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Frank E. Harrell, Jr.

Regression Modeling Strategies

With Applications to Linear Models, Logistic and Ordinal Regression, and Survival Analysis

Second Edition

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To the memories of Frank E. Harrell, Sr., Richard Jackson, L. Richard Smith, John Burdeshaw, and Todd Nick, and with appreciation to Liana and Charlotte Harrell, two high school math teachers: Carolyn Wailes (née Gaston) and Floyd Christian, two college professors: David Hurst (who advised me to choose the field of biostatistics) and Doug Stocks, and my graduate advisor P. K. Sen.

Chapter 12

Logistic Model Case Study 2: Survival of Titanic Passengers

This case study demonstrates the development of a binary logistic regression model to describe patterns of survival in passengers on the *Titanic*, based on passenger age, sex, ticket class, and the number of family members accompanying each passenger. Nonparametric regression is also used. Since many of the passengers had missing ages, multiple imputation is used so that the complete information on the other variables can be efficiently utilized. Titanic passenger data were gathered by many researchers. Primary references are the *Encyclopedia Titanica* at `www.encyclopedia-titanica.org` and Eaton and Haas.[169] Titanic survival patterns have been analyzed previously[151, 296, 571] but without incorporation of individual passenger ages. Thomas Cason while a University of Virginia student compiled and interpreted the data from the World Wide Web. One thousand three hundred nine of the passengers are represented in the dataset, which is available from this text's Web site under the name `titanic3`. An early analysis of Titanic data may be found in Bron[75].

12.1 Descriptive Statistics

First we obtain basic descriptive statistics on key variables.

```
require(rms)
```

```
getHdata(titanic3)      # get dataset from web site
# List of names of variables to analyze
v ← c('pclass','survived','age','sex','sibsp','parch')
t3 ← titanic3[, v]
units(t3$age) ← 'years'
latex(describe(t3), file='')
```

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```
                         t3
          6 Variables    1309  Observations
------------------------------------------------------------
pclass
     n missing unique
  1309       0      3

 1st (323, 25%), 2nd (277, 21%), 3rd (709, 54%)
------------------------------------------------------------
survived : Survived
     n missing unique Info Sum Mean
  1309       0      2 0.71  500 0.382
------------------------------------------------------------
age : Age [years]
     n missing unique Info  Mean .05 .10 .25 .50 .75 .90 .95
  1046     263     98    1 29.88   5  14  21  28  39  50  57

 lowest :  0.1667  0.3333  0.4167  0.6667  0.7500
 highest: 70.5000 71.0000 74.0000 76.0000 80.0000
------------------------------------------------------------
sex
     n missing unique
  1309       0      2

 female (466, 36%), male (843, 64%)
------------------------------------------------------------
sibsp : Number of Siblings/Spouses Aboard
     n missing unique Info  Mean
  1309       0      7 0.67 0.4989

              0   1  2  3  4 5 8
 Frequency  891 319 42 20 22 6 9
 %           68  24  3  2  2 0 1
------------------------------------------------------------
parch : Number of Parents/Children Aboard
     n missing unique Info  Mean
  1309       0      8 0.55 0.385

               0   1   2 3 4 5 6 9
 Frequency  1002 170 113 8 6 6 2 2
 %            77  13   9 1 0 0 0 0
------------------------------------------------------------
```

Next, we obtain access to the needed variables and observations, and save data distribution characteristics for plotting and for computing predictor effects. There are not many passengers having more than 3 siblings or spouses or more than 3 children, so we truncate two variables at 3 for the purpose of estimating stratified survival probabilities.

```
dd ← datadist(t3)
# describe distributions of variables to rms
options(datadist='dd')
s ← summary(survived ~ age + sex + pclass +
            cut2(sibsp,0:3) + cut2(parch,0:3), data=t3)
plot(s, main='', subtitles=FALSE)   # Figure 12.1
```

Note the large number of missing ages. Also note the strong effects of sex and passenger class on the probability of surviving. The age effect does not appear to be very strong, because as we show later, much of the effect is restricted to

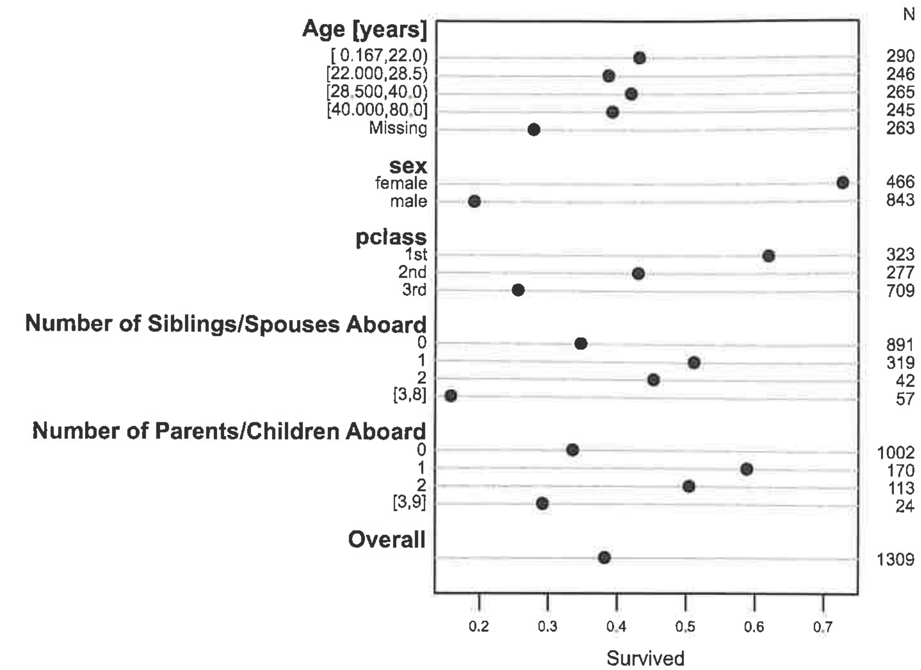

Fig. 12.1 Univariable summaries of Titanic survival

age < 21 years for one of the sexes. The effects of the last two variables are unclear as the estimated proportions are not monotonic in the values of these descriptors. Although some of the cell sizes are small, we can show four-way empirical relationships with the fraction of surviving passengers by creating four cells for `sibsp` × `parch` combinations and by creating two age groups. We suppress proportions based on fewer than 25 passengers in a cell. Results are shown in Figure 12.2.

