex` is significant, indicating that the fitted quadratics for males and females differ in "shape," meaning either their linear (slope) or quadratic (curvature) components.

These four models address the questions posed earlier. A compact summary of these models, giving the likelihood ratio tests of goodness of fit, together with AIC and BIC statistics are shown below, using the `LRstats()` method in vcdExtra for a list of "glm" models.

```
> library(vcdExtra)
> LRstats(donner.mod1, donner.mod2, donner.mod3, donner.mod4)

Likelihood summary table:
            AIC BIC LR Chisq Df Pr(>Chisq)
donner.mod1 117 125    111.1 87      0.042 *
donner.mod2 119 129    110.7 86      0.038 *
```

[12] Alternatively, we could use the term `ns(age,2)` or higher-degree polynomials or natural splines with more knots, but we don't do this here.

```
donner.mod3 115 125    106.7 86      0.064 .
donner.mod4 110 125     97.8 84      0.144
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

By AIC and BIC, `donner.mod4` is best, and it is also the only model with a non-significant LR χ^2 (residual deviance). Because these models comprise a 2×2 set of hypotheses, it is easier to compare models by extracting the LR statistics and arranging these in a table, together with the their row and column differences. The entries in the table below are calculated as follows.

```
> mods <- list(donner.mod1, donner.mod2, donner.mod3, donner.mod4)
> LR <- sapply(mods, function(x) x$deviance)
> LR <- matrix(LR, 2, 2)
> rownames(LR) <- c("additive", "non-add")
> colnames(LR) <- c("linear", "non-lin")
> LR <- cbind(LR, diff = LR[,1] - LR[,2])
> LR <- rbind(LR, diff = c(LR[1,1:2] - LR[2,1:2], NA))
```

	linear	non-linear	$\Delta\chi^2$	p-value
additive	111.128	106.731	4.396	0.036
non-additive	110.727	97.799	12.928	0.000
$\Delta\chi^2$	0.400	8.932		
p-value	0.527	0.003		

Thus, the answer to our questions seems to be that: (a) there is evidence that the relationship of survival to age differs for men and women in the Donner Party; (b) these relationships are not well-described by a linear logistic regression.

For simplicity, we used a quadratic effect, `poly(age,2)`, to test for non-linearity here. An alternative test of the same complexity could use a regression spline, `ns(age,2)`, also with 2 degrees of freedom for the main effect and interaction, or allow more knots. To illustrate, we fit two natural spline modes models with 2 and 4 df, and compare these with the quadratic model (`donner.mod4`), all of which include the interaction of age and sex.

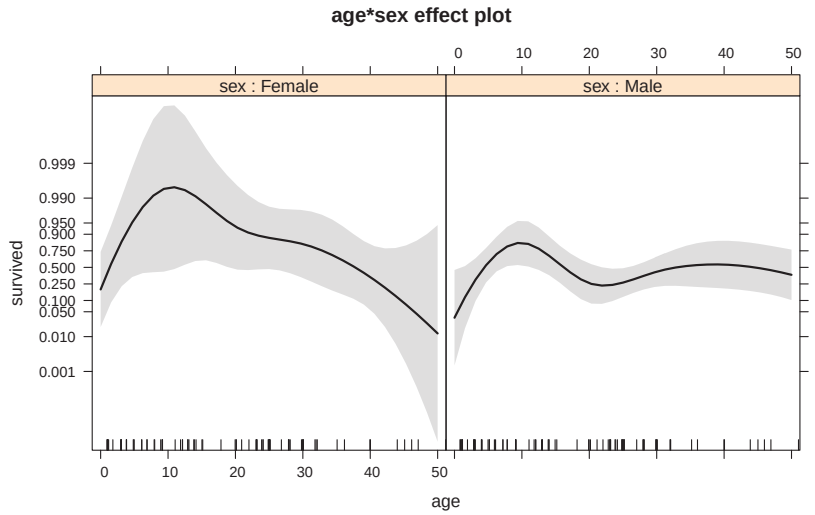
```
> library(splines)
> donner.mod5 <- glm(survived ~ ns(age,2) * sex,
+                    data = Donner, family = binomial)
> Anova(donner.mod5)

Analysis of Deviance Table (Type II tests)

Response: survived
              LR Chisq Df Pr(>Chisq)
ns(age, 2)        9.28  2     0.0097 **
sex               7.98  1     0.0047 **
ns(age, 2):sex    8.71  2     0.0129 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> donner.mod6 <- glm(survived ~ ns(age,4) * sex,
+                    data = Donner, family = binomial)
> Anova(donner.mod6)

Analysis of Deviance Table (Type II tests)

Response: survived
              LR Chisq Df Pr(>Chisq)
ns(age, 4)       22.05  4     0.0002 ***
sex              10.49  1     0.0012 **
```

```
ns(age, 4):sex     8.54  4     0.0737 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> LRstats(donner.mod4, donner.mod5, donner.mod6)

Likelihood summary table:
            AIC BIC LR Chisq Df Pr(>Chisq)
donner.mod4 110 125     97.8 84       0.14
donner.mod5 111 126     98.7 84       0.13
donner.mod6 106 131     86.1 80       0.30
```

With four more parameters, `donner.mod6` fits better and has a smaller AIC.

We conclude this example with an effect plot for the spline model `donner.mod6` shown in Figure 7.17. The complexity of the fitted relationships for men and women is intermediate between the two conditional plots shown in Figure 7.16. (However, note that the fitted effects are plotted on the logit scale in Figure 7.17 and labeled with the corresponding probabilities, whereas the conditional plots are plotted directly on the probability scale.)

```
> library(effects)
> donner.eff6 <- allEffects(donner.mod6, xlevels = list(age = seq(0, 50, 5)))
> plot(donner.eff6, ticks = list(at = c(0.001, 0.01, 0.05, 0.1, 0.25,
+                                       0.5, 0.75, 0.9, 0.95, 0.99, 0.999)))
```



{fig:donner-effect}

Figure 7.17: Effect plot for the Donner data

This plot confirms that for women in the Donner Party, survival was greatest for those aged 10–30. Survival among men was overall much less and there is a hint of greater survival for men aged 10–15.

Of course, this statistical analysis does not provide explanations for these effects, and it ignores the personal details of the Donner Party members and the individual causes and circumstances of death, which are generally well-documented in the historical record (Johnson, 1996). See `http://user.xmission.com/~octa/DonnerParty/` for a comprehensive collection of historical sources.

Grayson (1990) attributes the greater survival of women of intermediate age to demographic arguments that women are overall better able to withstand conditions of famine and extreme cold,

and high age-specific mortality rates among the youngest and oldest members of human societies. He also concludes (without much analysis) that members with larger social and kinship networks would be more likely to survive. △

{ex:arrests}

EXAMPLE 7.10: Racial profiling: Arrests for marijuana possession

In the summer of 2002, the *Toronto Star* newspaper launched an investigation on the topic of possible racial profiling by the Toronto police service. Through freedom of information requests, they obtained a data base of over 600,000 arrest records on all potential charges in the period from 1996–2002, the largest data bases on crime arrests and disposition ever assembled in Canada. An initial presentation of this study was given in Example 1.4.

In order to examine the issue of racial profiling (different treatment as a function of race) they excluded all charges such as assault, robbery, speeding and driving under the influence, where the police have no discretion regarding the laying of a charge. They focused instead on a subset of arrests, where the police had various options.

Among these, for people arrested for a single charge of simple possession of a small amount of marijuana, police have the option of releasing the arrestee, with a summons ("Form 9") to appear in court (similar to a parking ticket), or else the person could be given harsher treatment–brought to a police station or held in jail for a bail hearing ("Show cause"). The main question for the *Toronto Star* was whether the subject's skin color had any influence on the likelihood that the person would be released with a summons.[13]

Their results, published in a week-long series of articles in December 2002, concluded that there was strong evidence that black and white subjects were treated differently. For example, the analysis showed that blacks were 1.5 times more likely than whites to be given harsher treatment than release with a summons; if the subject was taken to the police station, a black was 1.6 times more likely to be held in jail for a bail hearing. An important part of the analysis and the public debate that ensued was to show that other variables that might account for these differences had been controlled or adjusted for.[14]

The data set `Arrests` in the effects package gives a simplified version of the *Star* database, containing records for 5,226 cases of arrest on the charge of simple possession of marijuana analyzed by the newspaper. The response variable here is `released` (Yes/No) and the main predictor of interest is skin color of the person arrested, `colour` (Black/White).[15] A random subset of the data set is shown below.

```
> library(effects)
> data("Arrests", package = "effects")
> Arrests[sample(nrow(Arrests), 6),]

     released colour year age  sex employed citizen checks
3768      Yes  Black 2000  23 Male       No     Yes      4
4576      Yes  Black 2001  17 Male      Yes     Yes      0
3976       No  White 2002  20 Male       No     Yes      3
4629      Yes  White 2000  18 Male      Yes     Yes      1
2384       No  Black 2000  19 Male      Yes     Yes      3
869       Yes  White 2001  15 Male      Yes     Yes      1
```

[13] Another discretionary charge they investigated was police stops for non-moving violations under the Ontario *Highway Traffic Act*, such as being pulled over for a faulty muffler or having an expired license plate renewal sticker. A disproportionate rate of charges against blacks is sometimes referred to as "driving while black" (DWB). This investigation found that the number of blacks so charged, but particularly young black males, far out-weighed their representation in the population.

[14] The Toronto Police Service launched a class-action libel law suit against the *Toronto Star* and the first author of this book, who served as their statistical consultant, claiming damages of $5,000 for every serving police officer in the city, a total of over 20 million dollars. The suit was thrown out of court, and the Toronto police took efforts to enhance training programs to combat the perception of racial profiling.

[15] The original data set also contained the categories Brown and Other, but these appeared with small frequencies.

Other available predictors, to be used as control variables included the `year` of the arrest, `age` and `sex` of the person, and binary indicators of whether the person was `employed` and a `citizen` of Canada. In addition, when someone is stopped by police, his/her name is checked in six police data bases that record previous arrests, convictions, whether on parole, etc. The variable `checks` records the number, 0–6, in which the person's name appeared.

A variety of logistic models were fit to these data including all possible main effects and some two-way interactions. To allow for possible non-linear effects of `year`, this variable was treated as a factor rather than as a (linear) numeric variable, but the effects of `age` and `checks` were reasonably linear on the logit scale. A reasonable model included the interactions of `colour` with both `year` and `age`, as fit below:

```
> Arrests$year <- as.factor(Arrests$year)
> arrests.mod <- glm(released ~ employed + citizen + checks
+                     + colour*year + colour*age,
+                     family = binomial, data = Arrests)
```

For such models, significance tests for the model terms are best carried out using the `Anova()` function in the car package that uses Type II tests:

```
> library(car)
> Anova(arrests.mod)

Analysis of Deviance Table (Type II tests)

Response: released
            LR Chisq Df Pr(>Chisq)
employed        72.7  1    < 2e-16 ***
citizen         25.8  1    3.8e-07 ***
checks         205.2  1    < 2e-16 ***
colour          19.6  1    9.7e-06 ***
year             6.1  5    0.29785
age              0.5  1    0.49827
colour:year     21.7  5    0.00059 ***
colour:age      13.9  1    0.00019 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The difficulty in interpreting these results from tables of coefficients can be seen in the output below:

```
> coeftest(arrests.mod)


z test of coefficients:

                     Estimate Std. Error z value Pr(>|z|)
(Intercept)           0.34443    0.31007    1.11  0.26665
employedYes           0.73506    0.08477    8.67  < 2e-16 ***
citizenYes            0.58598    0.11377    5.15  2.6e-07 ***
checks               -0.36664    0.02603  -14.08  < 2e-16 ***
colourWhite           1.21252    0.34978    3.47  0.00053 ***
year1998             -0.43118    0.26036   -1.66  0.09770 .
year1999             -0.09443    0.26154   -0.36  0.71805
year2000             -0.01090    0.25921   -0.04  0.96647
year2001              0.24306    0.26302    0.92  0.35541
year2002              0.21295    0.35328    0.60  0.54664
age                   0.02873    0.00862    3.33  0.00086 ***
colourWhite:year1998  0.65196    0.31349    2.08  0.03756 *
colourWhite:year1999  0.15595    0.30704    0.51  0.61152
colourWhite:year2000  0.29575    0.30620    0.97  0.33411
colourWhite:year2001 -0.38054    0.30405   -1.25  0.21073
colourWhite:year2002 -0.61732    0.41926   -1.47  0.14091
colourWhite:age      -0.03737    0.01020   -3.66  0.00025 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

By direct calculation (e.g., using `exp(coef(arrests.mod))`) you can find that the odds of a quick release was $\exp(0.735) = 2.08$ times greater for someone employed, $\exp(0.586) = 1.80$ times more likely for a Canadian citizen and $\exp(1.21) = 3.36$ times more likely for a white than a black person. It is much more difficult to interpret the interaction terms.

The primary question for the newspaper concerned the overall difference between the the treatment of blacks and whites– the main effect of `colour`. We plot this as shown below, giving the plot shown in Figure 7.18. This supports the claim by the *Star* because the 95% confidence limits for blacks and whites do not overlap, and all other relevant predictors that could account for this effect have been controlled or adjusted for.

