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cv: An R Package for Cross-Validation of Regression Models

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Abstract

The abstract of the article.

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1. Cross-validation

Cross-validation (CV) is an essentially simple and intuitively reasonable approach to estimating the predictive accuracy of regression models. CV is developed in many standard sources on regression modeling and "machine learning"—we particularly recommend James, Witten, Hastie, and Tibshirani (2021, Secs. 5.1, 5.3)—and so we will describe the method only briefly here before taking up computational issues and some examples. See Arlot and Celisse (2010) for a wide-ranging, if technical, survey of cross-validation and related methods that emphasizes the statistical properties of CV.

Validating research by replication on independently collected data is a common scientific norm. Emulating this process in a single study by data-division is less common: The data are randomly divided into two, possibly equal-size, parts; the first part is used to develop and fit a statistical model; and then the second part is used to assess the adequacy of the model fit to the first part of the data. Data-division, however, suffers from two problems: (1) Dividing the data decreases the sample size and thus increases sampling error; and (2), even more disconcertingly, particularly in smaller samples, the results can vary substantially based on the random division of the data: See Harrell (2015, Sec. 5.3) for this and other remarks about data-division and cross-validation.

Cross-validation speaks to both of these issues. In CV, the data are randomly divided as equally as possible into several, say k, parts, called "folds." The statistical model is fit k times, leaving each fold out in turn. Each fitted model is then used to predict the response

variable for the cases in the omitted fold. A CV criterion or "cost" measure, such as the mean-squared error ("MSE") of prediction, is then computed using these predicted values. In the extreme $k = n$, the number of cases in the data, thus omitting individual cases and refitting the model n times—a procedure termed "leave-one-out (LOO) cross-validation."

Because the n models are each fit to $n-1$ cases, LOO CV produces a nearly unbiased estimate of prediction error. The n regression models are highly statistical dependent, however, based as they are on nearly the same data, and so the resulting estimate of prediction error has relatively large variance. In contrast, estimated prediction error for k-fold CV with $k = 5$ or 10 (commonly employed choices) are somewhat biased but have smaller variance. It is also possible to correct k-fold CV for bias (see below).

2. Examples

2.1. Polynomial regression for the Auto data

The data for this example are drawn from the **ISLR2** package for R, associated with James *et al.* (2021). The presentation here is close (though not identical) to that in the original source (James *et al.* 2021, Secs. 5.1, 5.3), and it demonstrates the use of the `cv()` function in the **cv** package.[1]

The `Auto` dataset contains information about 392 cars:

```
R> data("Auto", package="ISLR2")
R> head(Auto)
```

```
  mpg cylinders displacement horsepower weight acceleration year origin
1  18         8          307        130   3504         12.0   70      1
2  15         8          350        165   3693         11.5   70      1
3  18         8          318        150   3436         11.0   70      1
4  16         8          304        150   3433         12.0   70      1
5  17         8          302        140   3449         10.5   70      1
6  15         8          429        198   4341         10.0   70      1
                       name
1 chevrolet chevelle malibu
2         buick skylark 320
3        plymouth satellite
4             amc rebel sst
5               ford torino
6          ford galaxie 500
```

```
R> dim(Auto)
```

```
[1] 392   9
```

[1] James *et al.* (2021) use the `cv.glm()` function in the **boot** package (Canty and Ripley 2022; Davison and Hinkley 1997). Despite its name, `cv.glm()` is an independent function and not a method of a `cv()` generic function.

With the exception of `origin` (which we don't use here), these variables are largely self-explanatory, except possibly for units of measurement: for details see `help("Auto", package="ISLR2")`.

We'll focus here on the relationship of `mpg` (miles per gallon) to `horsepower`, as displayed in the following scatterplot:

```
R> plot(mpg ~ horsepower, data=Auto)
```

The relationship between the two variables is monotone, decreasing, and nonlinear. Following James *et al.* (2021), we'll consider approximating the relationship by a polynomial regression, with the degree of the polynomial p ranging from 1 (a linear regression) to 10.[2] Polynomial fits for $p = 1$ to 5 are shown in the following figure:

```
R> plot(mpg ~ horsepower, data=Auto)
R> horsepower <- with(Auto,
+                     seq(min(horsepower), max(horsepower),
+                         length=1000))
R> for (p in 1:5){
+   m <- lm(mpg ~ poly(horsepower,p), data=Auto)
+   mpg <- predict(m, newdata=data.frame(horsepower=horsepower))
+   lines(horsepower, mpg, col=p + 1, lty=p, lwd=2)
+ }
R> legend("topright", legend=1:5, col=2:6, lty=1:5, lwd=2,
+        title="Degree", inset=0.02)
```

The linear fit is clearly inappropriate; the fits for $p = 2$ (quadratic) through 4 are very similar; and the fit for $p = 5$ may over-fit the data by chasing one or two relatively high `mpg` values at the right (but see the CV results reported below).