```
tn ← transform(t3,
  agec = ifelse(age < 21, 'child', 'adult'),
  sibsp= ifelse(sibsp == 0, 'no sib/sp', 'sib/sp'),
  parch= ifelse(parch == 0, 'no par/child', 'par/child'))

g ← function(y) if(length(y) < 25) NA else mean(y)
s ← with(tn, summarize(survived,
          llist(agec, sex, pclass, sibsp, parch), g))
# llist, summarize in Hmisc package
# Figure 12.2:
ggplot(subset(s, agec != 'NA'),
  aes(x=survived, y=pclass, shape=sex)) +
  geom_point() + facet_grid(agec ~ sibsp * parch) +
  xlab('Proportion Surviving') + ylab('Passenger Class') +
  scale_x_continuous(breaks=c(0, .5, 1))
```

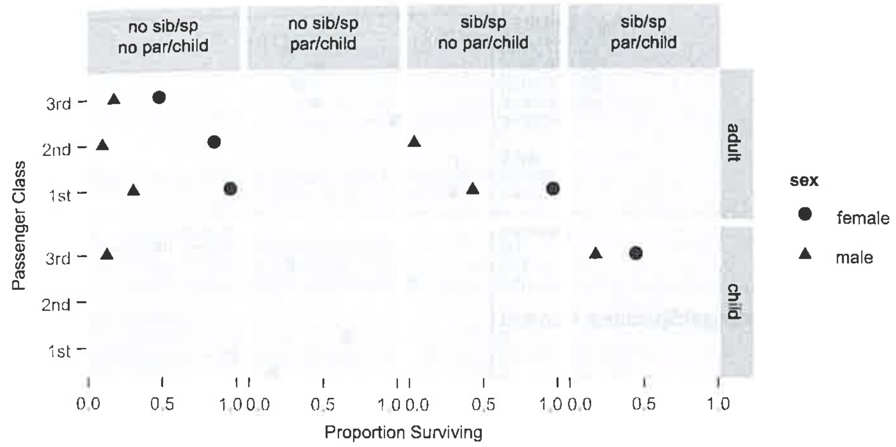

Fig. 12.2 Multi-way summary of Titanic survival

Note that none of the effects of `sibsp` or `parch` for common passenger groups appear strong on an absolute risk scale.

12.2 Exploring Trends with Nonparametric Regression

As described in Section 2.4.7, the `loess` smoother has excellent performance when the response is binary, as long as outlier detection is turned off. Here we use a `ggplot2` add-on function `histSpikeg` in the `Hmisc` package to obtain and plot the `loess` fit and age distribution. `histSpikeg` uses the "no iteration" option for the R `lowess` function when the response is binary.

```
# Figure 12.3
b  ← scale_size_discrete(range=c(.1, .85))
yl ← ylab(NULL)
p1 ← ggplot(t3, aes(x=age, y=survived)) +
      histSpikeg(survived ~ age, lowess=TRUE, data=t3) +
      ylim(0,1) + yl
p2 ← ggplot(t3, aes(x=age, y=survived, color=sex)) +
      histSpikeg(survived ~ age + sex, lowess=TRUE,
                 data=t3) + ylim(0,1) + yl
p3 ← ggplot(t3, aes(x=age, y=survived, size=pclass)) +
      histSpikeg(survived ~ age + pclass, lowess=TRUE,
                 data=t3) + b + ylim(0,1) + yl
p4 ← ggplot(t3, aes(x=age, y=survived, color=sex,
       size=pclass)) +
      histSpikeg(survived ~ age + sex + pclass,
                 lowess=TRUE, data=t3) +
      b + ylim(0,1) + yl
gridExtra::grid.arrange(p1, p2, p3, p4, ncol=2)  # combine 4
```


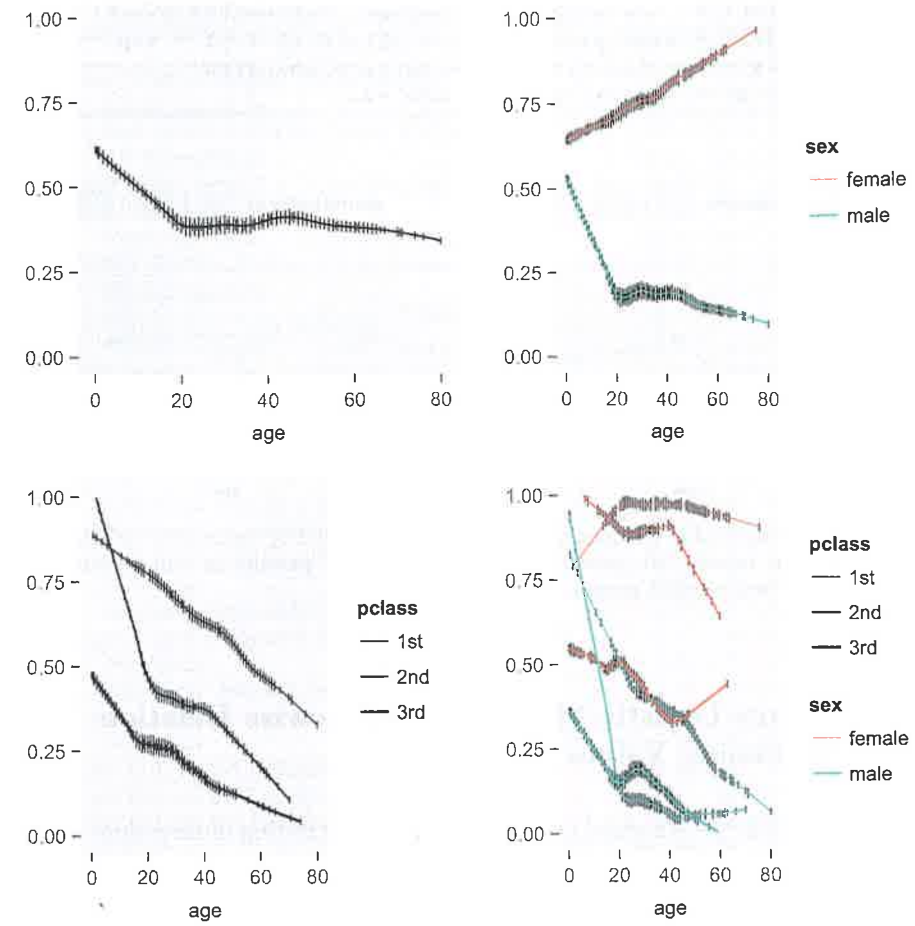

Fig. 12.3 Nonparametric regression (`loess`) estimates of the relationship between age and the probability of surviving the Titanic, with tick marks depicting the age distribution. The top left panel shows unstratified estimates of the probability of survival. Other panels show nonparametric estimates by various stratifications.

Figure 12.3 shows much of the story of passenger survival patterns. "Women and children first" seems to be true except for women in third class. It is interesting that there is no real cutoff for who is considered a child. For men, the younger the greater chance of surviving. The interpretation of the effects of the "number of relatives"-type variables will be more difficult, as their definitions are a function of age. Figure 12.4 shows these relationships.