```
> plot(Effect("colour", arrests.mod),
+      lwd = 3, ci.style = "bands", main = "",
+      xlab = list("Skin color of arrestee", cex = 1.25),
+      ylab = list("Probability(released)", cex = 1.25)
+   )
```

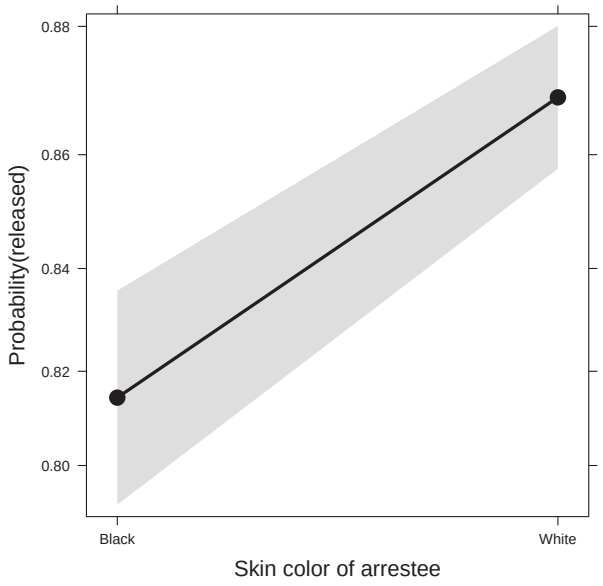


Figure 7.18: Effect plot for the main effect of skin color in the Arrests data. {fig:arrests-eff1}

Of course, one should be very wary of interpreting main effects when there are important interactions, and the story turned out to be far more nuanced than was reported in the newspaper. In particular, the interactions of color with with age and year provided a more complete account. Effect plots for these interactions are shown in Figure 7.19.

```
> # colour x age interaction
> plot(Effect(c("colour", "age"), arrests.mod),
+      lwd = 3, multiline = TRUE, ci.style = "bands",
+      xlab = list("Age", cex = 1.25),
+      ylab = list("Probability(released)", cex = 1.25),
+      key.args = list(x = .05, y = .99, cex = 1.2, columns = 1)
+      )
> # colour x year interaction
> plot(Effect(c("colour", "year"), arrests.mod),
```

```
+       lwd = 3, multiline = TRUE,
+       xlab = list("Year", cex = 1.25),
+       ylab = list("Probability(released)", cex = 1.25),
+       key.args = list(x = .7, y = .99, cex = 1.2, columns = 1)
+       )
```

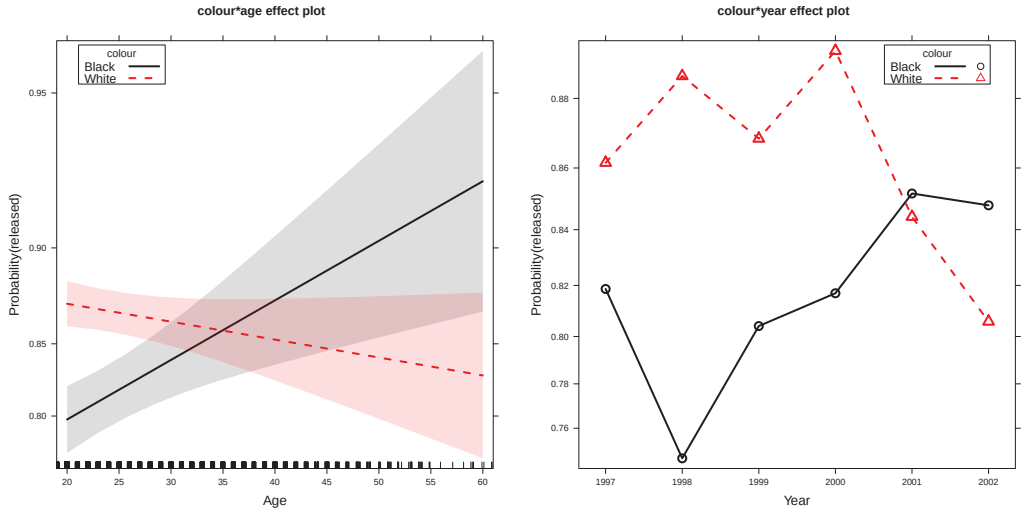


Figure 7.19: Effect plots for the interactions of color with age (left) and year (right) in the Arrests data.

{fig:arrests-eff2}

From the left panel in Figure 7.19, it is immediately apparent that the effect of age was in opposite directions for blacks and whites: Young blacks were indeed treated more severely than young whites; however for older people, blacks were treated less harshly than whites, controlling for all other predictors.

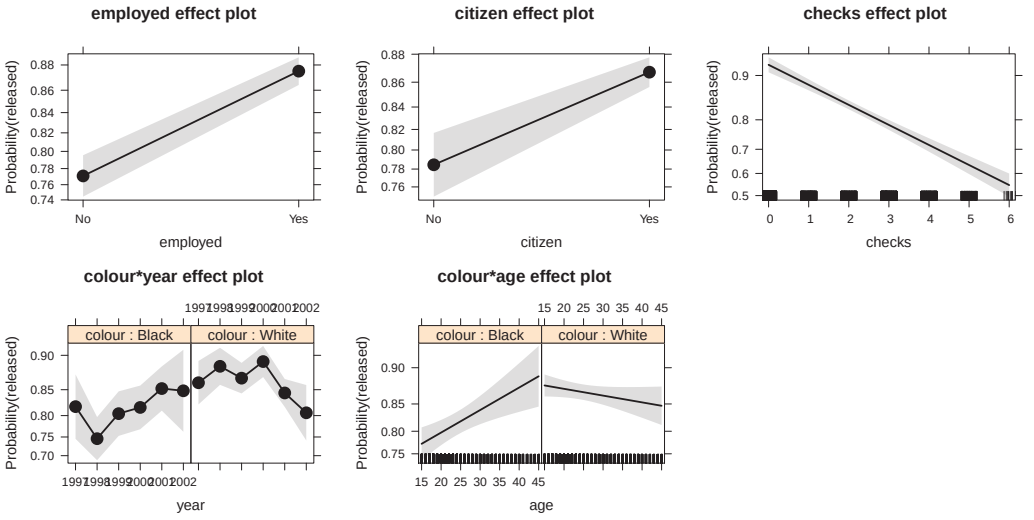
The right panel of Figure 7.19 shows the changes over time in the treatment of blacks and whites. It can be seen that up to the year 2000 there was strong evidence for differential treatment on these charges, again controlling for other predictors. There was also evidence to support the claim by the police that in the year 2001 they began training of officers to reduce racial effects in treatment.

Finally, the effects package provides a convenience function, `allEffects()`, that calculates the effects for all high-order terms in a given model. The `plot()` method for the "efflist" object can be used to plot individual terms selectively from a graphic menu, or plot all terms together in one comprehensive display using `ask=FALSE`.

```
> arrests.effects <- allEffects(arrests.mod,
+                               xlevels = list(age = seq(15, 45, 5)))
> plot(arrests.effects,
+       ylab = "Probability(released)", ci.style = "bands", ask = FALSE)
```

The result, shown in Figure 7.20 is a relatively compact and understandable summary of the `arrests.mod` model: (a) people were more likely to be released if they were employed and citizens. (b) each additional police check decreased the likelihood of release with a summons. (c) the effect of skin color varied with age and year of arrest, in ways that tell a far more nuanced story than reported in the newspaper.

Finally, another feature of this plot bears mention: by default, the scales for each effect plot are determined separately for each effect, to maximize use of the plot region. However, you have to



{fig:arrests-all} **Figure 7.20:** Effect plot for all high-order terms in the model for the Arrests data

read the Y scale values to judge the relative sizes of these effects. An alternative plot, using the *same* scale in each subplot[16] would show the relative sizes of these effects.

△

7.4.2 More complex models: Model selection and visualization

{sec:complex}

Models with more predictors or more complex terms (interactions, non-linear terms) present additional challenges for model fitting, summarization, and visualization and interpretation. These problems increase rapidly with the number of potential predictors.

A very complicated model, with many terms and interactions may fit the data at hand quite well. However, because goodness-of-fit is optimized in the sample, terms that appear significant are less likely to be important in a future sample, and we need to worry about inflation of Type I error rates that accompany multiple significance tests. As well, it becomes increasingly difficult to visualize and understand a fitted model as the model becomes increasingly complex. On the other hand, a very simple model may omit important predictors, interactions, or non-linear relationships with the response and give an illusion of a comfortable interpretation.

Model selection for logistic regression seeks to balance the trade-off between the competing goals of goodness-of-fit and simplicity. A full discussion of this topic is beyond the scope of this book, but is well treated in Agresti (2013, Chapter 6), and extensively in Harrell (2001, Chapter 10–13). Here, we illustrate some important ideas using the AIC and BIC statistics as parsimony-adjusted measures of goodness-of-fit. These are discussed Section 9.3.2. AIC is defined as

$$\text{AIC} = -2 \log \mathcal{L} + 2k$$

where $\log \mathcal{L}$ is the maximized log likelihood and k is the number of parameters estimated in the model. Better models correspond to *smaller* AIC. BIC is similar, but uses a penalty of $\log(n)k$, and so prefers smaller models as the sample size n increases.

{ex:icu1}

EXAMPLE 7.11: Death in the ICU

[16] With the effects package, you can set the `ylim` argument to equate the vertical range for all plots, but this should be done on the logit scale. For this plot, `ylim = plogis(c(0.5, 1))` would work.

In this example we examine briefly some aspects of logistic regression related to model selection and graphical display with a large collection of potential predictors, including both quantitative and discrete variables. We use data from a classic study by Lemeshow *et al.* (1988) of patients admitted to an intensive care unit at Baystate Medical Center in Springfield, Massachusetts. The major goal of this study was to develop a model to predict the probability of survival (until hospital discharge) of these patients and to study the risk factors associated with ICU mortality. The data, contained in the data set *ICU* in vcdExtra , gives the results for a sample of 200 patients that was presented in Hosmer *et al.* (2013) (and earlier editions).

The *ICU* data set contains 22 variables of which the first, `died` is a factor. Among the predictors, two variables (`race`, `coma`) were represented initially as 3-level factors, but then recoded to binary variables (`white`, `uncons`).

```
> data("ICU", package = "vcdExtra")
> names(ICU)

 [1] "died"      "age"       "sex"       "race"      "service"
 [6] "cancer"    "renal"     "infect"    "cpr"       "systolic"
[11] "hrtrate"   "previcu"   "admit"     "fracture"  "po2"
[16] "ph"        "pco"       "bic"       "creatin"   "coma"
[21] "white"     "uncons"

> ICU <- ICU[,-c(4, 20)]  # remove redundant race, coma
```

Removing the 3-level versions leaves 19 predictors, of which three (age, heart rate, systolic blood pressure) are quantitative and the remainder are either binary (service, cancer) or had previously been dichotomized (e.g., `ph<7.25`).

As an initial step, and a basis for comparison, we fit the full model containing all 19 predictors.

```
> icu.full <- glm(died ~ ., data = ICU, family = binomial)
> summary(icu.full)


Call:
glm(formula = died ~ ., family = binomial, data = ICU)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.8040  -0.5606  -0.2044  -0.0863   2.9773

Coefficients:
                Estimate Std. Error z value Pr(>|z|)
(Intercept)     -6.72670    2.38551   -2.82   0.0048 **
age              0.05639    0.01862    3.03   0.0025 **
sexMale          0.63973    0.53139    1.20   0.2286
serviceSurgical -0.67352    0.60190   -1.12   0.2631
cancerYes        3.10705    1.04585    2.97   0.0030 **
renalYes        -0.03571    0.80165   -0.04   0.9645
infectYes       -0.20493    0.55319   -0.37   0.7110
cprYes           1.05348    1.00661    1.05   0.2953
systolic        -0.01547    0.00850   -1.82   0.0686 .
hrtrate         -0.00277    0.00961   -0.29   0.7732
previcuYes       1.13194    0.67145    1.69   0.0918 .
admitEmergency   3.07958    1.08158    2.85   0.0044 **
fractureYes      1.41140    1.02971    1.37   0.1705
po2<=60          0.07382    0.85704    0.09   0.9314
ph<7.25          2.35408    1.20880    1.95   0.0515 .
pco>45          -3.01844    1.25345   -2.41   0.0160 *
bic<18          -0.70928    0.90978   -0.78   0.4356
creatin>2        0.29514    1.11693    0.26   0.7916
```

```
whiteNon-white   0.56573    0.92683    0.61   0.5416
unconsYes        5.23229    1.22630    4.27    2e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 200.16  on 199  degrees of freedom
Residual deviance: 120.78  on 180  degrees of freedom
AIC: 160.8

Number of Fisher Scoring iterations: 6
```

You can see that a few predictors are individually significant, but many are not.

However, it is useful to carry out a simultaneous global test of $H_0 : \boldsymbol{\beta} = 0$ that *all* regression coefficients are zero. If this test is not significant, it makes little sense to use selection methods to choose individually significant predictors. For convenience, we define a simple function, `LRtest()`, to calculate the likelihood ratio test from the model components.

