Logistic Regression

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Psych 6136

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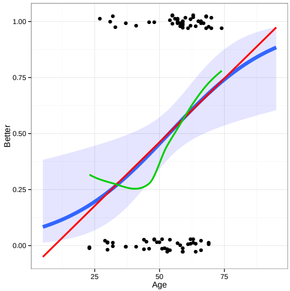

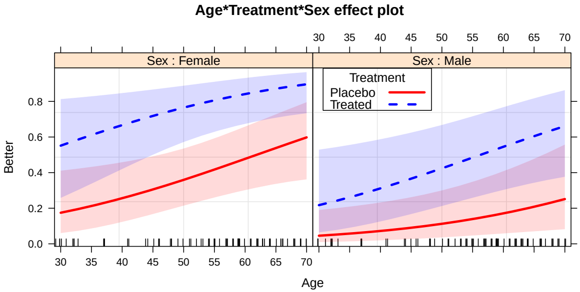

Model-based methods: Overview

Structure

- Explicitly assume some probability distribution for the data, e.g., binomial, Poisson, ...
- Distinguish between the systematic component— explained by the model— and a random component, which is not
- Allow a compact summary of the data in terms of a (hopefully) small number of parameters

Advantages

- Inferences: hypothesis tests *and* confidence intervals
- Methods for model selection: adjust balance between goodness-of-fit and parsimony
- Predicted values give model-smoothed summaries for plotting
- $\Longrightarrow$ Interpret the fitted model graphically

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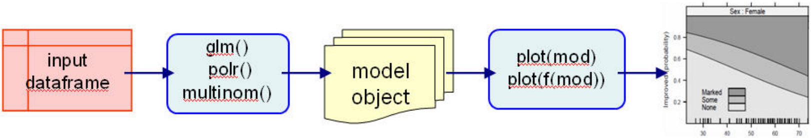
Fitting and graphing: Overview

Object-oriented approach in R:



- Fit model (`obj <- glm(...)`) $\rightarrow$ a model object
- `print(obj)` and `summary(obj)` $\rightarrow$ numerical results
- `anova(obj)` and `Anova(obj)` $\rightarrow$ tests for model terms
- `update(obj)`, `add1(obj)`, `drop1(obj)` for model selection

Plot methods:

- `plot(obj)` often gives diagnostic plots
- Other plot methods:
  - Mosaic plots: `mosaic(obj)` for `"loglm"` and `"glm"` objects
  - Effect plots: `plot(Effect(obj))` for nearly all linear models
  - Influence plots (car): `influencePlot(obj)` for `"glm"` objects

Objects and methods

How this works:

- Model objects have a ”class” attribute:
  - `loglm()`: `"loglm"`
  - `glm()`: `c("glm", "lm")` — inherits also from `lm()`
- Class-specific methods have names like `method.class`, e.g., `plot.glm()`, `mosaic.loglm()`
- Generic functions (`print()`, `summary()`, `plot()` . . .) call the appropriate method for the class

```
arth.mod <- glm(Better ~ Age + Sex + Treatment, data=Arthritis)
class(arth.mod)

## [1] "glm" "lm"
```

Objects and methods

Methods for "glm" objects

```
library(MASS); library(vcdExtra)
methods(class="glm")

##   [1] add1.glm*           addterm.glm*        anova.glm*
##   [4] asGnm.glm*          assoc.glm           confint.glm*
##   [7] cooks.distance.glm* deviance.glm*       drop1.glm*
##  [10] dropterm.glm*       effects.glm*        extractAIC.glm*
##  [13] family.glm*         formula.glm*        gamma.shape.glm*
##  [16] influence.glm*      logLik.glm*         model.frame.glm*
##  [19] modFit.glm          mosaic.glm          nobs.glm*
##  [22] predict.glm         print.glm*          profile.glm*
##  [25] residuals.glm       rstandard.glm*      rstudent.glm*
##  [28] sieve.glm           summarise.glm*      summary.glm
##  [31] vcov.glm*           weights.glm*
##
##    Non-visible functions are asterisked
```

Objects and methods

Some available `plot()` methods:

```
methods("plot")

##  [1] plot.acf*           plot.correspondence* plot.data.frame*
##  [4] plot.decomposed.ts* plot.default         plot.dendrogram*
##  [7] plot.density*       plot.ecdf            plot.factor*
## [10] plot.formula*       plot.function        plot.gnm*
## [13] plot.goodfit*       plot.hclust*         plot.histogram*
## [16] plot.HLtest*        plot.HoltWinters*    plot.isoreg*
## [19] plot.lda*           plot.lm*             plot.loddsratio*
## [22] plot.loglm*         plot.mca*            plot.medpolish*
## [25] plot.mlm*           plot.oddsratio*      plot.ppr*
## [28] plot.prcomp*        plot.princomp*       plot.profile*
## [31] plot.profile.gnm*   plot.profile.nls*    plot.qv*
## [34] plot.ridgelm*       plot.shingle*        plot.spec*
## [37] plot.stepfun        plot.stl*            plot.structable*
## [40] plot.table*         plot.trellis*        plot.ts
## [43] plot.tskernel*      plot.TukeyHSD*       plot.zoo*
##
##    Non-visible functions are asterisked
```

Modeling approaches: Overview

Association models

- **Loglinear models**

(Contingency table form)

[Admit][GenderDept]

[AdmitDept][GenderDept]

[AdmitDept][AdmitGender][GenderDept]

- **Poisson GLMs**

(Frequency data frame)

Freq ~ Admit + Gender*Dept

Freq ~ Admit*Dept + Gender*Dept

Freq ~ Admit*Dept + Admit*Gender + Gender*Dept

- **Ordered variables**

Freq ~ right+left+Diag(right,left)

Freq ~ right+left+Symm(right,left)

Response models

- **Binary response**
- Categorical predictors: Logit models

logit(Admit) ~ 1

logit(Admit) ~ Dept

logit(Admit) ~ Dept + Gender

- Continuous/mixed predictors: Logistic regression models

Pr(Admit) ~ Dept + Age + GRE

- **Polytomous response**
- Ordinal: proportional odds model

Improve ~ Age + Sex + Treatment

- General: multinomial model

WomenWork ~ Kids + HusbandInc

Logistic regression models

Response variable

- Binary response: success/failure, vote: yes/no
- Binomial data: x successes in n trials (grouped data)
- Ordinal response: none $<$ some $<$ severe depression
- Polytomous response: vote Liberal, Tory, NDP, Green

Explanatory variables

- Quantitative regressors: age, dose
- Transformed regressors: $\sqrt{\text{age}}$, log(dose)
- Polynomial regressors: age^2, age^3, $\cdots$ (or better: splines)
- Categorical predictors: treatment, sex (dummy variables, contrasts)
- Interaction regessors: treatment $\times$ age, sex $\times$ age