```
# Figure 12.4
top ← theme(legend.position='top')
p1 ← ggplot(t3, aes(x=age, y=survived, color=cut2(sibsp,
       0:2))) + stat_plsmo() + b + ylim(0,1) + yl + top +
     scale_color_discrete(name='siblings/spouses')
```

```
p2 ← ggplot(t3, aes(x=age, y=survived, color=cut2(parch,
       0:2))) + stat_plsmo() + b + ylim(0,1) + yl + top +
      scale_color_discrete(name='parents/children')
gridExtra::grid.arrange(p1, p2, ncol=2)
```

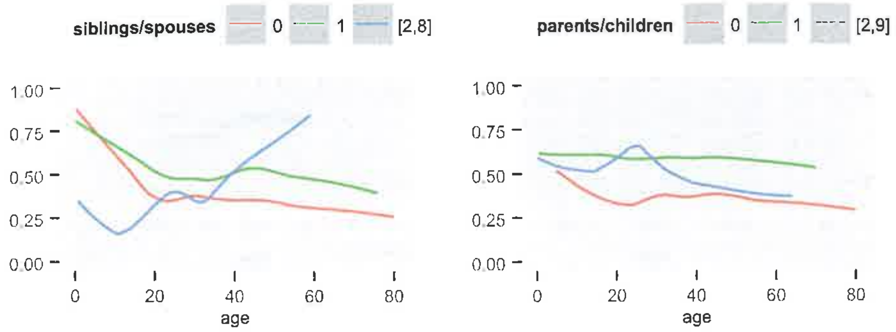

Fig. 12.4 Relationship between age and survival stratified by the number of siblings or spouses on board (left panel) or by the number of parents or children of the passenger on board (right panel).

12.3 Binary Logistic Model With Casewise Deletion of Missing Values

What follows is the standard analysis based on eliminating observations having any missing data. We develop an initial somewhat saturated logistic model, allowing for a flexible nonlinear age effect that can differ in shape for all six sex × class strata. The `sibsp` and `parch` variables do not have sufficiently dispersed distributions to allow for us to model them nonlinearly. Also, there are too few passengers with nonzero values of these two variables in sex × `pclass` × age strata to allow us to model complex interactions involving them. The meaning of these variables does depend on the passenger's age, so we consider only age interactions involving `sibsp` and `parch`.

```
f1 ← lrm(survived ~ sex*pclass*rcs(age,5) +
          rcs(age,5)*(sibsp + parch), data=t3)    # Table 12.1
latex(anova(f1), file='', label='titanic-anova3',
      size='small')
```

Three-way interactions are clearly insignificant ($P = 0.4$) in Table 12.1. So is `parch` ($P = 0.6$ for testing the combined main effect + interaction effects for `parch`, i.e., whether `parch` is important for any age). These effects would be deleted in almost all bootstrap resamples had we bootstrapped a variable selection procedure using $\alpha = 0.1$ for retention of terms, so we can safely ignore these terms for future steps. The model not containing those terms

Table 12.1 Wald Statistics for `survived`

	χ^2	d.f.	P
sex (Factor+Higher Order Factors)	187.15	15	< 0.0001
All Interactions	59.74	14	< 0.0001
pclass (Factor+Higher Order Factors)	100.10	20	< 0.0001
All Interactions	46.51	18	0.0003
age (Factor+Higher Order Factors)	56.20	32	0.0052
All Interactions	34.57	28	0.1826
Nonlinear (Factor+Higher Order Factors)	28.66	24	0.2331
sibsp (Factor+Higher Order Factors)	19.67	5	0.0014
All Interactions	12.13	4	0.0164
parch (Factor+Higher Order Factors)	3.51	5	0.6217
All Interactions	3.51	4	0.4761
sex × pclass (Factor+Higher Order Factors)	42.43	10	< 0.0001
sex × age (Factor+Higher Order Factors)	15.89	12	0.1962
Nonlinear (Factor+Higher Order Factors)	14.47	9	0.1066
Nonlinear Interaction : f(A,B) vs. AB	4.17	3	0.2441
pclass × age (Factor+Higher Order Factors)	13.47	16	0.6385
Nonlinear (Factor+Higher Order Factors)	12.92	12	0.3749
Nonlinear Interaction : f(A,B) vs. AB	6.88	6	0.3324
age × sibsp (Factor+Higher Order Factors)	12.13	4	0.0164
Nonlinear	1.76	3	0.6235
Nonlinear Interaction : f(A,B) vs. AB	1.76	3	0.6235
age × parch (Factor+Higher Order Factors)	3.51	4	0.4761
Nonlinear	1.80	3	0.6147
Nonlinear Interaction : f(A,B) vs. AB	1.80	3	0.6147
sex × pclass × age (Factor+Higher Order Factors)	8.34	8	0.4006
Nonlinear	7.74	6	0.2581
TOTAL NONLINEAR	28.66	24	0.2331
TOTAL INTERACTION	75.61	30	< 0.0001
TOTAL NONLINEAR + INTERACTION	79.49	33	< 0.0001
TOTAL	241.93	39	< 0.0001

is fitted below. The ^2 in the model formula means to expand the terms in parentheses to include all main effects and second-order interactions.

```
f ← lrm(survived ~ (sex + pclass + rcs(age,5))^2 +
          rcs(age,5)*sibsp, data=t3)
print(f, latex=TRUE)
```

Logistic Regression Model

```
lrm(formula = survived ~ (sex + pclass + rcs(age, 5))^2
    + rcs(age, 5) * sibsp, data = t3)
```

Frequencies of Missing Values Due to Each Variable

```
survived    sex  pclass    age   sibsp
       0      0       0    263       0
```

		Model Likelihood Ratio Test		Discrimination Indexes		Rank Discrim. Indexes	
Obs	1046	LR χ^2	553.87	R^2	0.555	C	0.878
0	619	d.f.	26	g	2.427	D_{xy}	0.756
1	427	$\Pr(>\chi^2)$	< 0.0001	g_r	11.325	γ	0.758
$\max \lvert \frac{\partial \log L}{\partial \beta} \rvert$	6×10^{-6}			g_p	0.365	τ_a	0.366
				Brier	0.130		

	Coef	S.E.	Wald Z	$\Pr(>\lvert Z\rvert)$
Intercept	3.3075	1.8427	1.79	0.0727
sex=male	-1.1478	1.0878	-1.06	0.2914
pclass=2nd	6.7309	3.9617	1.70	0.0893
pclass=3rd	-1.6437	1.8299	-0.90	0.3691
age	0.0886	0.1346	0.66	0.5102
age'	-0.7410	0.6513	-1.14	0.2552
age"	4.9264	4.0047	1.23	0.2186
age"'	-6.6129	5.4100	-1.22	0.2216
sibsp	-1.0446	0.3441	-3.04	0.0024
sex=male * pclass=2nd	-0.7682	0.7083	-1.08	0.2781
sex=male * pclass=3rd	2.1520	0.6214	3.46	0.0005
sex=male * age	-0.2191	0.0722	-3.04	0.0024
sex=male * age'	1.0842	0.3886	2.79	0.0053
sex=male * age"	-6.5578	2.6511	-2.47	0.0134
sex=male * age"'	8.3716	3.8532	2.17	0.0298
pclass=2nd * age	-0.5446	0.2653	-2.05	0.0401
pclass=3rd * age	-0.1634	0.1308	-1.25	0.2118
pclass=2nd * age'	1.9156	1.0189	1.88	0.0601
pclass=3rd * age'	0.8205	0.6091	1.35	0.1780
pclass=2nd * age"	-8.9545	5.5027	-1.63	0.1037
pclass=3rd * age"	-5.4276	3.6475	-1.49	0.1367
pclass=2nd * age"'	9.3926	6.9559	1.35	0.1769
pclass=3rd * age"'	7.5403	4.8519	1.55	0.1202
age * sibsp	0.0357	0.0340	1.05	0.2933
age' * sibsp	-0.0467	0.2213	-0.21	0.8330
age" * sibsp	0.5574	1.6680	0.33	0.7382
age"' * sibsp	-1.1937	2.5711	-0.46	0.6425