```
> LRtest <- function(model)
+   c(LRchisq = (model$null.deviance - model$deviance),
+     df = (model$df.null - model$df.residual))
>
> (LR <- LRtest(icu.full))

LRchisq      df
 79.383  19.000

> (pvalue <- 1 - pchisq(LR[1], LR[2]))

   LRchisq
2.3754e-09
```

At this point, it is tempting to examine the output from `summary(icu.full)` shown above and eliminate those predictors which fail significance at some specified level such as the conventional $\alpha = 0.05$. This is generally a bad idea for many reasons.[17]

A marginally better approach is to remove non-significant variables whose coefficients have signs that don't make sense from the substance of the problem. For example, in the full model, both `renal` (history of chronic renal failure) and `infect` (infection probable at ICU admission) have negative signs, meaning that their presence *decreases* the odds of death. We remove those variables using `update()`; as expected they make little difference.

```
> icu.full1 <- update(icu.full, . ~ . - renal - fracture)
> anova(icu.full1, icu.full, test = "Chisq")

Analysis of Deviance Table

Model 1: died ~ age + sex + service + cancer + infect + cpr + systolic +
    hrtrate + previcu + admit + po2 + ph + pco + bic + creatin +
    white + uncons
Model 2: died ~ age + sex + service + cancer + renal + infect + cpr +
    systolic + hrtrate + previcu + admit + fracture + po2 + ph +
    pco + bic + creatin + white + uncons
  Resid. Df Resid. Dev Df Deviance Pr(>Chi)
1       182        122
2       180        121  2      1.7     0.43
```

Before proceeding to consider model selection, it is useful to get a better visual overview of the

[17] It ignores the facts of (a) an arbitrary cutoff value for significance, (b) the strong likelihood that chance features of the data or outliers influence the result, (c) problems of collinearity, etc. See Harrell (2001, §4.3) for a useful discussion of these issues.

current model than is available from a table of coefficients and significance tests. Some very useful `print()`, `summary()` and `plot()` methods are available in the rsm (Lenth, 2014) package. Unfortunately, these require that the logistic model is fitted with `lrm()` in that package rather than with `glm()`. We pause here to refit the same model as `icu.full1` in order to show a plot of odds ratios for the terms in this model.

```
> library(rms)
> dd <- datadist(ICU[,-1])
> options(datadist = "dd")
> icu.lrm1 <- lrm(died ~ ., data = ICU)
> icu.lrm1 <- update(icu.lrm1, . ~ . - renal - fracture)
```

The `summary()` method for "rms" objects produces a much more detailed descriptive summary of a fitted model, and the `plot()` method for that summary object gives a sensible plot of the odds ratios for the model terms together with confidence intervals, at levels (0.9, 0.95, 0.99) by default. The following lines produce Figure 7.21.

```
> sum.lrm1 <- summary(icu.lrm1)
> plot(sum.lrm1, log = TRUE, main = "Odds ratio for 'died'", cex = 1.25,
+      col = rgb(0.1, 0.1, 0.8, alpha = c(0.3, 0.5, 0.8)))
```

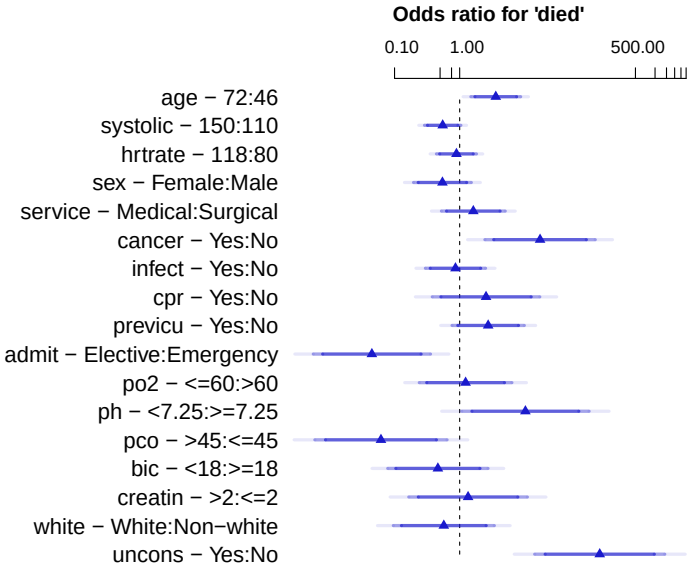


Figure 7.21: Odds ratios for the terms in the model for the ICU data. Each line shows the odds ratio for a term, together with lines for 90, 95 and 99% confidence intervals in progressively darker shades.

{fig:icu1-odds-ratios}

In this plot, continuous variables are shown at the top, followed by the discrete predictors. In each line, the range or levels of the predictors are given in the form $a : b$, such that the value a corresponds to the numerator of the odds ratio plotted. Confidence intervals that don't overlap the vertical line for odds ratio = 1 are significant, but this graph shows those at several confidence levels, allowing you to decide what is "significant" visually. As well, the widths of those intervals convey the precision of these estimates.

Among several stepwise selection methods in R for "glm" models, `stepAIC()` in the MASS package implements a reasonable collection of methods for forward, backward and stepwise selection

using penalized AIC-like criteria that balance goodness of fit against parsimony. The method takes an argument, `scope`, which is a list of two model formulae; `upper` defines the largest (most complex) model to consider and `lower` defines the smallest (simplest) model, e.g., `lower = ~ 1` is the intercept-only model.

By default, the function produces verbose printed output showing the details of each step, but we suppress that here to save space. It returns the final model as its result, along with an `anova` component that summarises the deviance and AIC from each step.

```
> library(MASS)
> icu.step1 <- stepAIC(icu.full1, trace = FALSE)
> icu.step1$anova

Stepwise Model Path
Analysis of Deviance Table

Initial Model:
died ~ age + sex + service + cancer + infect + cpr + systolic +
    hrtrate + previcu + admit + po2 + ph + pco + bic + creatin +
    white + uncons

Final Model:
died ~ age + cancer + systolic + admit + ph + pco + uncons


        Step Df Deviance Resid. Df Resid. Dev    AIC
1                              182     122.48 158.48
2      - po2  1 0.062446       183     122.54 156.54
3  - creatin  1 0.059080       184     122.60 154.60
4  - hrtrate  1 0.072371       185     122.67 152.67
5   - infect  1 0.122772       186     122.79 150.79
6    - white  1 0.334999       187     123.13 149.13
7  - service  1 0.671313       188     123.80 147.80
8      - bic  1 0.377521       189     124.18 146.18
9      - cpr  1 1.148260       190     125.33 145.33
10     - sex  1 1.543523       191     126.87 144.87
11 - previcu  1 1.569976       192     128.44 144.44
```

Alternatively, we can use the BIC criterion, by specifying `k`=$\log(n)$, which generally will select a smaller model when the sample size is reasonably large.

```
> icu.step2 <- stepAIC(icu.full, trace = FALSE, k = log(200))
> icu.step2$anova

Stepwise Model Path
Analysis of Deviance Table

Initial Model:
died ~ age + sex + service + cancer + renal + infect + cpr +
    systolic + hrtrate + previcu + admit + fracture + po2 + ph +
    pco + bic + creatin + white + uncons

Final Model:
died ~ age + cancer + admit + uncons


         Step Df  Deviance Resid. Df Resid. Dev    AIC
1                              180     120.78 226.74
2     - renal  1 0.0019881       181     120.78 221.45
3       - po2  1 0.0067968       182     120.79 216.16
4   - creatin  1 0.0621463       183     120.85 210.92
5   - hrtrate  1 0.0658870       184     120.92 205.69
6    - infect  1 0.2033221       185     121.12 200.59
```

```
7      - white  1 0.3673180       186     121.49 195.66
8        - bic  1 0.6002993       187     122.09 190.96
9    - service  1 0.7676303       188     122.85 186.43
10 - fracture  1 1.3245086       189     124.18 182.46
11       - cpr  1 1.1482598       190     125.33 178.31
12       - sex  1 1.5435228       191     126.87 174.55
13   - previcu  1 1.5699762       192     128.44 170.83
14        - ph  1 4.4412370       193     132.88 169.97
15       - pco  1 2.7302934       194     135.61 167.40
16 - systolic  1 3.5231028       195     139.13 165.63
```

This model differs from model `icu.step1` selected using AIC in the last three steps, which also removed `ph`, `pco` and `systolic`.

```
> coeftest(icu.step2)


z test of coefficients:

               Estimate Std. Error z value Pr(>|z|)
(Intercept)     -6.8698     1.3188   -5.21  1.9e-07 ***
age              0.0372     0.0128    2.91  0.00360 **
cancerYes        2.0971     0.8385    2.50  0.01238 *
admitEmergency   3.1022     0.9186    3.38  0.00073 ***
unconsYes        3.7055     0.8765    4.23  2.4e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

These two models are nested, so we can compare them directly using a likelihood ratio test from `anova()`.

```
> anova(icu.step2, icu.step1, test = "Chisq")

Analysis of Deviance Table

Model 1: died ~ age + cancer + admit + uncons
Model 2: died ~ age + cancer + systolic + admit + ph + pco + uncons
  Resid. Df Resid. Dev Df Deviance Pr(>Chi)
1       195        139
2       192        128  3     10.7    0.013 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The larger model is significantly better by this test, but the smaller model is simpler to interpret. We retain these both as "candidate models" to be explored further, but for ease in this example, we do so using the smaller model, `icu.step2`.

Another important step is to check for non-linearity of quantitative predictors such as `age` and interactions among the predictors. This is easy to do using `update()` and `anova()` as shown below. First, allow a non-linear term in `age`, and all two-way interactions of the binary predictors.

```
> icu.glm3 <- update(icu.step2, . ~ . -age + ns(age, 3) + (cancer + admit + uncons)^2)
> anova(icu.step2, icu.glm3, test = "Chisq")

Analysis of Deviance Table

Model 1: died ~ age + cancer + admit + uncons
Model 2: died ~ cancer + admit + uncons + ns(age, 3) + cancer:admit +
    cancer:uncons + admit:uncons
  Resid. Df Resid. Dev Df Deviance Pr(>Chi)
1       195        139
2       191        135  4     3.73     0.44
```

Next, we can check for interactions with `age`:

```
> icu.glm4 <- update(icu.step2, . ~ . + age * (cancer + admit + uncons))
> anova(icu.step2, icu.glm4, test = "Chisq")

Analysis of Deviance Table

Model 1: died ~ age + cancer + admit + uncons
Model 2: died ~ age + cancer + admit + uncons + age:cancer + age:admit +
    age:uncons
  Resid. Df Resid. Dev Df Deviance Pr(>Chi)
1       195        139
2       192        134  3     5.37     0.15
```

None of these additional terms have much effect. △

So, we will tentatively adopt the simple main effects model, `icu.step2`, and consider how to visualize and interpret this result. {ex:icu1a}

EXAMPLE 7.12: Death in the ICU – Visualization

One interesting display is a ***nomogram*** that shows how values on the various predictors translate into a predicted value of the log odds, and the relative strengths of their effects on this prediction. This kind of plot is shown in Figure 7.22, produced using `nomogram()` in the rms (Harrell, Jr., 2015) package as follows. It only works with models fit using `lrm()`, so we have to refit this model.

```
> icu.lrm2 <- lrm(died ~ age + cancer  + admit + uncons, data = ICU)
> plot(nomogram(icu.lrm2), cex.var = 1.2, lplabel = "Log odds death")
```

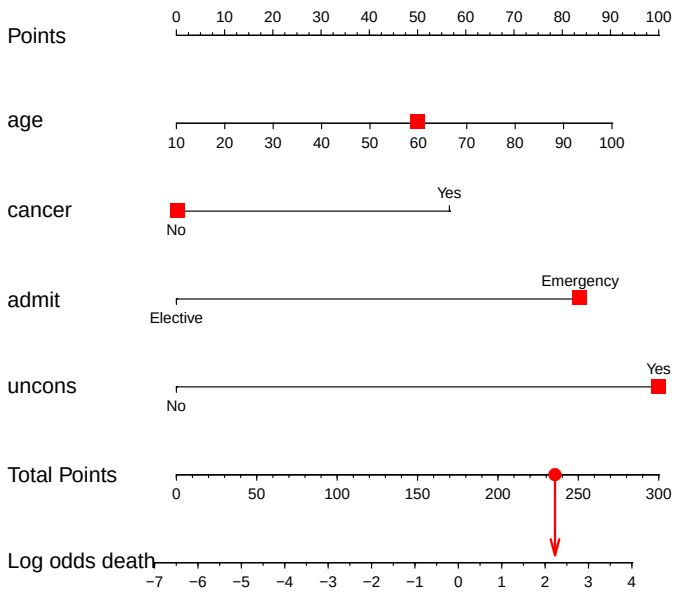


Figure 7.22: Nomogram for predicted values in the simple main effects model for the ICU data. Each predictor is scaled in relation to its effect on the outcome in terms of "points", 0–100. Adding the points for a given case gives total points that have a direct translation to log odds. The marked points show the prediction for someone of age 60, admitted to the emergency ward and unconscious. {fig:icu-nomogram}

In this nomogram, each predictor is scaled according to the size of its effect on a common scale of 0–100 "points." A representative observation is shown by the marked points, corresponding to a person of age 60, without cancer, who was admitted to emergency and was unconscious at that time. Adding the points associated with each variable value gives the result shown on the scale of total points. For this observation, the result is $50 + 0 + 84 + 100 = 234$, for which the scale of log odds at the bottom gives a predicted logit of 2.2, or a predicted probability of death of $1/(1 + \exp(-2.2)) = 0.90$.

This leaves us with the problem of how to visualize the fitted model compactly and comprehensively. Multi-panel full-model plots and effect plots, as we have used them, are somewhat unwieldy with four or more predictors if we want to view all effects simultaneously because it becomes more difficult to make comparisons across multiple panels (particularly if the vertical scales differ).

One way to reduce the visual complexity of such graphs is to combine some predictors that would otherwise be shown in separate panels into a recoding that can be shown as multiple curves for their combinations in fewer panels. In general, this can be done by combining some predictors *interactively*; for example with sex and education as factors, their combinations, `M:Hi`, `M:Lo`, etc. could be used to define a new variable, `group` used as the curves in one plot, rather than separate panels. This, in fact, is precisely what `binreg_plot()` does when there are two or more factors to be shown in a given plot.

In this case, because age is continuous, it makes sense to plot fitted values against age.[18] With `cancer`, `admit` and `uncons` as binary factors associated with risk of death, it is also convenient for plotting to represent them in a way that reflects the level assiciated with higher risk. We do this by recoding their levels using `"-"` for low risk.