This is exactly the same as in classical ANOVA, regression models

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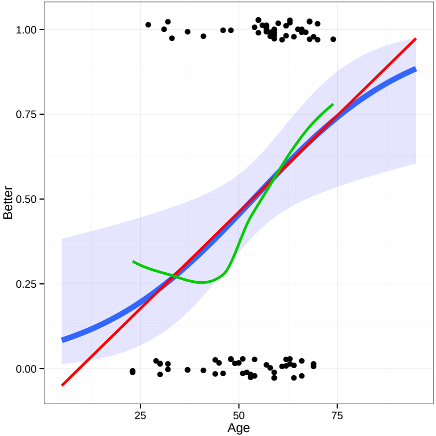
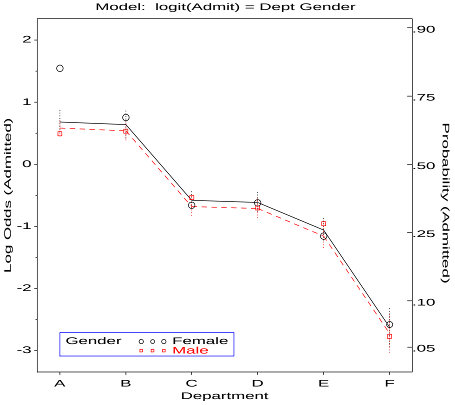
Arthritis treatment data



- The response variable, `Improved` is ordinal: `"None" < "Some" < "Marked"`
- A binary logistic model can consider just `Better = (Improved>"None")`
- Other important predictors: Sex, Treatment
- Main Q: how does treatment affect outcome?
- How does this vary with Age and Sex?
- This plot shows the binary observations, with several model-based smoothings

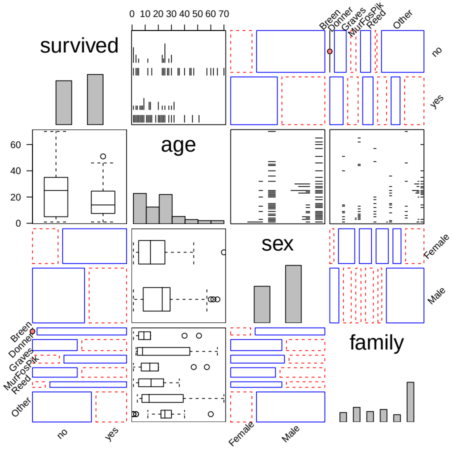
Berkeley admissions data



- Admit/Reject can be considered a binomial response for each Dept and Gender
- Logistic regression here is analogous to an ANOVA model, but for log odds(Admit)
- (With categorical predictors, these are often called logit models)
- Every such model has an equivalent loglinear model form.
- This plot shows fitted logits for the main effects model, `Dept + Gender`

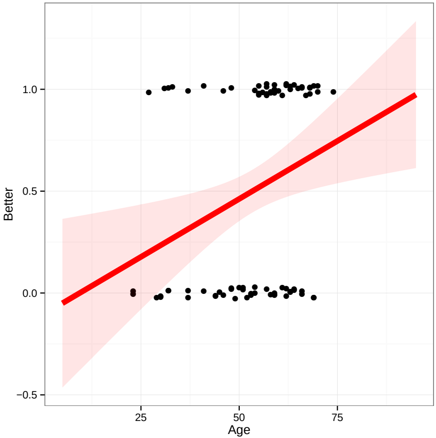
Survival in the Donner Party

- Binary response: `survived`
- Categorical predictors: `sex`, `family`
- Quantitative predictor: `age`
- Q: Is the effect of age linear?
- Q: Are there interactions among predictors?
- This is a generalized pairs plot, with different plots for each pair



Binary response: What's wrong with OLS?

- For a binary response, $Y \in (0, 1)$, want to predict $\pi = \Pr(Y = 1 \mid x)$
- A linear probability model uses classical linear regression (OLS)
- Problems:
  - Gives predicted values and CIs outside $0 \leq \pi \leq 1$
  - Homogeneity of variance is violated: $\mathcal{V}(\hat{\pi}) = \hat{\pi}(1 - \hat{\pi}) \neq$ constant
  - Inferences, hypothesis tests are wrong!



OLS vs. Logistic regression

OLS regression:
- Assume $y|x \sim N(0, \sigma^2)$

Logistic regression:
- Assume $Pr(y=1|x) \sim \text{binomial}(p)$

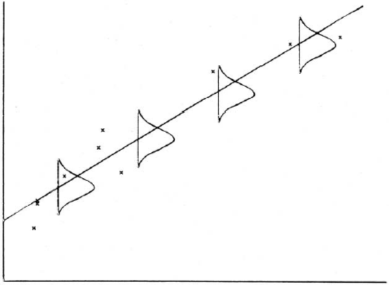


Fig. 2.1. Graphical representation of a simple linear normal regression.

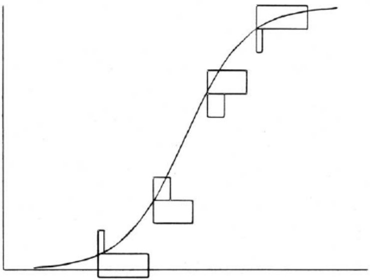
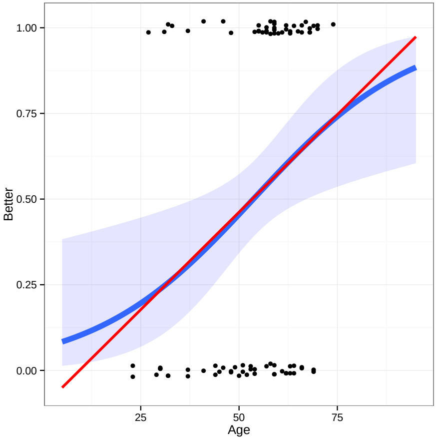


Fig. 2.2. Graphical representation of a simple linear logistic regression.

Logistic regression

- Logistic regression avoids these problems
- Models $\text{logit}(\pi_i) \equiv \log[\pi/(1-\pi)]$
- logit is interpretable as “log odds” that $Y = 1$
- A related probit model gives very similar results, but is less interpretable
- For $0.2 \leq \pi \leq 0.8$ fitted values are close to those from linear regression.