```
latex(anova(f),file='',label='titanic-anova2',size='small')
    #12.2
```

This is a very powerful model (ROC area $= c = 0.88$); the survival patterns are easy to detect. The Wald ANOVA in Table 12.2 indicates especially strong sex and `pclass` effects ($\chi^2 = 199$ and 109, respectively). There is a very strong

Table 12.2 Wald Statistics for `survived`

	χ^2	d.f.	P
sex (Factor+Higher Order Factors)	199.42	7	< 0.0001
All Interactions	56.14	6	< 0.0001
pclass (Factor+Higher Order Factors)	108.73	12	< 0.0001
All Interactions	42.83	10	< 0.0001
age (Factor+Higher Order Factors)	47.04	20	0.0006
All Interactions	24.51	16	0.0789
Nonlinear (Factor+Higher Order Factors)	22.72	15	0.0902
sibsp (Factor+Higher Order Factors)	19.95	5	0.0013
All Interactions	10.99	4	0.0267
sex × pclass (Factor+Higher Order Factors)	35.40	2	< 0.0001
sex × age (Factor+Higher Order Factors)	10.08	4	0.0391
Nonlinear	8.17	3	0.0426
Nonlinear Interaction : f(A,B) vs. AB	8.17	3	0.0426
pclass × age (Factor+Higher Order Factors)	6.86	8	0.5516
Nonlinear	6.11	6	0.4113
Nonlinear Interaction : f(A,B) vs. AB	6.11	6	0.4113
age × sibsp (Factor+Higher Order Factors)	10.99	4	0.0267
Nonlinear	1.81	3	0.6134
Nonlinear Interaction : f(A,B) vs. AB	1.81	3	0.6134
TOTAL NONLINEAR	22.72	15	0.0902
TOTAL INTERACTION	67.58	18	< 0.0001
TOTAL NONLINEAR + INTERACTION	70.68	21	< 0.0001
TOTAL	253.18	26	< 0.0001

sex × `pclass` interaction and a strong age × `sibsp` interaction, considering the strength of `sibsp` overall.

Let us examine the shapes of predictor effects. With so many interactions in the model we need to obtain predicted values at least for all combinations of sex and `pclass`. For `sibsp` we consider only two of its possible values.

```
p ← Predict(f, age, sex, pclass, sibsp=0, fun=plogis)
ggplot(p)          # Fig. 12.5
```

Note the agreement between the lower right-hand panel of Figure 12.3 with Figure 12.5. This results from our use of similar flexibility in the parametric and nonparametric approaches (and similar effective degrees of freedom). The estimated effect of `sibsp` as a function of age is shown in Figure 12.6.

```
ggplot(Predict(f, sibsp, age=c(10,15,20,50), conf.int=FALSE))
## Figure 12.6
```

Note that children having many siblings apparently had lower survival. Married adults had slightly higher survival than unmarried ones.

There will never be another Titanic, so we do not need to validate the model for prospective use. But we use the bootstrap to validate the model anyway, in an effort to detect whether it is overfitting the data. We do not penalize the calculations that follow for having examined the effect of `parch` or

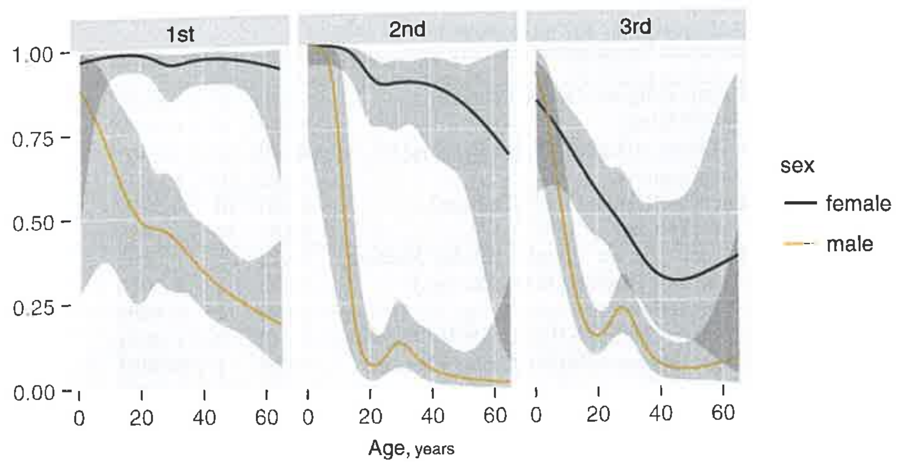

Fig. 12.5 Effects of predictors on probability of survival of Titanic passengers, estimated for zero siblings or spouses

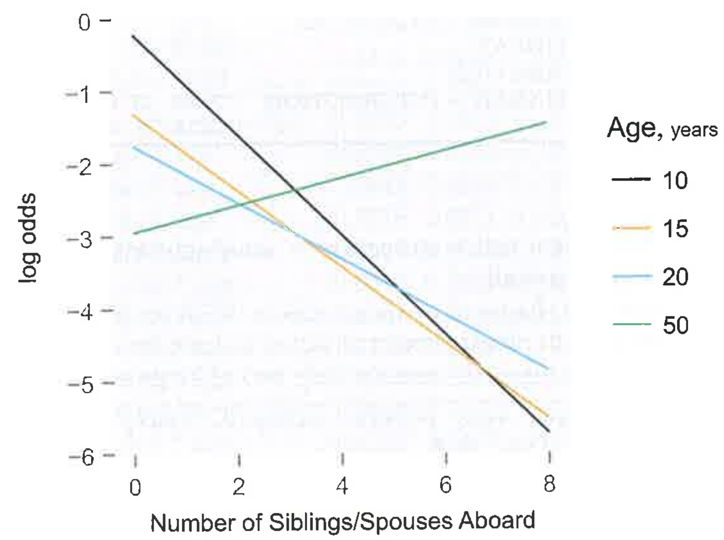

Fig. 12.6 Effect of number of siblings and spouses on the log odds of surviving, for third class males

for testing three-way interactions, in the belief that these tests would replicate well.