The following graph shows two measures of estimated (squared) error as a function of polynomial-regression degree: The mean-squared error ("MSE"), defined as $\mathsf{MSE} = \frac{1}{n}\sum_{i=1}^{n}(y_i - \widehat{y}_i)^2$, and the usual residual variance, defined as $\widehat{\sigma}^2 = \frac{1}{n-p-1}\sum_{i=1}^{n}(y_i - \widehat{y}_i)^2$. The former necessarily declines with p (or, more strictly, can't increase with p), while the latter gets slightly larger for the largest values of p, with the "best" value, by a small margin, for $p = 7$.

```
R> library("cv") # for mse() and other functions

Loading required package: doParallel

Loading required package: foreach

Loading required package: iterators

Loading required package: parallel
```

[2] Although it serves to illustrate the use of CV, a polynomial is probably not the best choice here. Consider, for example the scatterplot for log-transformed `mpg` and `horsepower`, produced by `plot(mpg ~ horsepower, data=Auto, log="xy")` (execution of which is left to the reader).

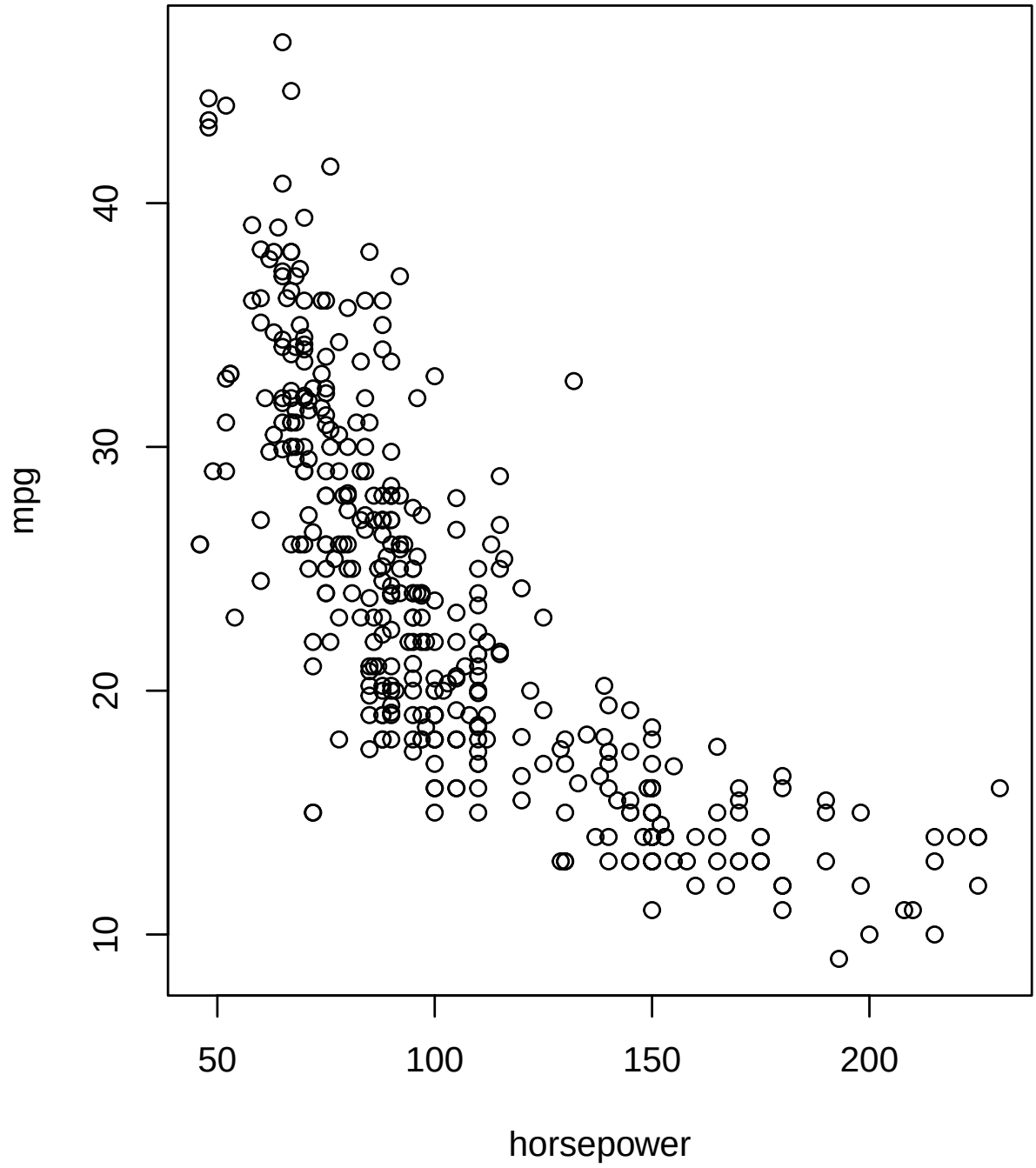


Figure 1: ‘mpg‘ vs ‘horsepower‘ for the ‘Auto‘ data

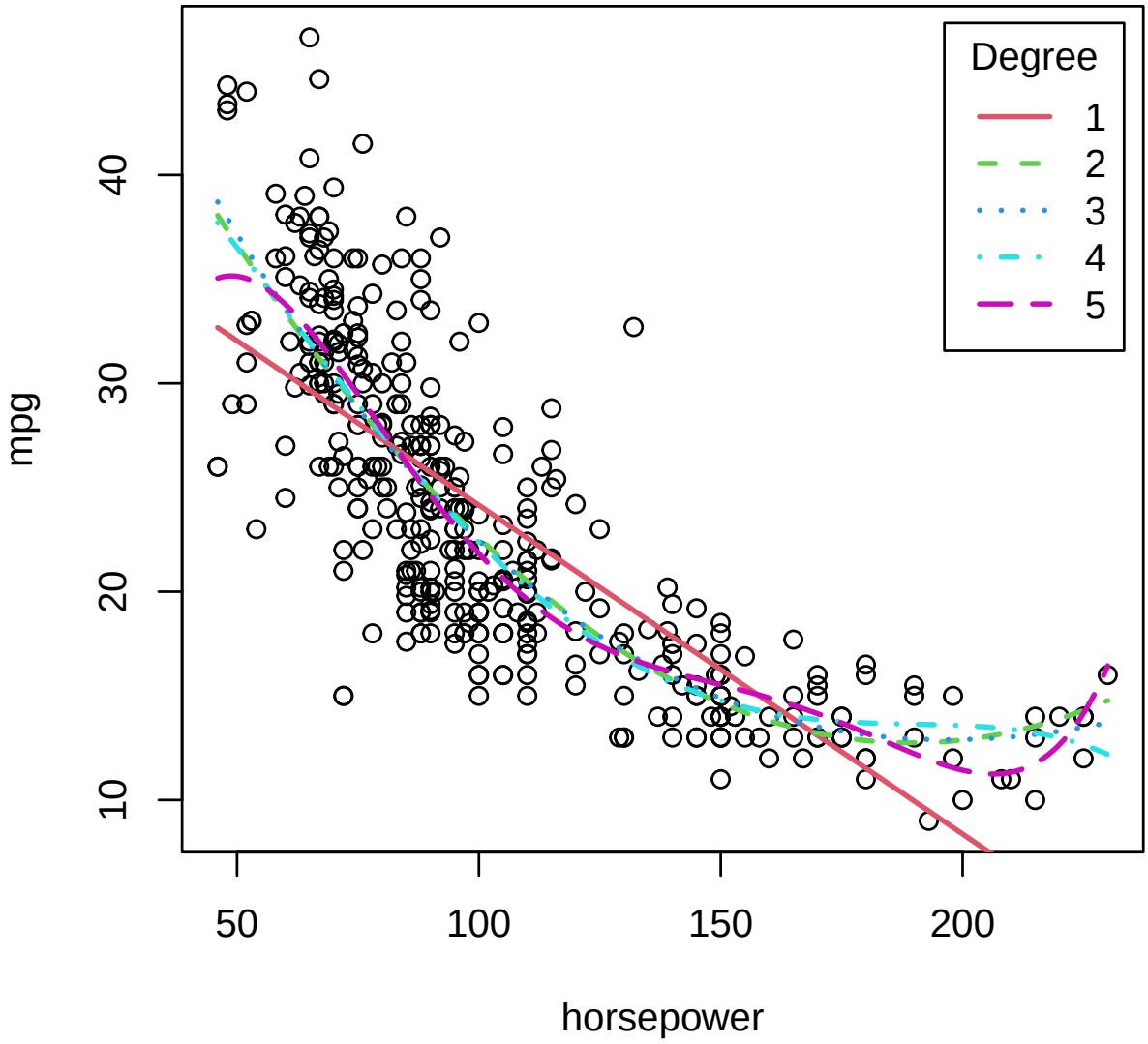


Figure 2: ‘mpg‘ vs ‘horsepower‘ for the ‘Auto‘ data

```
R> var <- mse <- numeric(10)
R> for (p in 1:10){
+   m <- lm(mpg ~ poly(horsepower, p), data=Auto)
+   mse[p] <- mse(Auto$mpg, fitted(m))
+   var[p] <- summary(m)$sigma^2
+ }
R>
R> plot(c(1, 10), range(mse, var), type="n",
+      xlab="Degree of polynomial, p",
+      ylab="Estimated Squared Error")
R> lines(1:10, mse, lwd=2, lty=1, col=2, pch=16, type="b")
R> lines(1:10, var, lwd=2, lty=2, col=3, pch=17, type="b")
R> legend("topright", inset=0.02,
+        legend=c(expression(hat(sigma)^2), "MSE"),
+        lwd=2, lty=2:1, col=3:2, pch=17:16)
```

The code for this graph uses the `mse()` function from the **cv** package to compute the MSE for each fit.

Using cv()

The generic `cv()` function has an `"lm"` method, which by default performs $k = 10$-fold CV:

```
R> m.auto <- lm(mpg ~ poly(horsepower, 2), data=Auto)
R> summary(m.auto)


Call:
lm(formula = mpg ~ poly(horsepower, 2), data = Auto)

Residuals:
     Min       1Q   Median       3Q      Max
-14.7135  -2.5943  -0.0859   2.2868  15.8961

Coefficients:
                     Estimate Std. Error t value Pr(>|t|)
(Intercept)           23.4459     0.2209  106.13   <2e-16
poly(horsepower, 2)1 -120.1377     4.3739  -27.47   <2e-16
poly(horsepower, 2)2   44.0895     4.3739   10.08   <2e-16

Residual standard error: 4.374 on 389 degrees of freedom
Multiple R-squared:  0.6876,    Adjusted R-squared:  0.686
F-statistic:   428 on 2 and 389 DF,  p-value: < 2.2e-16

R> cv(m.auto)

R RNG seed set to 44768
```