Logistic regression: One predictor

For a single quantitative predictor, x, the simple linear logistic regression model posits a linear relation between the ***log odds*** (or ***logit***) of $\Pr(Y = 1)$ and x,

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

- 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 $\pi(x)$

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

Logistic regression: One predictor

The coefficients of this model have simple interpretations in terms of odds and log odds:

- The odds can be expressed as a multiplicative model

$$\text{odds}(Y = 1) \equiv \frac{\pi(x)}{1 - \pi(x)} = \exp(\alpha + \beta x) = e^{\alpha}(e^{\beta})^{x} \; . \tag{1}$$

  Thus:
- 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.
- In R, use `exp(coef(obj))` to get these values.
- Another interpretation: In terms of probability, the slope of the logistic regression curve is $\beta\pi(1 - \pi)$
- This has the maximum value $\beta/4$ at $\pi = \frac{1}{2}$

Logistic regression models: Multiple predictors

- For a binary response, $Y \in (0, 1)$, let $\boldsymbol{x}$ be a vector of p regressors, and π_i be the probability, $\Pr(Y = 1 \mid \boldsymbol{x})$.
- The logistic regression model is a linear model for the *log odds*, or *logit* that $Y = 1$, given the values in $\boldsymbol{x}$,

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

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$$\frac{\pi_i}{1-\pi_i} = \exp(\alpha + \boldsymbol{x}_i^\mathsf{T} \boldsymbol{\beta}) = \exp(\alpha) \exp(\boldsymbol{x}_i^\mathsf{T} \boldsymbol{\beta})$$

Increasing x_{ij} by 1 increases $\text{logit}(\pi_i)$ by β_j, and multiplies the odds by e^{β_j}.

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Fitting the logistic regression model

Logistic regression models are the special case of generalized linear models, fit in R using `glm(..., family=binomial)`
For this example, we define `Better` as any improvement at all:

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

Fit and print:

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

##
## Call:  glm(formula = Better ~ Age, family = binomial, data = Arthritis)
##
## Coefficients:
## (Intercept)          Age
##     -2.6421       0.0492
##
## Degrees of Freedom: 83 Total (i.e. Null);  82 Residual
## Null Deviance:     116
## Residual Deviance: 109  AIC: 113
```

The **summary()** method gives details:

```
summary(arth.logistic)

##
## Call:
## glm(formula = Better ~ Age, family = binomial, data = Arthritis)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.5106  -1.1277   0.0794   1.0677   1.7611
##
## 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
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 116.45  on 83  degrees of freedom
## Residual deviance: 109.16  on 82  degrees of freedom
## AIC: 113.2
##
## Number of Fisher Scoring iterations: 4
```

Interpreting coefficients

```
coef(arth.logistic)

## (Intercept)         Age
##   -2.642071    0.049249
```

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

## (Intercept)         Age
##    0.071214    1.050482

exp(10*coef(arth.logistic)[2])

##    Age
## 1.6364
```

Interpretations:

- log odds(Better) increase by $\beta = 0.0492$ for each year of age
- odds(Better) multiplied by $e^{\beta} = 1.05$ for each year of age— a 5% increase
- over 10 years, odds(Better) are multiplied by $\exp(10 \times 0.0492) = 1.64$, a 64% increase.
- Pr(Better) increases by $\beta/4 = 0.0123$ for each year (near $\pi = \frac{1}{2}$)

Multiple predictors

The main interest here is the effect of Treatment. Sex and Age are control variables. Fit the main effects model (no interactions):

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

where x_1 is `Age` and x_2 and x_3 are the factors representing `Sex` and `Treatment`, respectively. R uses dummy (0/1) variables for factors.

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

- α doesn't have a sensible interpretation here. Why?
- β_1: increment in log odds(Better) for each year of age.
- β_2: difference in log odds for male as compared to female.
- β_3: difference in log odds for treated vs. the placebo group

Multiple predictors: Fitting

Fit the main effects model. Use `I(Age-50)` to center Age, making α interpretable.

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

coeftest() in lmtest gives just the tests of coefficients provided by **summary()**:

```
library(lmtest)
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
```