```
f ← update(f, x=TRUE, y=TRUE)
# x=TRUE, y=TRUE adds raw data to fit object so can bootstrap
set.seed(131)                 # so can replicate re-samples
latex(validate(f, B=200), digits=2, size='Ssize')
```


Index	Original Sample	Training Sample	Test Sample	Optimism	Corrected Index	n
D_{xy}	0.76	0.77	0.74	0.03	0.72	200
R^2	0.55	0.58	0.53	0.05	0.50	200
Intercept	0.00	0.00	−0.08	0.08	−0.08	200
Slope	1.00	1.00	0.87	0.13	0.87	200
$E_{\max}$	0.00	0.00	0.05	0.05	0.05	200
D	0.53	0.56	0.50	0.06	0.46	200
U	0.00	0.00	0.01	−0.01	0.01	200
Q	0.53	0.56	0.49	0.07	0.46	200
B	0.13	0.13	0.13	−0.01	0.14	200
g	2.43	2.75	2.37	0.37	2.05	200
g_p	0.37	0.37	0.35	0.02	0.35	200

```
cal ← calibrate(f, B=200)          # Figure 12.7
plot(cal, subtitles=FALSE)
```

```
n=1046   Mean absolute error=0.009   Mean squared error=0.00012
0.9 Quantile of absolute error=0.017
```

The output of `validate` indicates minor overfitting. Overfitting would have been worse had the risk factors not been so strong. The closeness of the calibration curve to the 45° line in Figure 12.7 demonstrates excellent validation on an absolute probability scale. But the extent of missing data casts some doubt on the validity of this model, and on the efficiency of its parameter estimates.

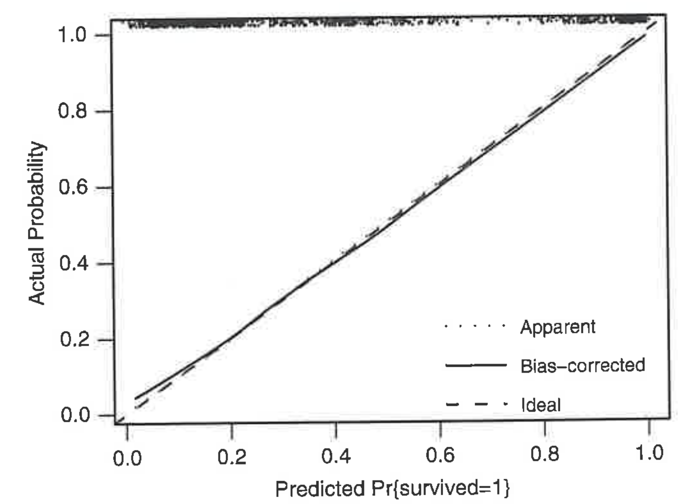

Fig. 12.7 Bootstrap overfitting-corrected loess nonparametric calibration curve for casewise deletion model

12.4 Examining Missing Data Patterns

The first step to dealing with missing data is understanding the patterns of missing values. To do this we use the Hmisc library's naclus and naplot functions, and the recursive partitioning library of Atkinson and Therneau. Below naclus tells us which variables tend to be missing on the same persons, and it computes the proportion of missing values for each variable. The rpart function derives a tree to predict which types of passengers tended to have age missing.

```
na.patterns ← naclus(titanic3)
require(rpart)      # Recursive partitioning package
```

```
who.na ← rpart(is.na(age) ~ sex + pclass + survived +
               sibsp + parch, data=titanic3, minbucket=15)
naplot(na.patterns, 'na per var')
plot(who.na, margin=.1); text(who.na) # Figure 12.8
plot(na.patterns)
```

We see in Figure 12.8 that age tends to be missing on the same passengers as the body bag identifier, and that it is missing in only 0.09 of first or second class passengers. The category of passengers having the highest fraction of missing ages is third class passengers having no parents or children on board. Below we use Hmisc's summary.formula function to plot simple descriptive statistics on the fraction of missing ages, stratified by other variables. We see that without adjusting for other variables, age is slightly more missing on nonsurviving passengers.

```
plot(summary(is.na(age) ~ sex + pclass + survived +
             sibsp + parch, data=t3))  # Figure 12.9
```

Let us derive a logistic model to predict missingness of age, to see if the survival bias maintains after adjustment for the other variables.

```
m ← lrm(is.na(age) ~ sex * pclass + survived + sibsp + parch,
        data=t3)
print(m, latex=TRUE, needspace='2in')
```

Logistic Regression Model

```
lrm(formula = is.na(age) ~ sex * pclass + survived + sibsp +
    parch, data = t3)
```

		Model Likelihood Ratio Test		Discrimination Indexes		Rank Discrim. Indexes	
Obs	1309	LR χ^2	114.99	R^2	0.133	C	0.703
FALSE	1046	d.f.	8	g	1.015	D_{xy}	0.406
TRUE	263	$\Pr(>\chi^2)$	<0.0001	g_r	2.759	γ	0.452
$\max\lvert\frac{\partial \log L}{\partial \beta}\rvert$	5×10^{-6}			g_p	0.126	τ_a	0.131
				Brier	0.148		

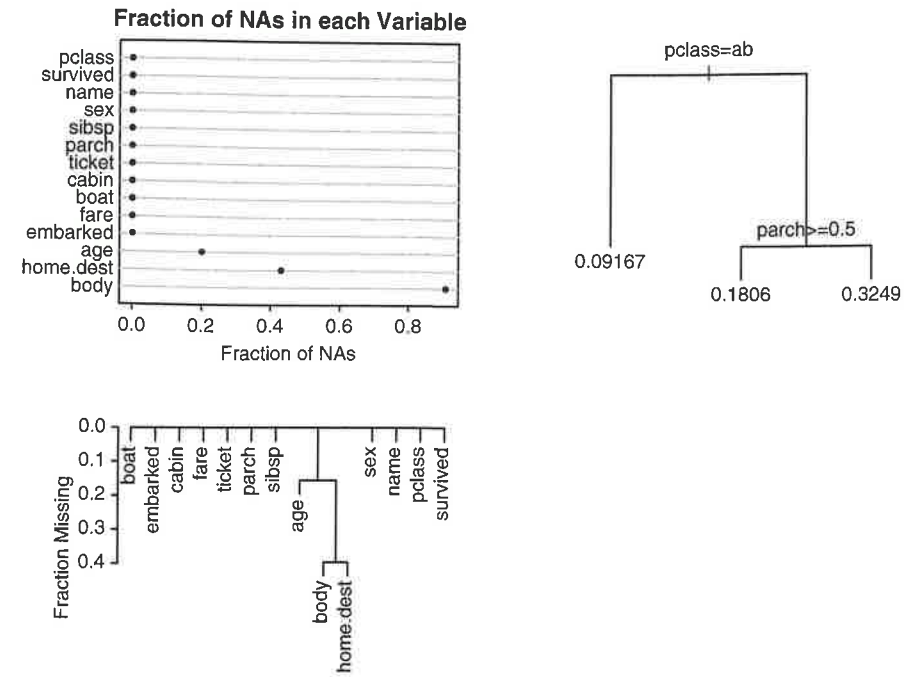

Fig. 12.8 Patterns of missing data. Upper left panel shows the fraction of observations missing on each predictor. Lower panel depicts a hierarchical cluster analysis of missingness combinations. The similarity measure shown on the Y-axis is the fraction of observations for which both variables are missing. Right panel shows the result of recursive partitioning for predicting is.na(age). The rpart function found only strong patterns according to passenger class.

	Coef	S.E.	Wald Z	$\Pr(>\lvert Z\rvert)$
Intercept	-2.2030	0.3641	-6.05	<0.0001
sex=male	0.6440	0.3953	1.63	0.1033
pclass=2nd	-1.0079	0.6658	-1.51	0.1300
pclass=3rd	1.6124	0.3596	4.48	<0.0001
survived	-0.1806	0.1828	-0.99	0.3232
sibsp	0.0435	0.0737	0.59	0.5548
parch	-0.3526	0.1253	-2.81	0.0049
sex=male * pclass=2nd	0.1347	0.7545	0.18	0.8583
sex=male * pclass=3rd	-0.8563	0.4214	-2.03	0.0422