```
> levels(ICU$cancer) <- c("-", "Cancer")
> levels(ICU$admit) <- c("-","Emerg")
> levels(ICU$uncons) <- c("-","Uncons")
>
> icu.glm2 <- glm(died ~ age + cancer + admit + uncons,
+                 data = ICU, family = binomial)
```

Then, `binreg_plot()` is called as follows, giving the plot shown in Figure 7.23. Such multiline graphs are more easily read with direct labels on the lines rather than a legend, so the legend is suppressed, and the lines are labeled using `labels = TRUE`. Points along the fitted lines are shown when `point_size>0`.

```
> binreg_plot(icu.glm2, type = "link", conf_level = 0.68,
+             legend = FALSE,
+             labels = TRUE, labels_just = c("right", "bottom"),
+             cex = 0, point_size = 0.8, pch = 15:17,
+             ylab = "Log odds (died)",
+             ylim = c(-7, 4))
```

From Figure 7.23, it is apparent that the log odds of mortality increases with age in all cases. Relative to the line labeled `"-:-:-"` (no risk factors) mortality is higher when any of these risk factors are present, particularly when the patient is admitted to Emergency; it is highest when the patient is also unconscious at admission. The vertical gaps between lines that share a common risk (e.g., `Cancer`, `CancerEmerg`) indicate the additional increment from one more risk.

Finally, the plotted points show the number and age distribution of these various combinations. The greatest number of patients have only `Emerg` as a risk factor and only one patient was unconscious with no other risk.

Before concluding that this model provides an adequate description of the data, we should examine whether any individual cases are unduly influencing the predicted results, and more importantly,

[18] By default, `binreg_plot()` uses the first numeric predictor as the horizontal variable.

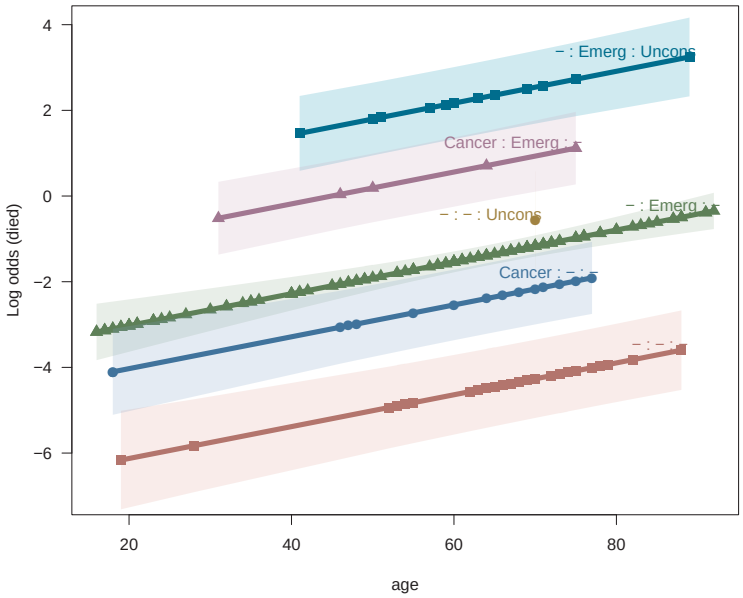


Figure 7.23: Fitted log odds of death in the ICU data for the model `icu.glm2`. Each line shows the relationship with age, for patients having various combinations of risk factors and 1 standard error confidence bands.

{fig:icu1-binreg-plot}

the choice of variables in the model. We examine this question in Section 7.5 where we return to these data (Example 7.14).

△

7.5 Influence and diagnostic plots

{sec:logist-infl}

In ordinary least squares (OLS) regression, measures of ***influence*** (leverage, Cook's D, DFBETAs, etc.) and associated plots help you to determine whether individual cases (or cells in grouped data) have undue impact on the fitted regression model and the coefficients of individual predictors. Analogs of most of these measures have been suggested for logistic regression and generalized linear models. Pregibon (1981) provided the theoretical basis for these methods, exploiting the relationship between logistic models and weighted least squares. Some additional problems occur in practical applications to logistic regression because the response is discrete, and because the leave-one-out diagnostics are more difficult to compute, but the ideas are essentially the same.

7.5.1 Residuals and leverage

{sec:logist-resids}

As in ordinary least squares regression, the influence (actual impact) of an observation in logistic models depends multiplicatively on its residual (disagreement between y_i and $\hat{y}_i$) and its leverage (how unusual $\boldsymbol{x}_i$ is in the space of the explanatory variables). A conceptual formula is

$$\text{Influence} = \text{Leverage} \times \text{Residual}$$

This multiplicative definition implies that a case is influential to the extent that it is both poorly fit *and* has unusual values of the predictors.

7.5.1.1 Residuals

In logistic regression, the simple raw residual is just $e_i \equiv y_i - \hat{p}_i$, where $\hat{p}_i = 1/[1 + \exp(-\boldsymbol{x}_i^\mathsf{T}\boldsymbol{b})]$.

The Pearson and deviance residuals are more useful for identifying poorly fitted observations, and are components of overall goodness-of-fit statistics. The (raw) ***Pearson residual*** is defined as

{eq:reschi}
$$r_i \equiv \frac{e_i}{\sqrt{\widehat{p}_i(1-\widehat{p}_i)}} \tag{7.7}$$

and the Pearson chi-square is therefore $\chi^2 = \sum r_i^2$. The ***deviance residual*** is

{eq:resdev}
$$g_i \equiv \pm -2[y_i \log \widehat{p}_i + (1-y_i)\log(1-\widehat{p}_i)]^{1/2} \tag{7.8}$$

where the sign of g_i is the same as that of e_i. Likewise, the sum of squares of the deviance residuals gives the overall deviance, $G^2 = -2\log\mathcal{L}(\boldsymbol{b}) = \sum g_i^2$.

When y_i is a binomial count based on n_i trials (grouped data), the Pearson residuals Eqn. (7.7) then become

$$r_i \equiv \frac{y_i - n_i\widehat{p}_i}{\sqrt{n_i\widehat{p}_i(1-\widehat{p}_i)}}$$

with similar modifications made to Eqn. (7.8).

In R, `residuals()` is the generic function for obtaining (raw) residuals from a model fitted with `glm()` (or `lm()`). However ***standardized residuals***, given by `rstandard()`, and ***studentized residuals***, provided by `rstudent()` are often more useful because they rescale the residuals to have unit variance. They use, respectively, an overall estimate, $\hat{\sigma}^2$ of error variance, and the leave-one-out estimate, $\hat{\sigma}^2_{(-i)}$, omitting the ith observation; the studentized version is usually to be preferred in model diagnostics because it also accounts for the impact of the observation on residual variance.

7.5.1.2 Leverage

Leverage measures the *potential* impact of an individual case on the results, which is directly proportional to how far an individual case is from the centroid in the space of the predictors. Leverage is defined as the diagonal elements, h_{ii}, of the "Hat" matrix, $\boldsymbol{H}$,

$$\boldsymbol{H} = \boldsymbol{X}^\star(\boldsymbol{X}^{\star\mathsf{T}}\boldsymbol{X}^\star)^{-1}\boldsymbol{X}^{\star\mathsf{T}}$$

where $\boldsymbol{X}^\star = \boldsymbol{V}^{1/2}\boldsymbol{X}$, and $\boldsymbol{V} = \text{diag}\,[\hat{\boldsymbol{p}}(1-\hat{\boldsymbol{p}})]$. As in OLS, leverage values are between 0 and 1, and a leverage value, $h_{ii} > \{2 \text{ or } 3\}k/n$ is considered "large"; here, $k = p + 1$ is the number of coefficients including the intercept and n is the number of cases. In OLS, however, the hat values depend only on the Xs, whereas in logistic regression, they also depend on the dependent variable values and the fitted probabilities (through $\boldsymbol{V}$). As a result, an observation may be extremely unusual on the predictors, yet not have a large hat value, if the fitted probability is near 0 or 1. The function `hatvalues()` calculates these values for a fitted "glm" model object.

7.5.2 Influence diagnostics

{sec:logist-infldiag}

Influence measures assess the effect that deleting an observation has on the regression parameters, fitted values, or the goodness-of-fit statistics. In OLS, these measures can be computed exactly from a single regression. In logistic regression, the exact effect of deletion requires refitting the model with each observation deleted in turn, a time-intensive computation. Consequently, Pregibon (1981) showed how analogous deletion diagnostics may be approximated by performing one additional step of the iterative procedure. Most modern implementations of these methods for generalized linear models follow Williams (1987).

The simplest measure of influence of observation i is the standardized change in the coefficient for each variable due to omitting that observation, termed ***DFBETA***s. From the relation (Pregibon, 1981, p. 716)

$$\boldsymbol{b} - \boldsymbol{b}_{(-i)} = (\boldsymbol{X}^\mathsf{T}\boldsymbol{V}\boldsymbol{X})^{-1}\boldsymbol{x}_i(y_i - \widehat{p}_i)/(1 - h_{ii}) \ ,$$

the estimated standardized change in the coefficient for variable j is

$$\text{DFBETA}ij \equiv \frac{b_{(-i)j} - b_j}{\hat{\sigma}(b_j)} \ , \tag{7.9}$$ {eq:dfbeta}

where $\hat{\sigma}(b_j)$ is the estimated standard error of b_j. With k regressors, there are $k + 1$ sets of DFBETAs, which makes their examination burdensome. Graphical displays ease this burden, as do various summary measures considered below.

The most widely used summary of the overall influence of observation i on the estimated regression coefficients is ***Cook's distance***, which measures the average squared distance between $\boldsymbol{b}$ for all the data and $\boldsymbol{b}_{(-i)}$ estimated without observation i. It is defined as

$$C_i \equiv (\boldsymbol{b} - \boldsymbol{b}_{(-i)})^\mathsf{T}\ \boldsymbol{X}^\mathsf{T}\boldsymbol{V}\boldsymbol{X}\ (\boldsymbol{b} - \boldsymbol{b}_{(-i)})/k\hat{\sigma}^2 \ .$$

However, Pregibon (1981) showed that C_i could be calculated simply as

$$C_i = \frac{r_i^2 h_{ii}}{k(1 - h_{ii})^2} \ , \tag{7.10}$$ {eq:cookd2}

where $r_i = y_i - \hat{p}_i/\sqrt{v_{ii}(1 - h_{ii})}$ is the ith standardized Pearson residual and v_{ii} is the ith diagonal element of $\boldsymbol{V}$. Rules of thumb for noticeably "large" values of Cook's D are only rough indicators, and designed so that only "noteworthy" observations are nominated as unusually influential. One common cutoff for an observation to be treated as influential is $C_i > 1$. Others refer the values of C_i to a χ^2_k or $F_{k,n-k}$ distribution.

Another commonly used summary statistic of overall influence is the ***DFFITS*** statistic, a standardized measure of the difference between the predicted value $\hat{y}_i$ using all the data and the predicted value $\hat{y}_{(-i)}$ calculated omitting the ith observation.

$$\text{DFFITS}_i = \frac{\hat{y}_i - \hat{y}_{(-i)}}{\hat{\sigma}_{(-i)}\sqrt{h_{ii}}} \ ,$$

where $\hat{\sigma}_{(-i)}$ is the estimated standard error with the ith observation deleted. For computation, DFFITS can be expressed in terms of the standardized Pearson residual and leverage as

$$\text{DFFITS}_i = r_i\sqrt{\frac{h_{ii}}{(1 - h_{ii})}\frac{v_{ii}}{v_{(-ii)}}} \ . \tag{7.11}$$ {eq:dffits}

From Eqn. (7.10) and Eqn. (7.11) it can be shown that Cook's distance is nearly the square of DFFITS divided by k,

$$C_i = \frac{v^2_{(-ii)}}{v^2_{ii}}\frac{\text{DFFITS}_i^2}{k} \ . \tag{7.12}$$ {eq:cook-dffits}

Noteworthy values of DFFITS are often nominated by the rule-of-thumb $\text{DFFITS}_i > 2$ or $3\sqrt{k/n - k}$.

In R, these influence measures are calculated for a fitted "glm" model using `cooks.distance()` and `dffits()`. A convenience function, `influence.measures()` gives a tabular display showing the DFBETA_{ij} for each model variable, DFFITS, Cook's distances and the diagonal elements of the hat matrix. Cases which are influential with respect to any of these measures are marked with an asterisk.[19]

[19] See `help(influence.measures)` for the description of all of these functions for residuals, leverage and influence diagnostics in generalized linear models.

Beyond printed output of these numerical summaries, plots of these measures can shed light on potential problems due to influential or other noteworthy cases. By highlighting them, such plots provide the opportunity to determine if and how any of these affect your conclusions, or to take some corrective action.

Basic diagnostic plots are provided by the `plot()` method for a "glm" model object. These are easy to do, but the results for discrete response data are often unsatisfactory. The car package contains a variety of enhanced and extended functions for model diagnostic plots. We illustrate some of these in the examples below.

{ex:donner2}

EXAMPLE 7.13: Donner Party

This example re-visits the data on the Donner Party examined in Example 7.9. For illustrative purposes, we consider the influence measures and diagnostic plots for one specific model, the model `donner.mod3`, that included a quadratic effect of age and a main effect of sex, but no interaction.

Details of all the diagnostic measures for a given model including the DFBETAs for individual coefficients can be obtained using `influence.measures`. This can be useful for custom plots not provided elsewhere (see Example 7.14).