Interpreting coefficients

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

##                         coef OddsRatio  2.5 % 97.5 %
## (Intercept)          -0.5781     0.561 0.2647  1.132
## I(Age - 50)           0.0487     1.050 1.0100  1.096
## SexMale              -1.4878     0.226 0.0652  0.689
## TreatmentTreated      1.7598     5.811 2.1187 17.727
```

- $\alpha = -0.578$: At age 50, females given placebo have odds(Better) of $e^{-0.578} = 0.56$.
- $\beta_1 = 0.0487$: Each year of age multiplies odds(Better) by $e^{0.0487} = 1.05$, a 5% increase.
- $\beta_2 = -1.49$: Males $e^{-1.49} = 0.26 \times$ less likely to show improvement as females. (Or, females $e^{1.49} = 4.437 \times$ more likely than males.)
- $\beta_3 = 1.76$: Treated $e^{1.76}$=5.81 $\times$ more likely Better than Placebo

Hypothesis testing: Questions

- **Overall test**: How does my model, $\text{logit}(\pi) = \alpha + \boldsymbol{x}^\mathsf{T}\boldsymbol{\beta}$ compare with the null model, $\text{logit}(\pi) = \alpha$?

$$H_0 : \beta_1 = \beta_2 = \cdots = \beta_p = 0$$

- **One predictor**: Does x_k significantly improve my model? Can it be dropped?

$$H_0 : \beta_k = 0 \quad \text{given other predictors retained}$$

- **Lack of fit**: How does my model compare with a perfect model (saturated model)?

For ANOVA, regression, these tests are carried out using F-tests and t-tests. In logistic regression (fit by maximum likelihood) we use

- F-tests $\rightarrow$ likelihood ratio G^2 tests
- t-tests $\rightarrow$ Wald z or χ^2 tests

Maximum likelihood estimation

- Likelihood, $\mathcal{L} = \Pr(\mathit{data} \,|\, \mathit{model})$, as function of model parameters
- For case i,

$$\mathcal{L}_i = \begin{cases} p_i & \text{if } Y = 1 \\ 1 - p_i & \text{if } Y = 0 \end{cases} = p_i^{Y_i}(1 - p_i^{Y_i}) \qquad \text{where} \qquad p_i = 1/(1 + \exp(\mathbf{x}_i \boldsymbol{\beta}))$$

- Under independence, joint likelihood is the product over all cases

$$\mathcal{L} = \prod_i^n p_i^{Y_i}(1 - p_i^{Y_i})$$

- $\Longrightarrow$ Find estimates $\widehat{\beta}$ that maximize $\log \mathcal{L}$. Iterative, but this solves the "estimating equations"

$$\boldsymbol{X}^\mathsf{T} \boldsymbol{y} = \boldsymbol{X}^\mathsf{T} \widehat{\boldsymbol{p}}$$

Overall test

- Likelihood ratio test (G^2)
  - Compare *nested* models, similar to incremental F tests in OLS
  - Let $\mathcal{L}_1$ = maximized likelihood for **our** model

    $\text{logit}(\pi_i) = \beta_0 + \mathbf{x}_i^T \boldsymbol{\beta}$ w/ k predictors
  - Let $\mathcal{L}_0$ = maximized likelihood for **null** model

    $\text{logit}(\pi_i) = \beta_0$ under $H_0 : \beta_1 = \beta_2 = \cdots = \beta_k = 0$
  - Likelihood-ratio test statistic:

$$G^2 = -2 \log \left(\frac{L_0}{L_1} \right) = 2(\log L_1 - \log L_0) \sim \chi_k^2$$

Wald tests and confidence intervals

- Analogous to *t*-tests in OLS
- H_0: $\beta_i = 0$

$$z = \frac{b_k}{s(b_k)} \sim \mathcal{N}(0,1) \quad \text{or} \quad z^2 \sim \chi^2_1$$

(Wald chi-square)

- Confidence interval:

$$b_k \pm z_{1-\alpha/2} s(b_k)$$

e.g.,

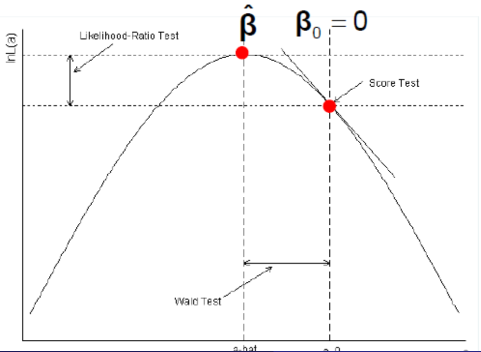
Analysis of Maximum Likelihood Estimates

Parameter		DF	Estimate	Standard Error	Wald Chi-Square	Pr > ChiSq
Intercept		1	-4.5033	1.3074	11.8649	0.0006
sex	Female	1	1.4878	0.5948	6.2576	0.0124
treat	Treated	1	1.7598	0.5365	10.7596	0.0010
age		1	0.0487	0.0207	5.5655	0.0183

LR, Wald and score tests

Testing Global Null Hypothesis: BETA=0

Test	Chi-Square	DF	Pr > ChiSq
Likelihood Ratio	24.3859	3	<.0001
Score	22.0051	3	<.0001
Wald	17.5147	3	0.0006



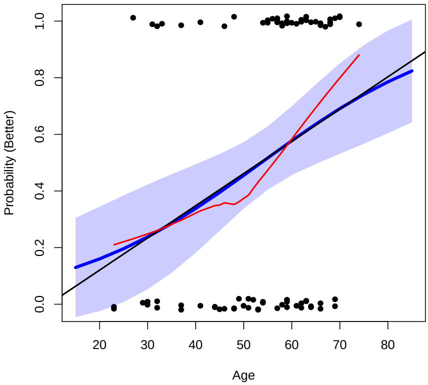
Different ways to measure departure from H_0 : $\boldsymbol{\beta} = 0$

- LR test: diff in log L
- Wald test: $(\hat{\boldsymbol{\beta}} - \boldsymbol{\beta}_0)^2$
- Score test: slope at $\boldsymbol{\beta} = 0$

Plotting logistic regression data

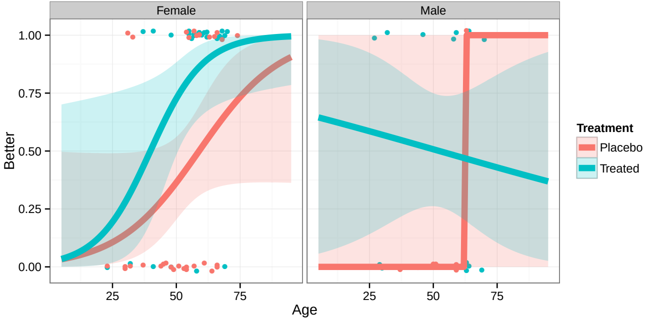
Plotting a binary response together with a fitted logistic model can be difficult because the 0/1 response leads to much overplottting.

- Need to jitter the points
- Useful to show the fitted logistic curve
- Confidence band gives a sense of uncertainty
- Adding a non-parametric (loess) smooth shows possible nonlinearity
- NB: Can plot either on the response scale (probability) or the link scale (logit) where effects are linear



Types of plots

- Conditional plots: Stratified plot of Y or logit(Y) vs. one X, conditioned by other predictors— only that subset is plotted for each
- Full-model plots: plots of fitted response surface, showing all effects; usually shown in separate panels



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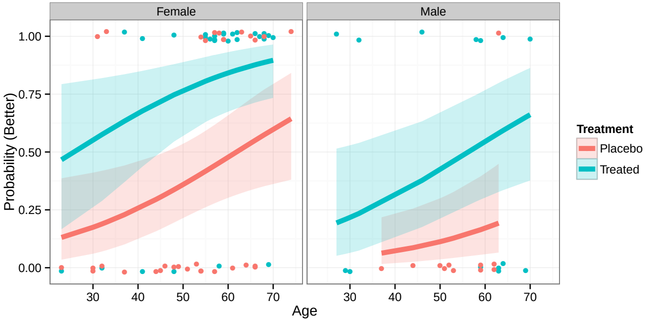

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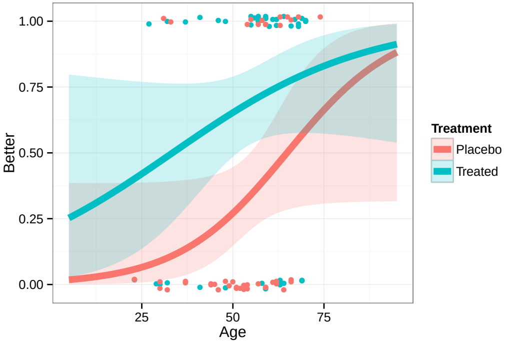
Conditional plots with ggplot2

Plot of Arthritis treatment data, by Treatment (ignoring Sex)

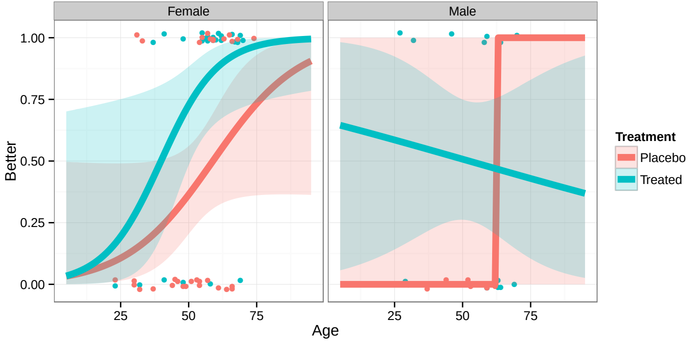
```
library(ggplot2)
gg <- ggplot(Arthritis, aes(Age, Better, color=Treatment)) +
  xlim(5, 95) + theme_bw() +
  geom_point(position = position_jitter(height = 0.02, width = 0)) +
  stat_smooth(method = "glm", family = binomial, alpha = 0.2,
              aes(fill=Treatment), size=2.5, fullrange=TRUE)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



Conditional plots with ggplot2

Conditional plot, faceted by Sex

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



The data is too thin for males to estimate each regression separately

Full-model plots

Full-model plots show the fitted values on the logit scale or on the response scale (probability), usually with confidence bands. This often requires a bit of custom programming.