```
latex(anova(m), file='', label='titanic-anova.na')
   # Table 12.3
```

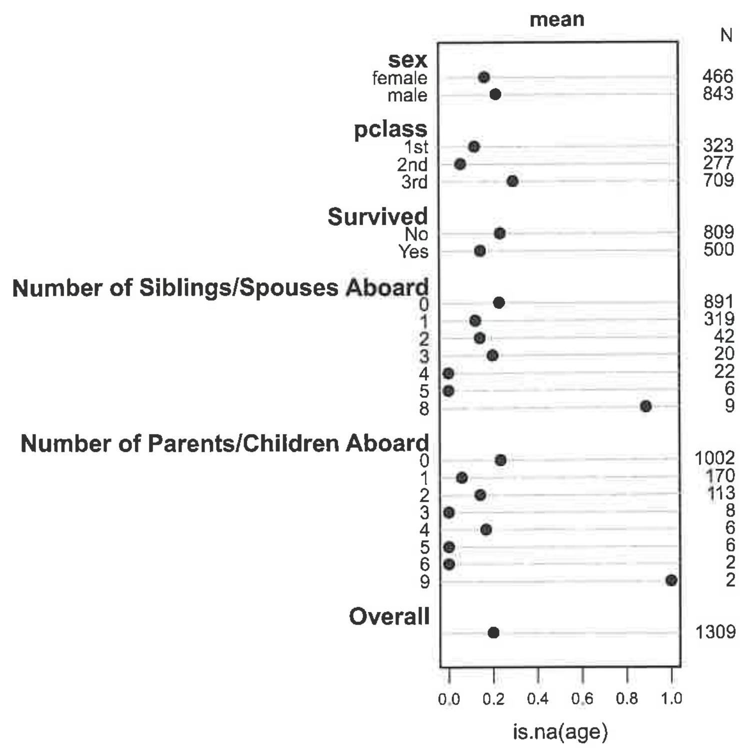

Fig. 12.9 Univariable descriptions of proportion of passengers with missing age

Fortunately, after controlling for other variables, Table 12.3 provides evidence that nonsurviving passengers are no more likely to have age missing. The only important predictors of missingness are `pclass` and `parch` (the more parents or children the passenger has on board, the less likely age was to be missing).

12.5 Multiple Imputation

Multiple imputation is expected to reduce bias in estimates as well as to provide an estimate of the variance–covariance matrix of $\hat{\beta}$ penalized for imputation. With multiple imputation, survival status can be used to impute missing ages, so the age relationship will not be as attenuated as with single conditional mean imputation. `aregImpute` The following uses the Hmisc package `aregImpute` function to do predictive mean matching, using van Buuren's "Type 1" matching [85, Section 3.4.2] in conjunction with bootstrapping to incorporate all uncertainties, in the context of smooth additive imputation

Table 12.3 Wald Statistics for `is.na(age)`

	χ^2	d.f.	P
sex (Factor+Higher Order Factors)	5.61	3	0.1324
All Interactions	5.58	2	0.0614
pclass (Factor+Higher Order Factors)	68.43	4	< 0.0001
All Interactions	5.58	2	0.0614
survived	0.98	1	0.3232
sibsp	0.35	1	0.5548
parch	7.92	1	0.0049
sex × pclass (Factor+Higher Order Factors)	5.58	2	0.0614
TOTAL	82.90	8	< 0.0001

models. Sampling of donors is handled by distance weighting to yield better distributions of imputed values. By default, `aregImpute` does not transform `age` when it is being predicted from the other variables. Four knots are used to transform `age` when used to impute other variables (not needed here as no other missings were present in the variables of interest). Since the fraction of observations with missing age is $\frac{263}{1309} = 0.2$ we use 20 imputations.

```
set.seed(17)          # so can reproduce random aspects
mi ← aregImpute(~ age + sex + pclass +
                sibsp + parch + survived,
                data=t3, n.impute=20, nk=4, pr=FALSE)
```

```
mi
```

```
Multiple Imputation using Bootstrap and PMM

aregImpute(formula = ~age + sex + pclass + sibsp + parch + survived,
    data = t3, n.impute = 20, nk = 4, pr = FALSE)

n: 1309        p: 6    Imputations: 20         nk: 4

Number of NAs:
      age      sex    pclass     sibsp     parch survived
      263        0         0         0         0        0

         type d.f.
age         s    1
sex         c    1
pclass      c    2
sibsp       s    2
parch       s    2
survived    l    1

Transformation of Target Variables Forced to be Linear

R-squares for Predicting Non-Missing Values for Each Variable
Using Last Imputations of Predictors
  age
0.295
```

```
# Print the first 10 imputations for the first 10 passengers
#  having missing age
mi$imputed$age[1:10, 1:10]
```

```
    [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10]
16    40   49   24   29 60.0   58   64   36   50    61
38    33   45   40   49 80.0    2   38   38   36    53
41    29   24   19   31 40.0   60   64   42   30    65
47    40   42   29   48 36.0   46   64   30   38    42
60    52   40   22   31 38.0   22   19   24   40    33
70    16   14   23   23 18.0   24   19   27   59    23
71    30   62   57   30 42.0   31   64   40   40    63
75    43   23   36   61 45.5   58   64   27   24    50
81    44   57   47   31 45.0   30   64   62   39    67
107   52   18   24   62 32.5   38   64   47   19    23
```

```
plot(mi)
Ecdf(t3$age, add=TRUE, col='gray', lwd=2,
     subtitles=FALSE) #Fig. 12.10
```

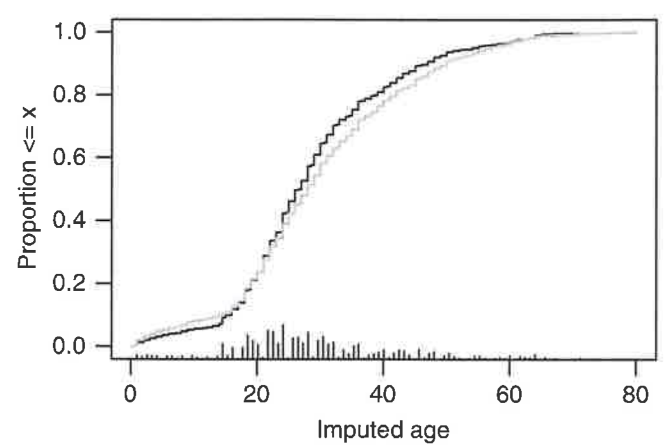

Fig. 12.10 Distributions of imputed and actual ages for the Titanic dataset. Imputed values are in black and actual ages in gray.

We now fit logistic models for five completed datasets. The `fit.mult.impute` function fits five models and examines the within– and between–imputation variances to compute an imputation-corrected variance–covariance matrix that is stored in the fit object `f.mi`. `fit.mult.impute` will also average the five $\hat{\beta}$ vectors, storing the result in `f.mi$coefficients`. The function also prints the ratio of imputation-corrected variances to average ordinary variances.