```
> infl <- influence.measures(donner.mod3)
> names(infl)

[1] "infmat" "is.inf" "call"
```

The `summary()` method for the "infl" object prints those observations considered noteworthy on one or more of these statistics, as indicated by a "*" next to the value.

```
> summary(infl)

Potentially influential observations of
 glm(formula = survived ~ poly(age, 2) + sex, family = binomial,      data = Donner) :

                    dfb.1_ dfb.p(,2)1 dfb.p(,2)2 dfb.sxMl dffit   cov.r   cook.d hat
Breen, Patrick        0.08   0.65       0.56       0.23     0.69_*  0.93    0.32   0.09
Donner, Elizabeth    -0.26  -0.34      -0.22       0.12    -0.40    1.15_*  0.03   0.14_*
Graves, Elizabeth C. -0.24  -0.37      -0.26       0.10    -0.42    1.20_*  0.03   0.16_*
```

The simplest overview of adequacy of a fitted model is provided by the `plot()` method for a "glm" (or "lm") object, which can produce up to six different diagnostic plots. Among them, we consider the residual-leverage graph (number 5) being the most useful for assessing influential observations, plotting residuals against leverages. An extended version is produced by the function `influencePlot()` in the car package, which additionally uses the size (area) of the plotting symbol to also show the value of Cook's D as shown in Figure 7.24. Like other diagnostic plots in car , it is considerably more general than illustrated here, because it allows for different `id.methods` to label noteworthy points, including `id.method = "identify"` for interactive point identification by clicking with the mouse. The `id.n` argument works differently than with `plot()`, because it selects the most extreme `id.n` observations on *each* of the studentized residual, hat value and Cook's D, and labels all of these.

```
> op <- par(mar = c(5, 4, 1, 1) + .1, cex.lab = 1.2)
> res <- influencePlot(donner.mod3, id.col = "blue", scale = 8, id.n = 2)
>
> k <- length(coef(donner.mod3))
> n <- nrow(Donner)
> text(x = c(2, 3) * k / n, y = -1.8, c("2k/n", "3k/n"), cex = 1.2)
```

Conveniently, `influencePlot()` returns a data frame containing the influence statistics for the points identified in the plot (`res` in the call above). We can combine this with the data values to help learn why these points are considered influential.

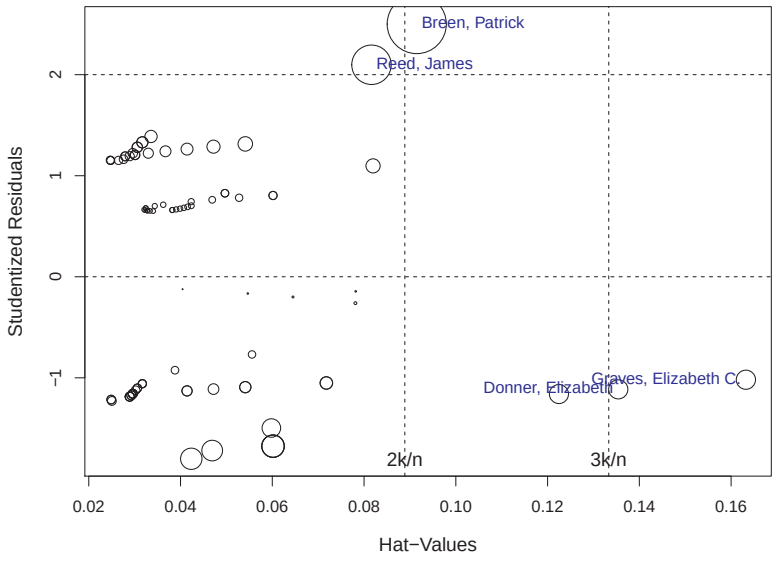


Figure 7.24: Influence plot (residual vs. leverage) for the Donner data model, showing Cook's D as the size of the bubble symbol. Horizontal and vertical reference lines show typical cutoff values for noteworthy residuals and leverage.

{fig:donner2-inflplot}

```
> # show data together with diagnostics for influential cases
> idx <- which(rownames(Donner) %in% rownames(res))
> cbind(Donner[idx,2:4], res)

                     age    sex survived StudRes     Hat  CookD
Breen, Patrick        51   Male      yes   2.501 0.09148 0.5688
Donner, Elizabeth     45 Female       no  -1.114 0.13541 0.1846
Graves, Elizabeth C.  47 Female       no  -1.019 0.16322 0.1849
Reed, James           46   Male      yes   2.098 0.08162 0.3790
```

We can see that Patrick Breen and James Reed[20] are unusual because they were both older men who survived, and have large positive residuals; Breen is the most influential by Cook's D, but this value is not excessively large. The two women were among the older women who died. They are selected here because they have the largest hat values, meaning they are unusual in terms of the distribution of age and sex, but they are not particularly influential in terms of Cook's D.

A related graphical display is the collection of index plots provided by `influenceIndexPlot()` in car , which plots various influence diagnostics against the observation numbers in the data. The `id.n` argument here works to label that number of the most extreme observations *individually* for each measure plotted. The following call produces Figure 7.25.

```
> influenceIndexPlot(donner.mod3, vars=c("Cook", "Studentized", "hat"),
+                    id.n=4)
```

In our opinion, *separate* index plots are often less useful than combined plots such as the leverage-influence plot that shows residuals, leverage and Cook's D together. However, the car version in Figure 7.25 does that too, and allows us to consider how unusual the labeled observations are both individually and in combination.

[20] Breen and Reed, both born in Ireland, were the leaders of their family groups. Among others, both kept detailed diaries of their experiences, from which most of the historical record derives. Reed was also the leader of two relief parties sent out to find rescue or supplies over the high Sierra mountains, so it is all the more remarkable that he survived.

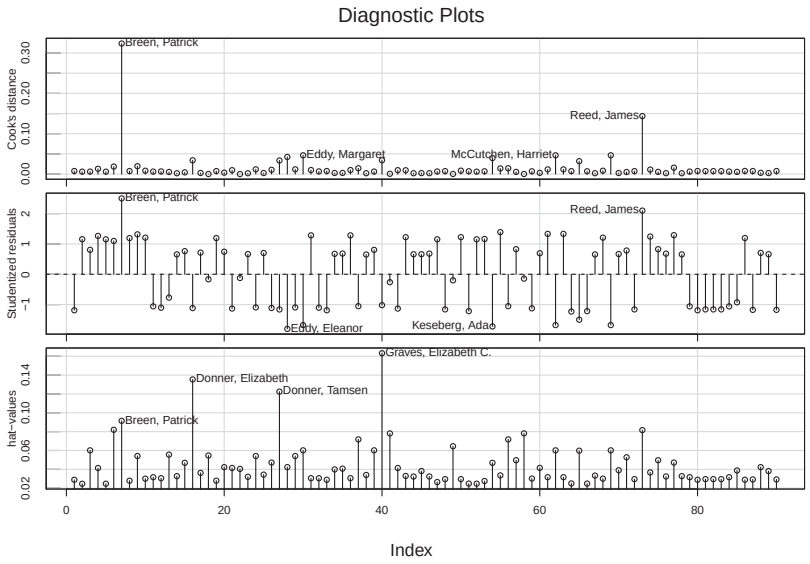


Figure 7.25: Index plots of influence measures for the Donner data model. The four most extreme observations on each measure are labeled. {fig:donner2-indexinfl}

△

{ex:icu2}

EXAMPLE 7.14: Death in the ICU

In Example 7.11 we examined several models to account for death in the *ICU* data set. We continue this analysis here, with a focus on the simple main effects model, `icu.glm2`, for which the fitted logits were shown in Figure **??**. For ease of reference, we restate that model here:

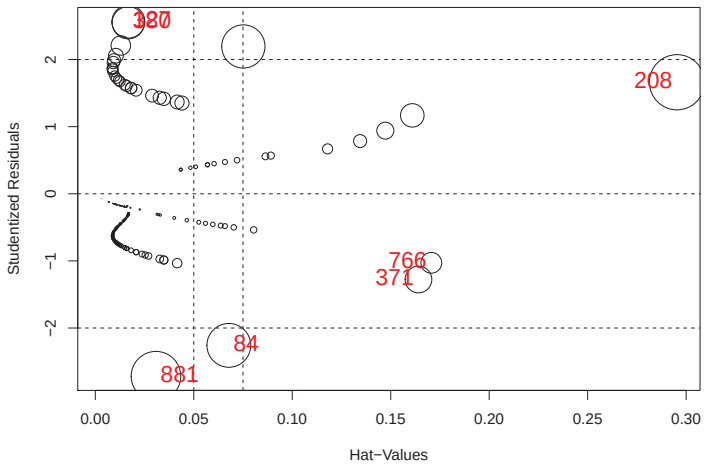
```
> icu.glm2 <- glm(died ~ age + cancer  + admit + uncons,
+                 data = ICU, family = binomial)
```

The plot of residual vs. leverage for this model is shown in Figure 7.26.

```
> library(car)
> res <- influencePlot(icu.glm2, id.col  ="red", scale = 8, id.cex = 1.5, id.n = 3)
```

Details for the cases identified in the figure are shown below, again using `rownames(res)` to select the relevant observations from the *ICU* data.

```
> idx <- which(rownames(ICU) %in% rownames(res))
> cbind(ICU[idx, c("died", "age", "cancer", "admit", "uncons")], res)

    died age cancer admit uncons StudRes     Hat  CookD
84    No  59      -  Emerg Uncons  -2.258 0.06781 0.3626
371   No  46 Cancer  Emerg      -  -1.277 0.16408 0.2210
766   No  31 Cancer  Emerg      -  -1.028 0.17062 0.1719
881   No  89      -  Emerg Uncons  -2.718 0.03081 0.4106
127  Yes  19      -  Emerg      -   2.565 0.01679 0.2724
208  Yes  70      -      - Uncons   1.662 0.29537 0.4568
380  Yes  20      -  Emerg      -   2.548 0.01672 0.2668
```



{fig:icu2-inflplot} **Figure 7.26:** Influence plot for the main effects model for the ICU data

None of the cases are particularly influential on the model coefficients overall: the largest Cook's D is only 0.45 for case 208. This observation also has the largest hat value. It is unusual on the predictors in this sample: a 70 year old man without cancer, admitted on an elective basis, who nonetheless died. However, this case is also highly unusual in having been unconscious on admission for an elective procedure, and signals that there might have been a coding error or other anomaly for this observation.

Another noteworthy observation identified here is case 881, an 89 year old male, admitted unconscious as an emergency; this case is poorly predicted because he survived. Similarly, two other cases (127, 380) with large studentized residuals are poorly predicted because they died, although they were young, did not have cancer, and conscious at admission. However, these cases have relatively small Cook's D values. From this evidence we might conclude that, case 208 bears further scrutiny, but none of these cases greatly affects the model, its coefficients, or interpretation.

For comparison with Figure 7.26, the related index plot of these measures is shown in Figure 7.27.

```
> influenceIndexPlot(icu.glm2, vars = c("Cook", "Studentized", "hat"), id.n = 4)
```

Cook's D and DFFITS are *overall* measures of the total influence that cases have on the regression coefficients and fitted values respectively. It might be that some cases have a large impact on some individual regression coefficients, but don't appear particularly unusual in these aggregate measures.

One way to study this is to make plots of the DFBETA$_{ij}$ statistics. Such plots are not available (as far as we know) in R packages, but it is not hard to construct them from the result returned by `influence.measures()`. To do this, we select the appropriate columns from the `infmat` component returned by that function.