Steps:

- Obtain fitted values with `predict(model, se.fit=TRUE)`— `type="link"` (logit) is the default
- Can use `type="response"` for probability scale
- Join this to your data (**`cbind()`**)
- Plot as you like: **`plot()`**, **`ggplot()`**, $\cdots$

```
arth.fit2 <- cbind(Arthritis,
                   predict(arth.logistic2, se.fit = TRUE))
head(arth.fit2[,-9], 4)

##   ID Treatment  Sex Age Improved Better   fit se.fit
## 1 57   Treated Male  27     Some      1 -1.43  0.758
## 2 46   Treated Male  29     None      0 -1.33  0.728
## 3 77   Treated Male  30     None      0 -1.28  0.713
## 4 17   Treated Male  32   Marked      1 -1.18  0.684
```

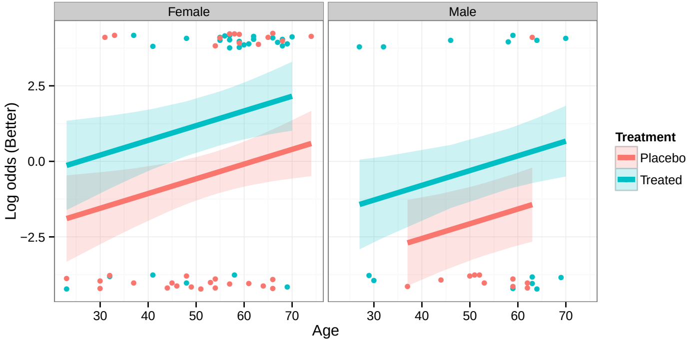
Plotting with ggplot2 package

```
arth.fit2$obs <- c(-4, 4 )[1+arth.fit2$Better]

gg2 <- ggplot( arth.fit2, aes(x=Age, y=fit, color=Treatment)) +
  geom_line(size = 2) +
  geom_ribbon(aes(ymin = fit - 1.96 * se.fit,
                  ymax = fit + 1.96 * se.fit,
                  fill = Treatment), alpha = 0.2,
              color = "transparent") +
  labs(x = "Age", y = "Log odds (Better)") +
  geom_point(aes(y=obs), position=position_jitter(height=0.25, width=0))
gg2 + facet_wrap(~ Sex)
```

Full-model plots

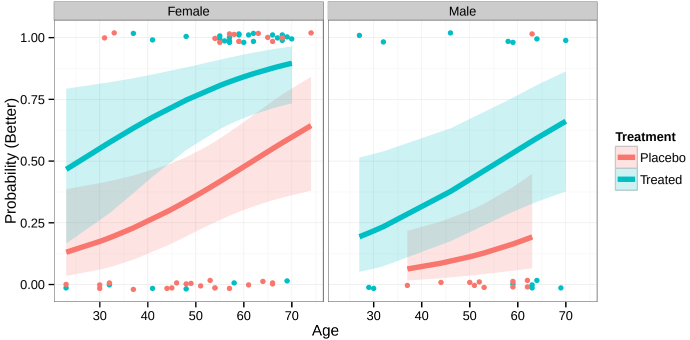
Ploting on the logit scale shows the additive effects of age, treatment and sex



These plots show the data (jittered) as well as model uncertainty (confidence bands)

Full-model plots

Ploting on the probability scale may be simpler to interpret



These plots show the data (jittered) as well as model uncertainty (confidence bands)

Models with interactions

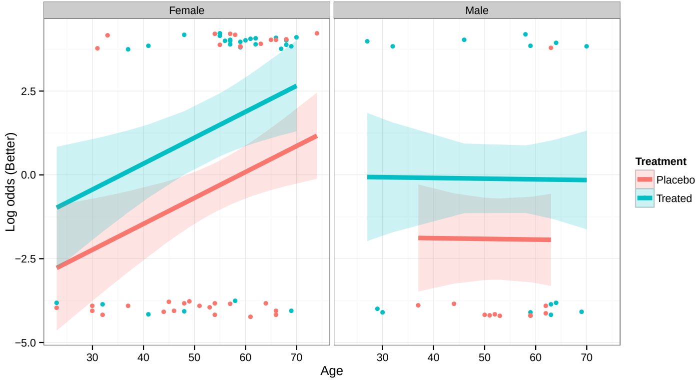
Allow an interaction of Age x Sex

```
arth.logistic4 <- update(arth.logistic2, . ~ . + Age:Sex)
Anova(arth.logistic4)

## Error in eval(expr, envir, enclos):  could not find function "Anova"
```

Interaction is NS, but we can plot it the model anyway

Models with interactions

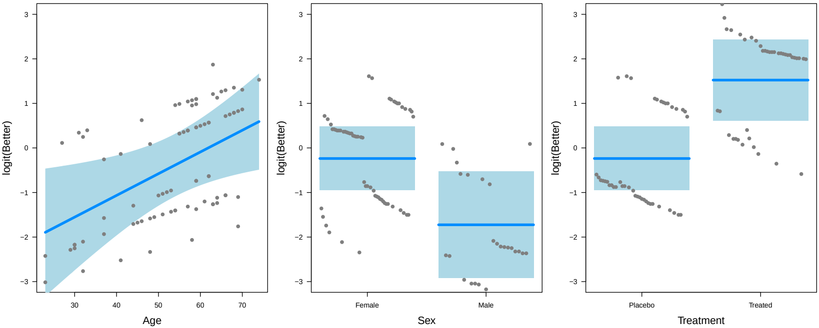


- Only the model changes
- `predict()` automatically incorporates the revised model terms
- Plotting steps remain the same
- This interpretation is quite different!

The `visreg` package

- Provides a more convenient way to plot model results from the model object
- A consistent interface for linear models, generalized linear models, robust regression, etc.
- Shows the data as partial residuals or rug plots
- Can plot on the response or logit scale
- Can produce plots with separate panels for conditioning variables

```r
library(visreg)
visreg(arth.logistic2, ylab="logit(Better)", ...)
```



- One plot for each variable in the model
- Other variables: continuous— held fixed at median; factors— held fixed at most frequent value
- Partial residuals ($\boldsymbol{r}_j$): the coefficient $\widehat{\beta}_j$ in the full model is the slope of the simple fit of $\boldsymbol{r}_j$ on $\boldsymbol{x}_j$.