```
f.mi ← fit.mult.impute(
  survived ~ (sex + pclass + rcs(age,5))^2 +
  rcs(age,5)*sibsp,
```


Table 12.4 Wald Statistics for `survived`

	χ^2	d.f.	P
sex (Factor+Higher Order Factors)	240.42	7	< 0.0001
All Interactions	54.56	6	< 0.0001
pclass (Factor+Higher Order Factors)	114.21	12	< 0.0001
All Interactions	36.43	10	0.0001
age (Factor+Higher Order Factors)	50.37	20	0.0002
All Interactions	25.88	16	0.0557
Nonlinear (Factor+Higher Order Factors)	24.21	15	0.0616
sibsp (Factor+Higher Order Factors)	24.22	5	0.0002
All Interactions	12.86	4	0.0120
sex × pclass (Factor+Higher Order Factors)	30.99	2	< 0.0001
sex × age (Factor+Higher Order Factors)	11.38	4	0.0226
Nonlinear	8.15	3	0.0430
Nonlinear Interaction : f(A,B) vs. AB	8.15	3	0.0430
pclass × age (Factor+Higher Order Factors)	5.30	8	0.7246
Nonlinear	4.63	6	0.5918
Nonlinear Interaction : f(A,B) vs. AB	4.63	6	0.5918
age × sibsp (Factor+Higher Order Factors)	12.86	4	0.0120
Nonlinear	1.84	3	0.6058
Nonlinear Interaction : f(A,B) vs. AB	1.84	3	0.6058
TOTAL NONLINEAR	24.21	15	0.0616
TOTAL INTERACTION	67.12	18	< 0.0001
TOTAL NONLINEAR + INTERACTION	70.99	21	< 0.0001
TOTAL	298.78	26	< 0.0001

```
  lrm, mi, data=t3, pr=FALSE)
latex(anova(f.mi), file='', label='titanic-anova.mi',
      size='small')   # Table 12.4
```

The Wald χ^2 for age is reduced by accounting for imputation but is increased (by a lesser amount) by using patterns of association with survival status to impute missing age. The Wald tests are all adjusted for multiple imputation. Now examine the fitted age relationship using multiple imputation vs. casewise deletion.

```
p1 ← Predict(f,     age, pclass, sex, sibsp=0, fun=plogis)
p2 ← Predict(f.mi,  age, pclass, sex, sibsp=0, fun=plogis)
p  ← rbind('Casewise Deletion'=p1, 'Multiple Imputation'=p2)
ggplot(p, groups='sex', ylab='Probability of Surviving')
# Figure 12.11
```

12.6 Summarizing the Fitted Model

In this section we depict the model fitted using multiple imputation, by computing odds ratios and by showing various predicted values. For age, the odds ratio for an increase from 1 year old to 30 years old is computed, instead of the default odds ratio based on outer quartiles of age. The estimated odds

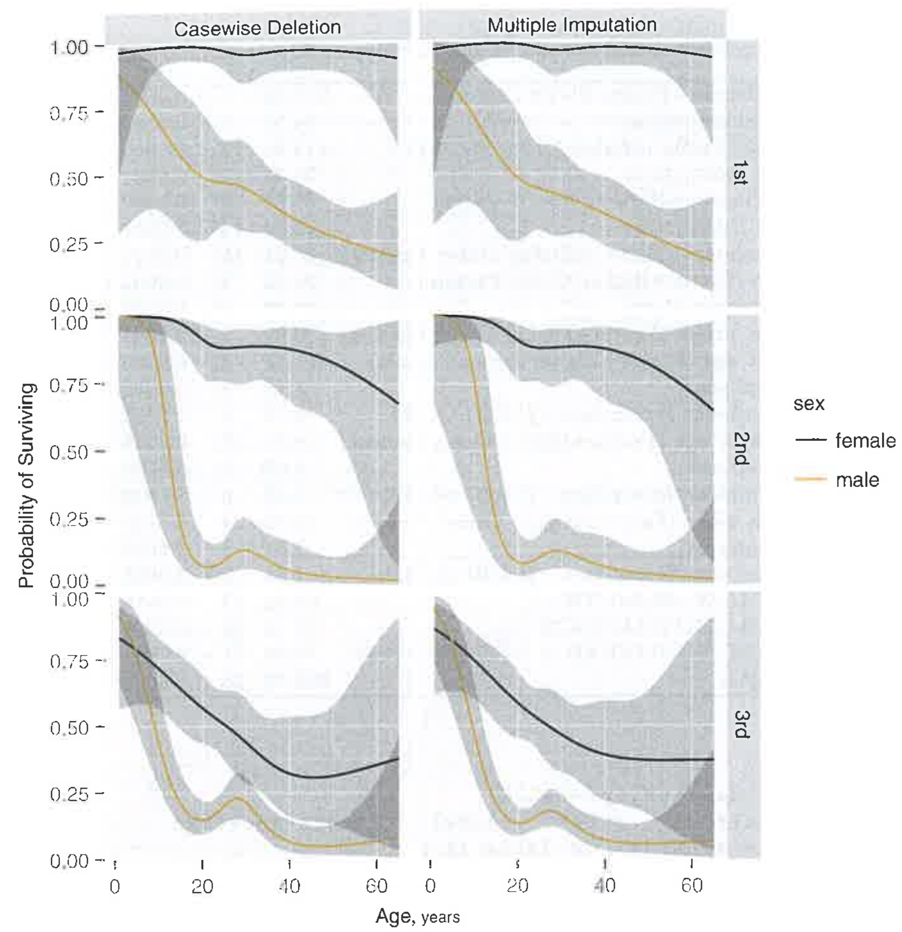

Fig. 12.11 Predicted probability of survival for males from fit using casewise deletion again (top) and multiple random draw imputation (bottom). Both sets of predictions are for `sibsp`=0.

ratios are very dependent on the levels of interacting factors, so Figure 12.12 depicts only one of many patterns.