```
> infl <- influence.measures(icu.glm2)
> dfbetas <- data.frame(infl$infmat[,2:5])
> colnames(dfbetas) <- c("dfb.age", "dfb.cancer", "dfb.admit", "dfb.uncons")
> head(dfbetas)

     dfb.age dfb.cancer dfb.admit dfb.uncons
```

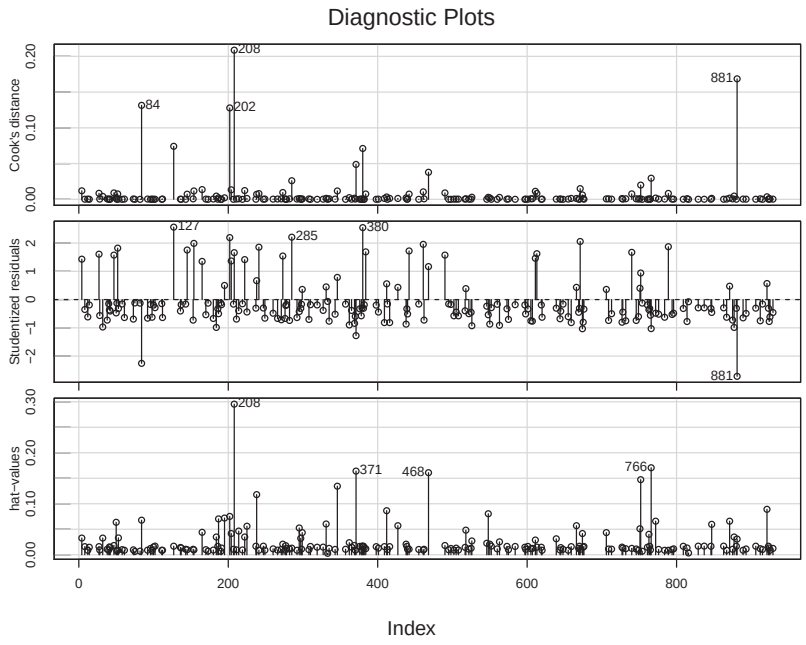


Figure 7.27: Index plots of influence measures for the ICU data model. The four most extreme observations on each measure are labeled. {fig:icu2-infl-index}

```
8    0.047340   0.013418  0.004067   0.009254
12   0.018988   0.018412 -0.004174   0.018106
14  -0.001051   0.014882  0.026278   0.005555
28   0.031562   0.018424 -0.001511   0.016640
32  -0.164084   0.003788 -0.036505   0.023488
38  -0.021525   0.016539 -0.011937   0.020803
```

To illustrate this idea, plotting an individual column of `dfbetas` using `type = "h"` gives an index plot against the observation number. This is shown in Figure 7.28 for the impact on the coefficient for age. The lines and points are colored blue or red according to whether the patient lived or died. Observations for which the $|\text{DFBETA}_{\text{age}}| > 0.2$ (an arbitrary value) are labeled.

```
> cols <- ifelse(ICU$died == "Yes", "red", "blue")
> op <- par(mar = c(5, 5, 1, 1) + .1)
> plot(dfbetas[,1], type = "h", col = cols,
+      xlab = "Observation index",
+      ylab = expression(Delta * beta[Age]),
+      cex.lab = 1.3)
> points(dfbetas[,1], col = cols)
> # label some points
> big <- abs(dfbetas[,1]) > .25
> idx <- 1 : nrow(dfbetas)
> text(idx[big], dfbetas[big, 1], label = rownames(dfbetas)[big],
+      cex = 0.9, pos = ifelse(dfbetas[big, 1] > 0, 3, 1),
+      xpd = TRUE)
> abline(h = c(-.25, 0, .25), col = "gray")
> par(op)
```

None of the labeled points here are a cause for concern, since the standardized DFBETAs are all

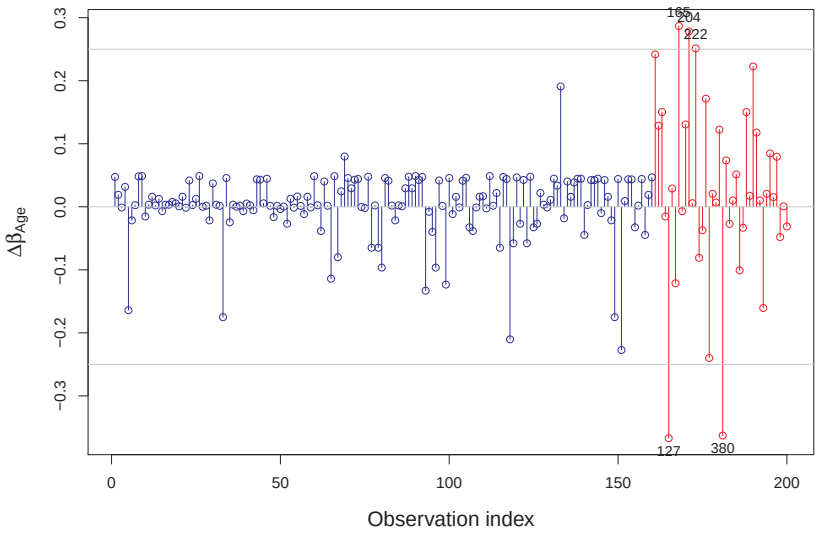


Figure 7.28: Index plot for DFBETA (Age) in the ICU data model. The observations are colored blue or red according to whether the patient lived or died.

{fig:icu2-dbage}

relatively small. However, the plot shows that patients who died have generally larger impacts on this coefficient.

An interesting alternative to individual index plots is a scatterplot matrix (Figure 7.29), that shows the pairwise changes in the regression coefficients for the various predictors. Here we use `scatterplotMatrix()` from car that offers features for additional plot annotations, including identifying the most unusual points in each pairwise plot. In each off-diagonal panel, a 95% data ellipse and linear regression line helps to show the marginal relationship between the two measures and highlight why the labeled points are atypical in each plot.[21]

```
> scatterplotMatrix(dfbetas, smooth = FALSE, id.n = 2,
+   ellipse = TRUE, levels = 0.95, robust = FALSE,
+   diagonal = "histogram",
+   groups = ICU$died, col = c("blue", "red"))
```

As Figure 7.29 illustrates, the *joint* effect of observations on *pairs* of coefficients is more complex than is apparent from the univariate views that appear in the plots along the diagonal. The DFBETAs for `cancer`, `admit` and `uncons` are all extremely peaked, yet the pairwise plots show considerable structure. The points identified would be worthy of further study.

△

7.5.3 Other diagnostic plots*

{sec:logist-partial}

The graphical methods described in this section are relatively straight-forward indicators of the adequacy of a particular model, with a specified set of predictors, each expressed in a given way. More sophisticated methods have also been proposed, which focus on the need to include a particular predictor and whether its relationship is linear. These include the ***component-plus-residual plot***, the ***added-variable plot***, and the ***constructed variable plot***, which are all analogous to techniques developed in OLS.

[21] This plot uses the `id.method = "mahal"` method to label the most extreme observations according to the Mahalanobis distance of each point from the centroid in the plot.

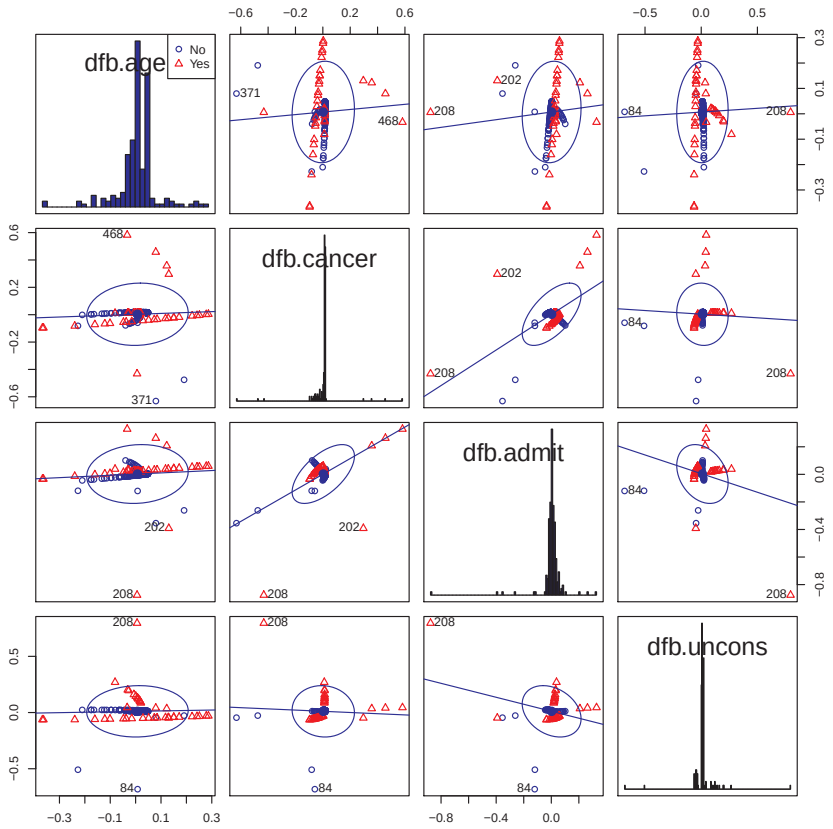


Figure 7.29: Scatterplot matrix for DFBETAs from the model for the ICU data. Those who lived or died are shown with blue circles and red triangles, respectively. The diagonal panels show histograms of each variable.

{fig:icu2-dbscatmat}

7.5.3.1 Component-plus-residual plots

{sec:component-plus-residual}

The ***component-plus-residual plot*** (also called a ***partial residual plot***) proposed originally by Larsen and McCleary (1972) is designed to show whether a given quantitative predictor, $\boldsymbol{x}_j$, included linearly in the model, actually shows a nonlinear relation, requiring transformation. The essential idea is to move the linear term for $\boldsymbol{x}_j$ back into the residual, by calculating the *partial residuals*,

$$\boldsymbol{r}_j^\star = \boldsymbol{r} + \beta_j \boldsymbol{x}_j$$

Then, a plot of $\boldsymbol{r}_j^\star$ against $\boldsymbol{x}_j$ will have the same slope, β_j, as the full model including it among other predictors. However, any non-linear trend will be shown in the pattern of the points, usually aided by a smoothed non-parametric curve.

As adapted to logistic regression by Landwehr *et al.* (1984), the partial residual for variable $\boldsymbol{x}_j$ is defined as

$$\boldsymbol{r}_j^\star = \boldsymbol{V}^{-1}\boldsymbol{r} + \beta_j \boldsymbol{x}_j$$

The partial residual plot is then a plot of $\boldsymbol{r}_j^\star$ against $\boldsymbol{x}_j$, possibly with the addition of a smoothed lowess curve (Fowlkes, 1987) and a linear regression line to aid interpretation. The linear regression of the partial residuals on $\boldsymbol{x}_j$ has the same slope, β_j, as in the full model.

If $\boldsymbol{x}_j$ affects the binary response linearly, the plot should be approximately linear with a slope approximately equal to β_j. A nonlinear plot suggests that x_j needs to be transformed, and the shape of the relation gives a rough guide to the required transformation. For example, a parabolic shape would suggest a term in $\boldsymbol{x}_j^2$. These plots complement the conditional data plots described earlier (Section 7.3.1), and are most useful when there several quantitative predictors, so that it is more convenient and sensible to examine their relationships individually.

The car package implements these plots in the `crPlots()` and `crPlot()` functions. They also work for models with factor predictors (using parallel boxplots for the factor levels) but not for those with interaction terms.

{ex:donner3}

EXAMPLE 7.15: Donner Party

In Example 7.13, we fit several models for the Donner Party data, and we recall two here to illustrate component-plus-residual plots. Both assert additive effects of age and sex, but the model `donner.mod3` allows a quadratic effect of age.

```
> donner.mod1 <- glm(survived ~ age + sex, data = Donner, family = binomial)
> donner.mod3 <- glm(survived ~ poly(age, 2) + sex, data = Donner, family = binomial)
```

Had we not made exploratory plots earlier (Example 7.13), and naively fit only the linear model in age, `donner.mod1`, we could use `crPlots()` to check for a non-linear relationship of survival with age as follows, giving Figure 7.30.

```
> crPlots(donner.mod1, ~age, id.n=2)
```

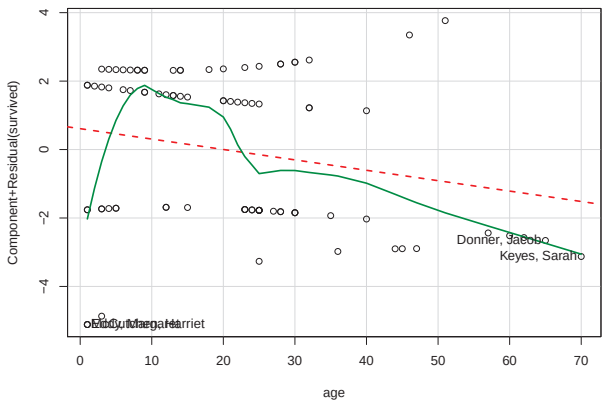


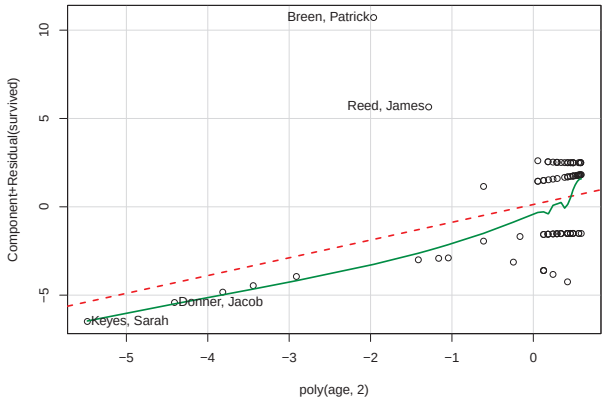
Figure 7.30: Component-plus-residual plot for the simple additive linear model, `donner.mod1`. The dashed red line shows the slope of age in the full model; the smoothed green curve shows a loess fit with span = 0.5.

{fig:donner-cr1}

The smoothed loess curve in this plot closely resembles the trend we saw in the conditional plot for age by sex (Figure 7.16), suggesting the need to include a non-linear term for age. The points identified in this plot, by default, are those with either the most extreme x values (giving them high leverage) or the largest absolute Pearson residuals in the full model. The four structured bands of points in the plot correspond to the combinations of sex and survival.

For comparison, you can see the result of allowing for a non-linear relationship in age in a partial residual plot for the model `donner.mod.3` that includes the effect `poly(age, 2)` for age. Note that the syntax of the `crPlots()` function requires that you specify a *term* in the model, rather than just a predictor variable.