Effect plots: basic ideas

Show a given effect (and low-order relatives) controlling for other model effects.

Data

	x1	x2	sex	x1x2	y	yhat
1	1	1	F	1	4.73	4.46
2	2	1	M	0	6.10	5.55
3	3	1	F	-1	4.32	4.34
4	1	1	F	1	4.84	4.46
5	2	1	F	0	4.73	4.40
...	...	...	...	...	...	...
29	2	2	M	0	6.10	6.15
30	3	2	F	1	6.71	7.14

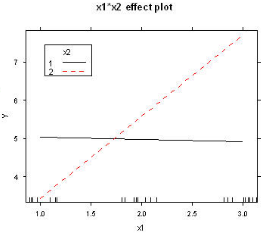
- Fit data: $\mathbf{X}\hat{\boldsymbol{\beta}} \Rightarrow \hat{\mathbf{y}}$
- Score data $\mathbf{X}^*\hat{\boldsymbol{\beta}} \Rightarrow \hat{\mathbf{y}}^*$
  - plot vars: vary over range
  - control vars: fix at means

Score data

	x1	x2	sex	x1:x2	y	yhat*
31	1	1	0.5	1	NA	5.030
32	2	1	0.5	2	NA	4.971
33	3	1	0.5	3	NA	4.912
34	1	2	0.5	2	NA	3.437
35	2	2	0.5	4	NA	5.574
36	3	2	0.5	6	NA	7.710

plot vars control vars

plot



Effect plots for generalized linear models: Details

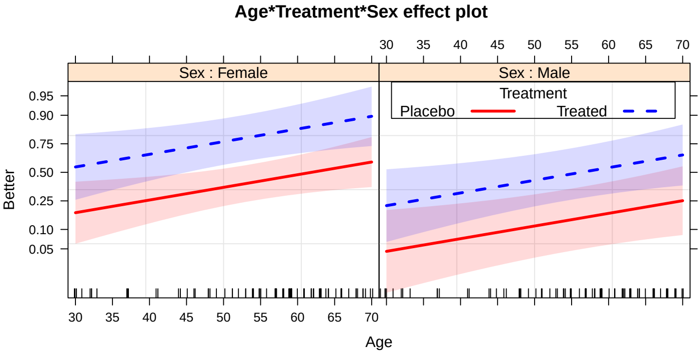
- For simple models, full model plots show the complete relation between response and *all predictors*.
- Fox(1987)— For complex models, often wish to plot a specific main effect or interaction (including lower-order relatives)— *controlling for other effects*
  - Fit full model to data with linear predictor (e.g., logit) $\boldsymbol{\eta} = \boldsymbol{X}\beta$ and link function $g(\boldsymbol{\mu}) = \boldsymbol{\eta} \rightarrow$ estimate $\boldsymbol{b}$ of β and covariance matrix $\widehat{V(\boldsymbol{b})}$ of $\boldsymbol{b}$.
  - Construct "score data"
    - Vary each predictor in the term over its' range
    - Fix other predictors at "typical" values (mean, median, proportion in the data)
    - $\rightarrow$ "effect model matrix," $\boldsymbol{X}^*$
  - Use `predict()` on $\boldsymbol{X}^*$
    - Calculate fitted effect values, $\hat{\boldsymbol{\eta}}^* = \boldsymbol{X}^* \boldsymbol{b}$.
    - Standard errors are square roots of $\mathrm{diag}\, \boldsymbol{X}^* \widehat{V(\boldsymbol{b})} \boldsymbol{X}^{*\mathsf{T}}$
  - Plot $\hat{\boldsymbol{\eta}}^*$, or values transformed back to scale of response, $g^{-1}(\hat{\boldsymbol{\eta}}^*)$.
- *Note*: This provides a general means to visualize interactions in *all* linear and generalized linear models.

Plotting main effects:

```
library(effects)
arth.eff2 <- allEffects(arth.logistic2)
plot(arth.eff2, rows=1, cols=3)
```

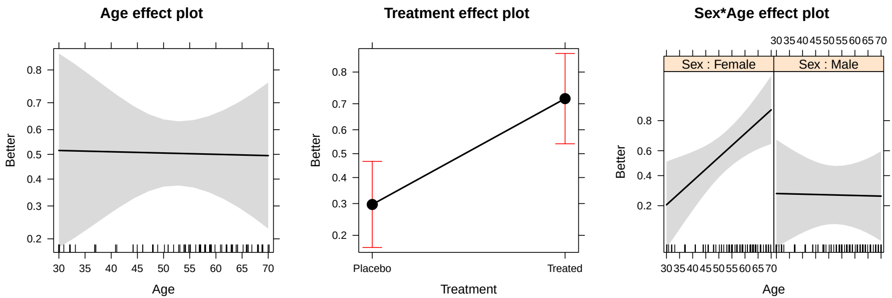
Full model plots:

```
arth.full <- Effect(c("Age", "Treatment", "Sex"), arth.logistic2)
plot(arth.full, multiline=TRUE, ci.style="bands", colors = c("red"
"blue"), lwd=3, ...)
```



Model with interaction of Age x Sex

```
plot(allEffects(arth.logistic4), rows=1, cols=3)
```



- Only the high-order terms for Treatment and Sex*Age need to be interpreted
- (How would you describe this?)
- The main effect of Age looks very different, averaged over Treatment and Sex

Case study: Arrests for Marijuana Possession

Context & background

- In Dec. 2002, the *Toronto Star* examined the issue of racial profiling, by analyzing a data base of 600,000+ arrest records from 1996-2002.
- They focused on a subset of arrests for which police action was discretionary, e.g., simple possession of small quantities of marijuana, where the police could:
  - Release the arrestee with a summons— like a parking ticket
  - Bring to police station, hold for bail, etc.— harsher treatment
- Response variable: `released` – `Yes, No`
- Main predictor of interest: skin-`colour` of arrestee (black, white)

The *Toronto Star* meets mosaic displays...