```
# Get predicted values for certain types of passengers
s ← summary(f.mi, age=c(1,30), sibsp=0:1)
# override default ranges for 3 variables
plot(s, log=TRUE, main='')          # Figure 12.12
```

Now compute estimated probabilities of survival for a variety of settings of the predictors.

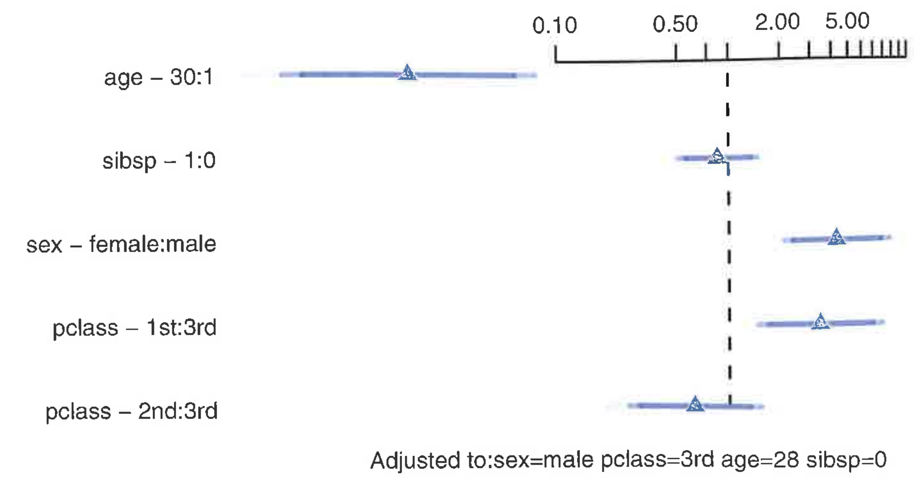

Fig. 12.12 Odds ratios for some predictor settings

```
phat ← predict(f.mi,
               combos ←
         expand.grid(age=c(2,21,50), sex=levels(t3$sex),
                     pclass=levels(t3$pclass),
                     sibsp=0), type='fitted')
# Can also use Predict(f.mi, age=c(2,21,50), sex, pclass,
#                      sibsp=0, fun=plogis)$yhat
options(digits=1)
data.frame(combos, phat)
```

	age	sex	pclass	sibsp	phat
1	2	female	1st	0	0.97
2	21	female	1st	0	0.98
3	50	female	1st	0	0.97
4	2	male	1st	0	0.88
5	21	male	1st	0	0.48
6	50	male	1st	0	0.27
7	2	female	2nd	0	1.00
8	21	female	2nd	0	0.90
9	50	female	2nd	0	0.82
10	2	male	2nd	0	1.00
11	21	male	2nd	0	0.08
12	50	male	2nd	0	0.04
13	2	female	3rd	0	0.85
14	21	female	3rd	0	0.57
15	50	female	3rd	0	0.37
16	2	male	3rd	0	0.91
17	21	male	3rd	0	0.13
18	50	male	3rd	0	0.06

```
options(digits=5)
```

We can also get predicted values by creating an R function that will evaluate the model on demand.

```
pred.logit ← Function(f.mi)
# Note: if don't define sibsp to pred.logit, defaults to 0
# normally just type the function name to see its body
latex(pred.logit, file='', type='Sinput', size='small',
      width.cutoff=49)
```

```
pred.logit ← function (sex = "male", pclass = "3rd",
    age = 28, sibsp = 0)
{
    3.2427671 − 0.95431809 * (sex == "male") + 5.4086505 *
        (pclass == "2nd") − 1.3378623 * (pclass ==
        "3rd") + 0.091162649 * age − 0.00031204327 *
        pmax(age − 6, 0)^3 + 0.0021750413 * pmax(age −
        21, 0)^3 − 0.0027627032 * pmax(age − 27, 0)^3 +
        0.0009805137 * pmax(age − 36, 0)^3 − 8.0808484e−05 *
        pmax(age − 55.8, 0)^3 − 1.1567976 * sibsp +
        (sex == "male") * (−0.46061284 * (pclass ==
            "2nd") + 2.0406523 * (pclass == "3rd")) +
        (sex == "male") * (−0.22469066 * age + 0.00043708296 *
            pmax(age − 6, 0)^3 − 0.0026505136 * pmax(age −
            21, 0)^3 + 0.0031201404 * pmax(age − 27,
            0)^3 − 0.00097923749 * pmax(age − 36,
            0)^3 + 7.2527708e−05 * pmax(age − 55.8,
            0)^3) + (pclass == "2nd") * (−0.46144083 *
        age + 0.00070194849 * pmax(age − 6, 0)^3 −
        0.0034726662 * pmax(age − 21, 0)^3 + 0.0035255387 *
        pmax(age − 27, 0)^3 − 0.0007900891 * pmax(age −
        36, 0)^3 + 3.5268151e−05 * pmax(age − 55.8,
        0)^3) + (pclass == "3rd") * (−0.17513289 *
        age + 0.00035283358 * pmax(age − 6, 0)^3 −
        0.0023049372 * pmax(age − 21, 0)^3 + 0.0028978962 *
        pmax(age − 27, 0)^3 − 0.00105145 * pmax(age −
        36, 0)^3 + 0.00010565735 * pmax(age − 55.8,
        0)^3) + sibsp * (0.040830773 * age − 1.5627772e−05 *
        pmax(age − 6, 0)^3 + 0.00012790256 * pmax(age −
        21, 0)^3 − 0.00025039385 * pmax(age − 27,
        0)^3 + 0.00017871701 * pmax(age − 36, 0)^3 −
        4.0597949e−05 * pmax(age − 55.8, 0)^3)
}
```

```
# Run the newly created function
plogis(pred.logit(age=c(2,21,50), sex='male', pclass='3rd'))
```

```
[1] 0.914817 0.132640 0.056248
```

A nomogram could be used to obtain predicted values manually, but this is not feasible when so many interaction terms are present.

Chapter 13
Ordinal Logistic Regression

13.1 Background

Many medical and epidemiologic studies incorporate an ordinal response variable. In some cases an ordinal response Y represents levels of a standard measurement scale such as severity of pain (none, mild, moderate, severe). In other cases, ordinal responses are constructed by specifying a hierarchy of separate endpoints. For example, clinicians may specify an ordering of the severity of several component events and assign patients to the worst event present from among none, heart attack, disabling stroke, and death. Still another use of ordinal response methods is the application of rank-based methods to continuous responses so as to obtain robust inferences. For example, the proportional odds model described later allows for a continuous Y and is really a generalization of the Wilcoxon–Mann–Whitney rank test. Thus the semiparametric proportional odds model is a direct competitor of ordinary linear models.

There are many variations of logistic models used for predicting an ordinal response variable Y. All of them have the advantage that they do not assume a spacing between levels of Y. In other words, the same regression coefficients and P-values result from an analysis of a response variable having levels $0, 1, 2$ when the levels are recoded $0, 1, 20$. Thus ordinal models use only the rank-ordering of values of Y.

In this chapter we consider two of the most popular ordinal logistic models, the proportional odds (PO) form of an ordinal logistic model[647] and the forward continuation ratio (CR) ordinal logistic model.[190] Chapter 15 deals with a wider variety of ordinal models with emphasis on analysis of continuous Y. 1

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