```
> crPlots(donner.mod3, ~poly(age,2), id.n=2)
```



{fig:donner-cr2} **Figure 7.31:** Component-plus-residual plot for the non-linear additive model, `donner.mod3`

Except possibly at the extreme right, this plot (Figure 7.31) shows no indication of a (further) non-linear relationship.

△

7.5.3.2 Added-variable plots

Added-variable plots (Cook and Weisberg, 1999, Wang, 1985) (also called ***partial-regression plot***s) are another important tool for diagnosing problems in logistic regression and other linear or generalized linear models. These are essentially plots, for each $\boldsymbol{x}_i$, of an adjusted response, $\boldsymbol{y}_i^\star = \boldsymbol{y} \,|\, \text{others}_i$, against an adjusted predictor, $\boldsymbol{x}_i^\star = \boldsymbol{x}_i \,|\, \text{others}_i$, where $\text{others}_i = \boldsymbol{X} \notin \boldsymbol{x}_i \equiv \boldsymbol{X}^{(-i)}$ indicates all other predictors excluding $\boldsymbol{x}_i$. As such, they show the *conditional* relationship between the response and the predictor $\boldsymbol{x}_i$, controlling for, or adjusting for, all other predictors. Here, $\boldsymbol{y}_i^\star$ and $\boldsymbol{x}_i^\star$ represent respectively the residuals from the regressions of $\boldsymbol{y}$ and $\boldsymbol{x}_i$ on all the other xs excluding $\boldsymbol{x}_i$.

It might seem from this description that each added-variable plot requires two additional auxiliary logistic regressions to calculate the residuals $\boldsymbol{y}_i^\star$ and $\boldsymbol{x}_i^\star$. However, Wang (1985) showed that the added-variable plot may be constructed by following the logistic regression for the model $\boldsymbol{y} \sim \boldsymbol{X}^{(-i)}$ with one weighted least squares regression of $\boldsymbol{x}_i$ on $\boldsymbol{X}^{(-i)}$ to find the residual part, $\boldsymbol{x}_i^\star$, of $\boldsymbol{x}$ not predicted by the other regressors.

Let $\boldsymbol{r}$ be the vector of Pearson residuals from the initial logistic fit of $\boldsymbol{y}$ on the variables in $\boldsymbol{X}^{(-i)}$, and let $\boldsymbol{H}$ and $\boldsymbol{V} = \text{diag}\,[\hat{\boldsymbol{p}}(1-\hat{\boldsymbol{p}})]$ be the hat matrix and $\boldsymbol{V}$ matrix from this analysis. Then, the added-variable plot is a scatterplot of the residuals $\boldsymbol{r}$ against the $\boldsymbol{x}_i$-residuals,

$$\boldsymbol{x}_i^\star = (\boldsymbol{I} - \boldsymbol{H})\boldsymbol{V}^{1/2}\boldsymbol{x} \ .$$

There are several important uses of added-variable plots:

First, *marginal* plots of the response variable $\boldsymbol{y}$ against the predictor variables $\boldsymbol{x}_i$ can conceal or misrepresent the relationships in a model including several predictors together due to correlations or associations among the predictors. This problem is compounded by the fact that graphical methods for discrete responses (boxplots, mosaic plots) cannot easily show influential observations or non-linear relationships. Added-variable plots solve this problem by plotting the residuals, $\boldsymbol{y}_i^\star = \boldsymbol{y} \,|\, \text{others}_i$, which are less discrete than the marginal responses in $\boldsymbol{y}$.

Second, the numerical measures and graphical methods for detecting influential observations described earlier in this section are based on the idea of *single-case deletion*, comparing coefficients or fitted values for the full data, with those that result from deleting each case in turn. Yet, it is well-known (Lawrance, 1995), that sets of two (or more) observations can have ***joint influence***, that greatly exceeds their individual influential. Similarly, the influence of one discrepant point can be offset by another influential point in an opposite direction, a phenomenon called ***masking***. The main cases of joint influence are illustrated in Figure 7.32. Added-variable plots, showing the partial regression for one predictor controlling all others can make such cases visually apparent.

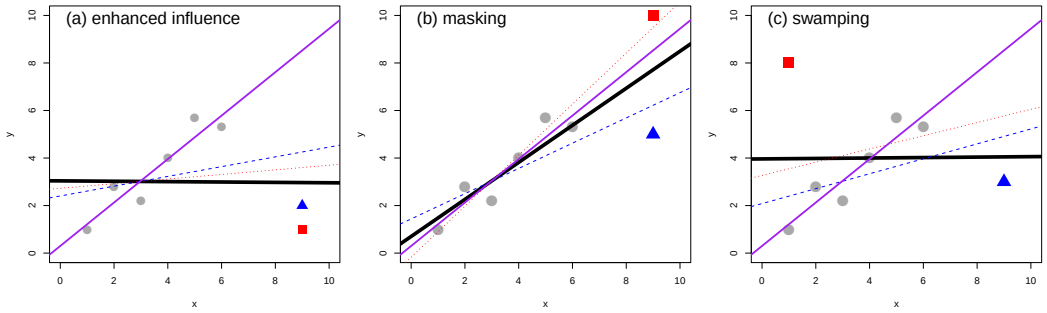


Figure 7.32: Jointly influential points in regression models. In each panel, the thick black line shows the regression of y on x using all the data points. The solid purple line shows the regression deleting *both* the red and blue points and the broken and dotted lines show the regression retaining only the point in its color in addition to the constant gray points. (a) Two points whose joint influence enhance each other; (b) two points where the influence of one is masked by that of the other; (c) two points whose combined influence greatly exceeds the effect of either one individually. {fig:joint}

Finally, given a tentative model using predictors $\boldsymbol{x}$, the added-variable plot for another regressor, z can provide a useful visual assessment of its additional contribution. An overall test could be based on the difference in G^2 for the enlarged model $\text{logit}(\boldsymbol{p}) = \boldsymbol{X\beta}+\gamma\boldsymbol{z}$, compared to the reduced model $\text{logit}(\boldsymbol{p}) = \boldsymbol{X\beta}$. But the added-variable plot shows whether the evidence for including z is spread throughout the sample or confined to a small subset of observations. The regressor z may be a new explanatory variable, or a higher-order term for variable(s) already in the model.

The car package implements these plots with the function `avPlot()` for a single term and `avPlots()` for all terms in a linear or generalized linear model, as shown in the example(s) below. See `http://www.datavis.ca/gallery/animation/duncanAV/` for an animated graphic showing the transition between a marginal plot of the relationship of $\boldsymbol{y}$ to $\boldsymbol{x}$ and the added-variable plot of $\boldsymbol{y}^\star$ to $\boldsymbol{x}^\star$ for the case of multiple linear regression with a quantitative response. {ex:donner4}

EXAMPLE 7.16: Donner Party

The simple additive model `donner.mod1` for the Donner Party data can be used to illustrate some features of added-variable plots. In the call to `avPlots()` below, we use color the plotting symbol to distinguish those who survived vs. died, shape to distinguish men from women.

```
> col <- ifelse(Donner$survived == "yes", "blue", "red")
> pch <- ifelse(Donner$sex == "Male", 16, 17)
> avPlots(donner.mod1, id.n = 2, col = col, pch = pch, col.lines = "darkgreen")
```

These plots have the following properties:

1. The slope in the simple regression of $\boldsymbol{y}_i^\star$ on $\boldsymbol{x}_i^\star$ is the same as the partial coefficient β_i in the full multiple regression model including both predictors here (or all predictors in general).

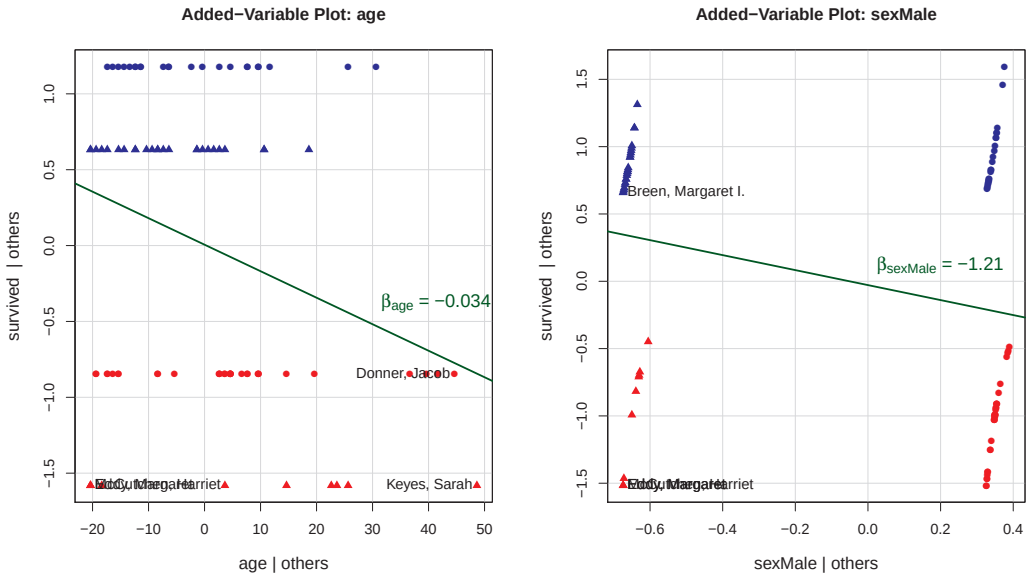


Figure 7.33: Added-variable plots for age (left) and sex (right) in the Donner Party main effects model. Those who survived are shown in blue; those who died in red. Men are plotted with filled circles; women with filled triangles.

{fig:donner4-avp}

2. The residuals from this regression line are the same as the residuals in the full model.

3. Because the response, `survived`, is binary, the vertical axis $\boldsymbol{y}^{\star}_{\text{age}}$ in the left panel for `age` is the part of the logit for survival that cannot be predicted from `sex`. Similarly, the vertical axis in the right panel is the part of survival that cannot be predicted from `age`. This property allows the clusters of points corresponding to discrete variables to be seen more readily, particularly if they are distinguished by visual attributes such as color and shape, as in Figure 7.33.

△

{ex:icu3}

EXAMPLE 7.17: Death in the ICU

We illustrate some of the uses of added-variable plots using the main effects model, `icu.glm2`, predicting death in the ICU from the variables `age`, `cancer`, `admit` and `uncons`.

To see why marginal plots of the discrete response against each predictor are often unrevealing for the purpose of model assessment, consider the collection of plots in Figure 7.34 showing the default plots (spineplots) for the factor response, `died` against each predictor. These show the marginal distribution of each predictor by the widths of the bars, and highlight the proportion who died by color. Such plots are useful for some purposes, but not for assessing the adequacy of the fitted model.

```
> plot(died ~ age, data = ICU, col = c("lightblue", "pink"))
> plot(died ~ cancer, data = ICU, col = c("lightblue", "pink"))
> plot(died ~ admit, data = ICU, col = c("lightblue", "pink"))
> plot(died ~ uncons, data = ICU, col = c("lightblue", "pink"))
> par(op)
```

The added-variable plot for this model is shown in Figure 7.35. In each plot, the solid red line shows the partial slope, β_j for the focal predictor, controlling for all others.

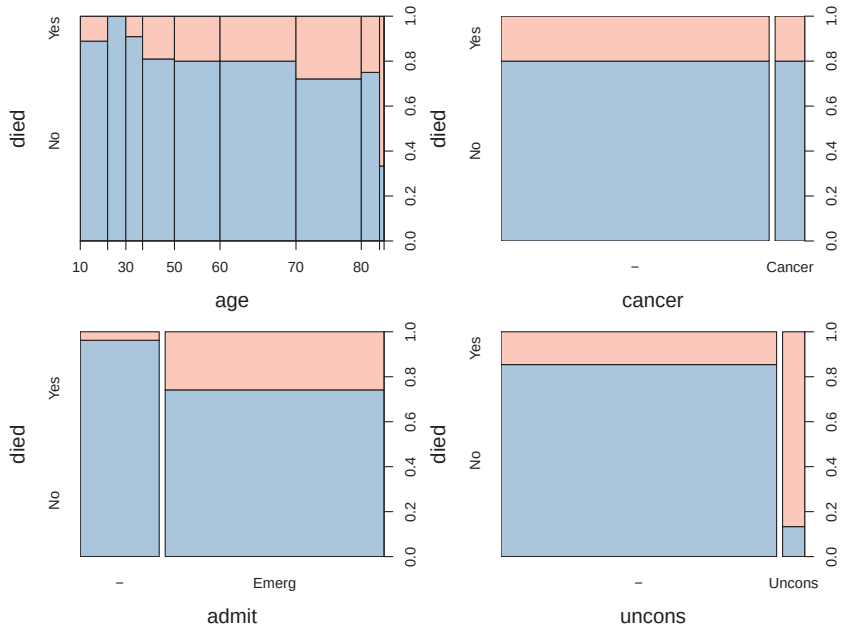


Figure 7.34: Marginal plots of the response `died` against each of the predictors in the model `icu.glm2` for the *ICU* data

{fig:icu3-marginal}

```
> pch <- ifelse(ICU$died=="No", 1, 2)
> avPlots(icu.glm2, id.n=2, pch=pch, cex.lab=1.3)
```

The labeled points in each panel use the default `id.method` for `avPlots()`, selecting those with either large absolute model residuals or extreme $x_i^\star$ residuals, given all other predictors. Cases 127 and 881, identified earlier as influential stand out in all these plots.

Next, we illustrate the use of added-variable plots for checking the effect of influential observations on the decision to include an additional predictor in some given model. In the analysis of the *ICU* data using model selection methods, the variable `systolic` (systolic blood pressure at admission) was nominated by several different procedures. Here we take a closer look at the evidence for inclusion of this variable in a predictive model. We fit a new model adding `systolic` to the others and test the improvement with a likelihood ratio test:

```
> icu.glm2a <- glm(died ~ age + cancer  + admit + uncons + systolic,
+                  data = ICU, family = binomial)
> anova(icu.glm2, icu.glm2a, test = "Chisq")

Analysis of Deviance Table

Model 1: died ~ age + cancer + admit + uncons
Model 2: died ~ age + cancer + admit + uncons + systolic
  Resid. Df Resid. Dev Df Deviance Pr(>Chi)
1       195        139
2       194        136  1     3.52    0.061 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

So, the addition of systolic blood pressure is nearly significant at the conventional $\alpha = 0.05$ level. The added-variable plot for this variable in Figure 7.36 shows the strength of evidence for its contribution, above and beyond the other variables in the model, as well as the partial leverage and influence of individual points.