B SECTION TORONTO STAR WEDNESDAY, DECEMBER 11, 2002 ★ thestar.com

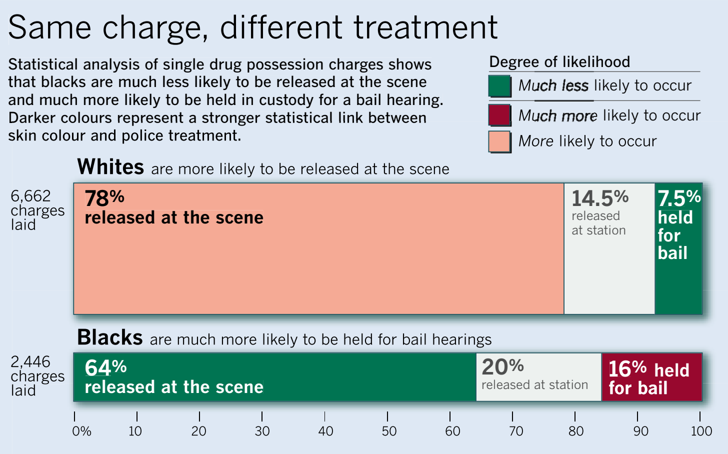
Race and Crime

VINCE TALOTTA/TORONTO STAR

York University professor Michael Friendly's expert statistical analysis provided confirmation for the Toronto Star's series on racial profiling by city police.

Man behind the numbers

... Which got turned into this infographic:



SOURCE: Toronto police arrest records 1996-2002

... Hey, they even spelled likelihood correctly!

Arrests for Marijuana Possession: Data

Data

Control variables:

- year, age, sex
- employed, citizen – Yes, No
- checks — Number of police data bases (previous arrests, previous convictions, parole status, etc.) in which the arrestee's name was found.

```
library(effects)    # for Arrests data
library(car)        # for Anova()
data(Arrests)
some(Arrests)


##      released colour year age    sex employed citizen checks
## 751       Yes  White 1999  21   Male      Yes     Yes      2
## 937       Yes  White 2001  22   Male      Yes     Yes      3
## 1116      Yes  White 2000  38   Male       No     Yes      4
## 1836       No  Black 1998  18   Male       No      No      4
## 2653      Yes  White 2000  17   Male      Yes     Yes      1
## 3638      Yes  White 1999  20   Male      Yes     Yes      0
## 3816      Yes  White 1998  48 Female      Yes     Yes      0
## 4137      Yes  White 2001  21   Male      Yes     Yes      2
## 4914       No  White 2001  24   Male      Yes      No      3
## 5206       No  White 2000  27   Male      Yes     Yes      2
```

Arrests for Marijuana Possession: Model

To allow possibly non-linear effects of `year`, we treat it as a factor:

```
> Arrests$year <- as.factor(Arrests$year)
```

Logistic regression model with all main effects, plus interactions of `colour:year` and `colour:age`

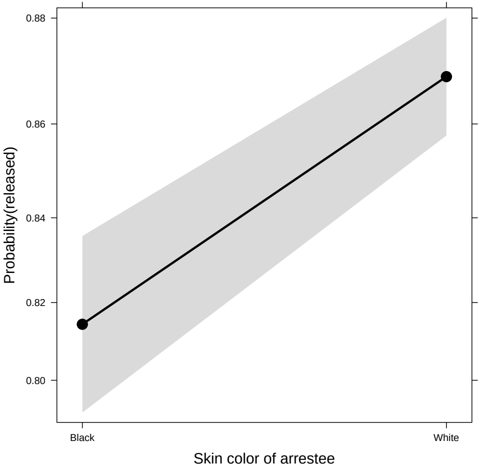
```
> arrests.mod <- glm(released ~ employed + citizen + checks + colour *
+     year + colour * age, family = binomial, data = Arrests)
> Anova(arrests.mod)
```

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

Response: released
            LR Chisq Df Pr(>Chisq)
employed      72.673  1  < 2.2e-16 ***
citizen       25.783  1  3.820e-07 ***
checks       205.211  1  < 2.2e-16 ***
colour        19.572  1  9.687e-06 ***
year           6.087  5  0.2978477
age            0.459  1  0.4982736
colour:year   21.720  5  0.0005917 ***
colour:age    13.886  1  0.0001942 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Effect plots: colour

```
plot(Effect("colour", arrests.mod), ci.style="bands", ...)
```

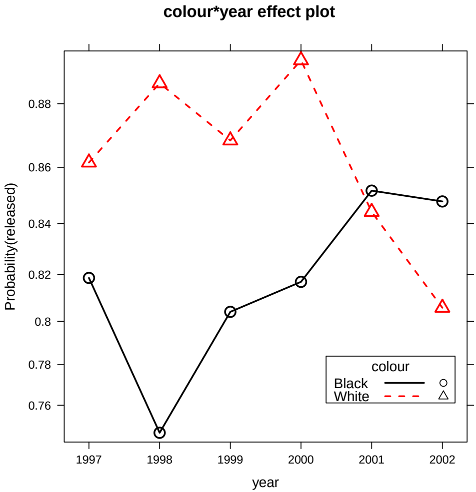


- Effect plot for colour shows average effect controlling (adjusting) for *all* other factors simultaneously
- (The *Star* analysis, controlled for these one at a time.)
- $\Longrightarrow$ Evidence for different treatment of blacks and whites ("racial profiling")
- (Even Frances Nunziata could understand this.)
- NB: Effects smaller than claimed by *the Star*

Effect plots: Interactions

The story turned out to be more nuanced than reported by the *Toronto Star*, as shown in effect plots for interactions with colour.

```
> plot(effect("colour:year", arrests.mod), multiline = TRUE, ...)
```

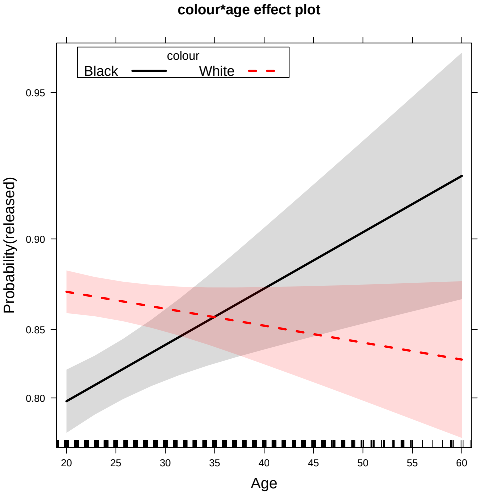


- Up to 2000, strong evidence for differential treatment of blacks and whites
- Also evidence to support Police claim of effect of training to reduce racial effects in treatment

Effect plots: Interactions

The story turned out to be more nuanced than reported by the *Toronto Star*, as shown in effect plots for interactions with colour.

```
> plot(effect("colour:age", arrests.mod), multiline = TRUE, ...)
```



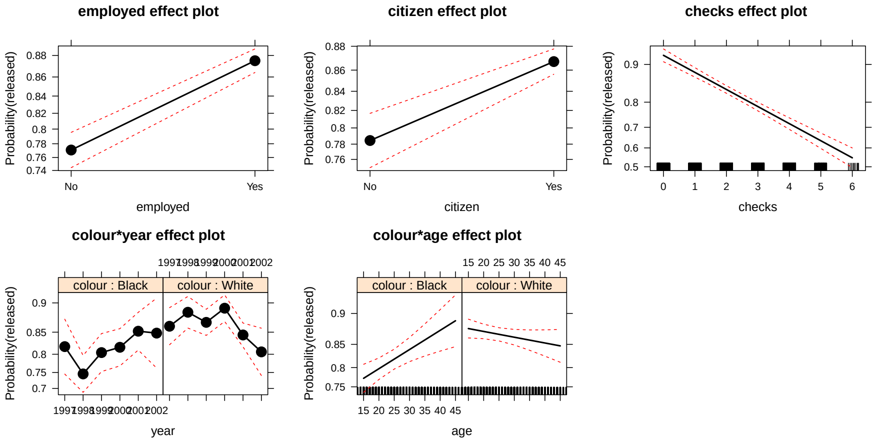
A more surprising finding:

- Opposite age effects for blacks and whites—
- Young blacks treated *more* harshly than young whites
- Older blacks treated *less* harshly than older whites

Effect plots: allEffects

All model effects can be viewed together using `plot(allEffects(mod))`

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



Model diagnostics

As in regression and ANOVA, the validity of a logistic regression model is threatened when:

- Important predictors have been omitted from the model
- Predictors assumed to be linear have non-linear effects on $\Pr(Y = 1)$
- Important interactions have been omitted
- A few "wild" observations have a large impact on the fitted model or coefficients

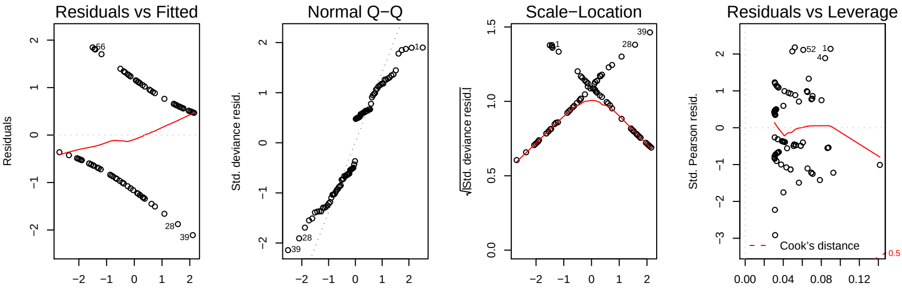
Model specification: Tools and techniques

- Use non-parametric smoothed curves to detect non-linearity
- Consider using polynomial terms ($X^2, X^3, \dots$) or regression splines (e.g., `ns(X, 3)`)
- Use `update(model, ...)` to test for interactions— formula: $. \sim .^2$

Diagnostic plots in R

In R, plotting a `glm` object gives the "regression quartet" — basic diagnostic plots

```
arth.mod1 <- glm(Better ~ Age + Sex + Treatment, data=Arthritis,
                 family='binomial')
plot(arth.mod1)
```



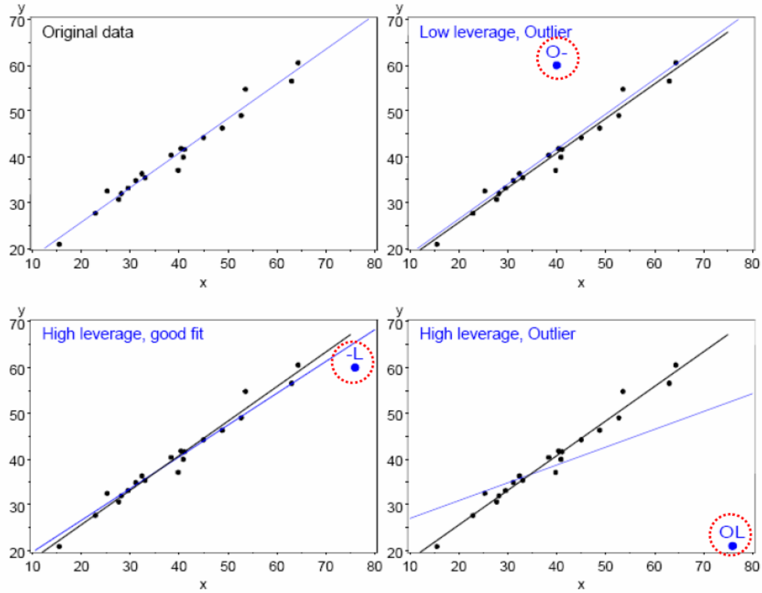
Better versions of these plots are available in the car package

Unusual data: Leverage and Influence

- "Unusual" observations can have dramatic effects on estimates in linear models
  - Can change the coefficients for the predictors
  - Can change the predicted values for all observations
- Three archetypal cases:
  - Typical X (low leverage), bad fit — Not much harm
  - Unusual X (high leverage), good fit — Not much harm
  - Unusual X (high leverage), bad fit — BAD, BAD, BAD
- Influential observations: unusual in both X and Y
- Heuristic formula:

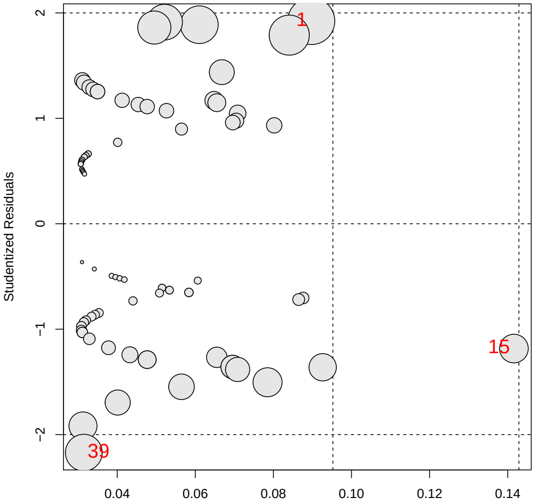
$$\mathit{Influence} = \mathit{Leverage}_X \times \mathit{Residual}_Y$$

Effect of adding one more point in simple linear regression (new point in blue)



Influence plots in R

```
library(car)
influencePlot(arth.logistic2)
```



- X axis: Leverage ("hat values")
- Y axis: Studentized residuals
- Bubble size ∼ Cook D (influence on coefficients)

Which cases are influential?

	ID	Treatment	Sex	Age	Better	StudRes	Hat	CookD
1	57	Treated	Male	27	1	1.922	0.08968	0.3358
15	66	Treated	Female	23	0	-1.183	0.14158	0.2049
39	11	Treated	Female	69	0	-2.171	0.03144	0.2626