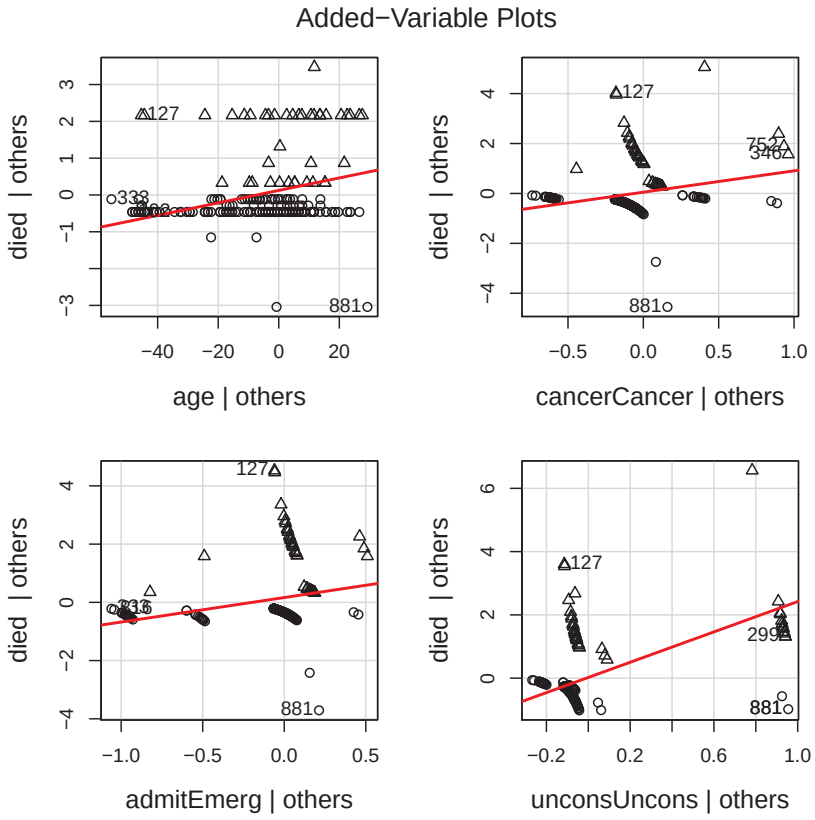


Figure 7.35: Added-variable plots for the predictors in the model for the ICU data. Those who died and survived are shown by triangles (△) and circles (◯) respectively. {fig:icu3-avp1}

```
> avPlot(icu.glm2a, "systolic", id.n = 3, pch = pch)
```

In this plot, cases 331 and 921 have high partial leverage, but they are not influential. Case 84, however, has high leverage and a large residual, so is possibly influential on the evidence for inclusion of `systolic` in the model. Note also that the partial regression line in this plot nicely separates nearly all the patients who died from those who survived.

△

7.6 Chapter summary

{sec:ch07-summary}

- Model-based methods for categorical data provide confidence intervals for parameters and predicted values for observed and unobserved values of the explanatory variables. Graphical displays of predicted values help us to interpret the fitted relations by smoothing a discrete response.
- The logistic regression model (Section 7.2) describes the relationship between a categorical response variable, usually dichotomous, and a set of one or more quantitative or discrete explanatory variables (Section 7.3) It is conceptually convenient to specify this model as a linear model predicting the log odds (or logit) of the probability of a success from the explanatory variables.

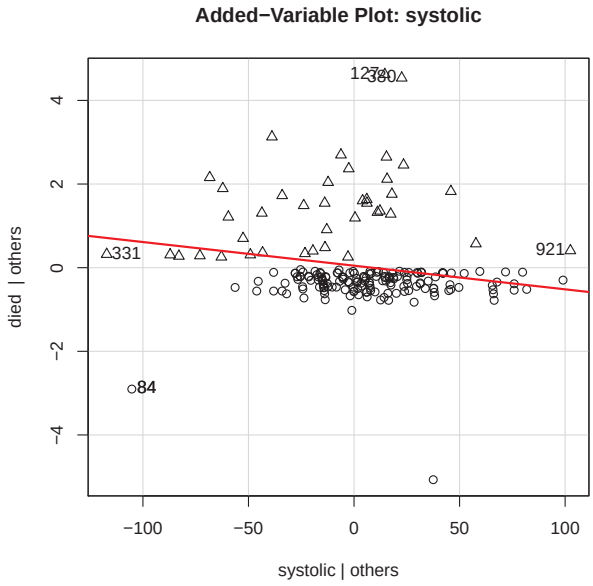


Figure 7.36: added-variable plot for the effect of adding systolic blood pressure to the main effects model for the ICU data. {fig:icu3-avp2}

- The relationship between a discrete response and a quantitative predictor may be explored graphically by plotting the binary observations against the predictor with some smoothed curve(s), either parametric or non-parametric, possibly stratified by other predictors.
- For both quantitative and discrete predictors, the results of a logistic regression are most easily interpreted from full-model plots of the fitted values against the predictors, either on the scale of predicted probabilities or log odds (Section 7.3.2). In these plots, confidence intervals provide a visual indication of the precision of the predicted results.
- When there are multiple predictors and/or higher-order interaction terms, effect plots (Section 7.3.3) provide an important method for constructing simplified displays, focusing on the higher-order terms in a given model.
- Influence diagnostics (Section 7.5) assess the impact of individual cases or groups on the fitted model, predicted values, and the coefficients of individual predictors. Among other displays, plots of residuals against leverage showing Cook's D are often most useful.
- Other diagnostic plots (Section 7.5.3) include component-plus-residual plots, that are useful for detecting non-linear relationships for a quantitative predictor, and added-variable plots, that show the partial relations of the response to a given predictor, controlling or adjusting for all other predictors.

7.7 Lab exercises

{lab:7.1} {sec:ch07-exercises}

Exercise 7.1 Arbuthnot's data on the sex ratio of births in London was examined in Example 3.1. Use a binomial logistic regression model to assess whether the proportion of male births varied with the variables `Year`, `Plague` and `Mortality` in the *`Arbuthnot`* data set. Produce effect plots for the terms in this model. What do you conclude?

{lab:7.2}

Exercise 7.2 For the Donner Party data in *Donner*, examine Grayson's 1990 claim that survival in the Donner Party was also mediated by the size of the family unit. This takes some care, because the `family` variable in the *Donner* data is a simplified grouping based on the person's name and known alliances among families from the historical record. Use the following code to compute a `family.size variable` from each individual's last name:

```
> data("Donner", package="vcdExtra")
> Donner$survived <- factor(Donner$survived, labels=c("no", "yes"))
> # use last name for family
> lame <- strsplit(rownames(Donner), ",")
> lame <- sapply(lame, function(x) x[[1]])
> Donner$family.size <- as.vector(table(lname)[lname])
```

(a) Choose one of the models (`donner.mod4`, `donner.mod6`) from Example 7.9 that include the interaction of age and sex and non-linear terms in age. Fit a new model that adds a main effect of `family.size`. What do you conclude about Grayson's claim?
(b) Produce an effect plot for this model.
(c) Continue, by examining whether the effect of family size can be taken as linear, or whether a non-linear term should be added.

{lab:7.3}

Exercise 7.3 Use component+residual plots (Section 7.5.3) to examine the additive model for the *ICU* data given by

```
> icu.glm2 <- glm(died ~ age + cancer  + admit + uncons,
+                 data=ICU, family=binomial)
```

(a) What do you conclude about the linearity of the (partial) relationship between age and death in this model?
(b) An alternative strategy is to allow some non-linear relation for age in the model using a quadratic (or cubic) term like `poly(age, 2)` (or `poly(age, 3)`) in the model formula. Do these models provide evidence for a non-linear effect of age on death in the ICU?

{lab:7.4}

Exercise 7.4 Explore the use of other marginal and conditional plots to display the relationships among the variables predicting death in the ICU in the model `icu.glm2`. For example, you might begin with a marginal `gpairs()` plot showing all bivariate marginal relations, something like this:

```
> library(gpairs)
> gpairs(ICU[,c("died", "age", "cancer", "admit", "uncons")],
+   diag.pars=list(fontsize=16, hist.color="lightgray"),
+   mosaic.pars=list(gp=shading_Friendly,
+                    gp_args=list(interpolate=1:4)))
```

{lab:caesar-logis} {lab:7.5}

Exercise 7.5 The data set *Caesar* in vcdExtra gives a 3×2^3 frequency table classifying 251 women who gave birth by Caesarian section by `Infection` (three levels: none, Type 1, Type2) and `Risk`, whether `Antibiotics` were used and whether the Caesarian section was `Planned` or not. `Infection` is a natural response variable. In this exercise, consider only the binary outcome of infection vs. no infection.

```
> data("Caesar", package="vcdExtra")
> Caesar.df <- as.data.frame(Caesar)
> Caesar.df$Infect <- as.numeric(Caesar.df$Infection %in% c("Type 1", "Type 2"))
```

(a) Fit the main-effects logit model for the binary response `Infect`. Note that with the data in the form of a frequency data frame you will need to use `weights=Freq` in the call to `glm()`. (It might also be convenient to reorder the levels of the factors so that `"No"` is the baseline level for each.)
(b) Use `summary()` or car ::`Anova()` to test the terms in this model.
(c) Interpret the coefficients in the fitted model in terms of their effect on the odds of infection.
(d) Make one or more effects plots for this model, showing separate terms, or their combinations.

{lab:7.6}

Exercise 7.6 The data set *birthwt* in the MASS package gives data on 189 babies born at Baystate Medical Center, Springfield, MA during 1986. The quantitative response is `bwt` (birth weight in grams), and this is also recorded as `low`, a binary variable corresponding to `bwt < 2500` (2.5 Kg). The goal is to study how this varies with the available predictor variables. The variables are all recorded as numeric, so in R it may be helpful to convert some of these into factors and possibly collapse some low frequency categories. The code below is just an example of how you might do this for some variables.

```
> data("birthwt", package="MASS")
> birthwt <- within(birthwt, {
+   race <- factor(race, labels = c("white", "black", "other"))
+         ptd <- factor(ptl > 0)   # premature labors
+         ftv <- factor(ftv)       # physician visits
+         levels(ftv)[-(1:2)] <- "2+"
+         smoke <- factor(smoke>0)
+         ht <- factor(ht>0)
+         ui <- factor(ui>0)
+   })
```

(a) Make some exploratory plots showing how low birth weight varies with each of the available predictors. In some cases, it will probably be helpful to add some sort of smoothed summary curves or lines.
(b) Fit several logistic regression models predicting low birth weight from these predictors, with the goal of explaining this phenomenon adequately, yet simply.
(c) Use some graphical displays to convey your findings.

{lab:7.7}

Exercise 7.7 Refer to Exercise 5.9 for a description of the *Accident* data. The interest here is to model the probability that an accident resulted in death rather than injury from the predictors `age`, `mode` and `gender`. With `glm()`, and the data in the form of a frequency table, you can use the argument `weight=Freq` to take cell frequency into account.

(a) Fit the main effects model, `result=="Died" ~ age + mode + gender`. Use car ::`Anova()` to assess the model terms.
(b) Fit the model that allows all two-way interactions. Use `anova()` to test whether this model is significantly better than the main effects model.
(c) Fit the model that also allows the three-way interaction of all factors. Does this offer any improvement over the two-way model?
(d) Interpret the results of the analysis using effect plots for the two-way model, separately for each of the model terms. Describe verbally the nature of the `age*gender` effect. Which mode of transportation leads to greatest risk of death?

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