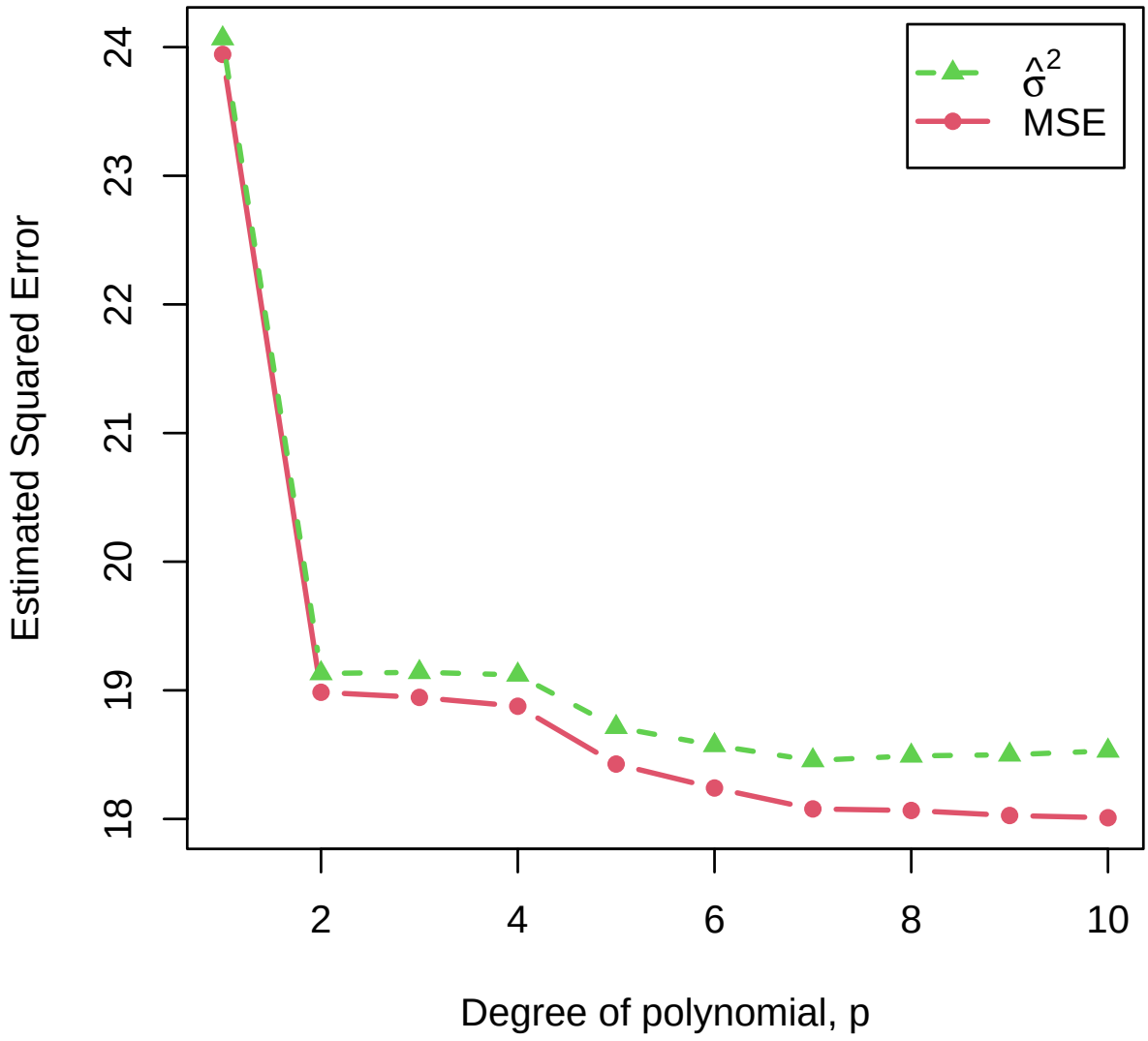


Figure 3: Estimated squared error as a function of polynomial degree, p

```
10-Fold Cross Validation
method: Woodbury
criterion: mse
cross-validation criterion = 19.52622
bias-adjusted cross-validation criterion = 19.49747
full-sample criterion = 18.98477
```

The `"lm"` method by default uses `mse()` as the CV criterion and the Woodbury matrix identity to update the regression with each fold deleted without having literally to refit the model. Computational details are discussed in the final section of this vignette. The function reports the CV estimate of MSE, a biased-adjusted estimate of the MSE (the bias adjustment is explained in the final section), and the MSE is also computed for the original, full-sample regression. Because the division of the data into 10 folds is random, `cv()` explicitly (randomly) generates and saves a seed for R's pseudo-random number generator, to make the results replicable. The user can also specify the seed directly via the `seed` argument to `cv()`.

To perform LOO CV, we can set the `k` argument to `cv()` to the number of cases in the data, here `k=392`, or, more conveniently, to `k="loo"` or `k="n"`:

```
R> cv(m.auto, k="loo")

n-Fold Cross Validation
method: hatvalues
criterion: mse
cross-validation criterion = 19.24821
```

For LOO CV of a linear model, `cv()` by default uses the hatvalues from the model fit to the full data for the LOO updates, and reports only the CV estimate of MSE. Alternative methods are to use the Woodbury matrix identity or the "naive" approach of literally refitting the model with each case omitted. All three methods produce exact results for a linear model (within the precision of floating-point computations):

```
R> cv(m.auto, k="loo", method="naive")

n-Fold Cross Validation
method: naive
criterion: mse
cross-validation criterion = 19.24821
bias-adjusted cross-validation criterion = 19.24787
full-sample criterion = 18.98477

R> cv(m.auto, k="loo", method="Woodbury")

n-Fold Cross Validation
method: Woodbury
criterion: mse
cross-validation criterion = 19.24821
bias-adjusted cross-validation criterion = 19.24787
full-sample criterion = 18.98477
```

The "naive" and "Woodbury" methods also return the bias-adjusted estimate of MSE and the full-sample MSE, but bias isn't an issue for LOO CV.

This is a small regression problem and all three computational approaches are essentially instantaneous, but it is still of interest to investigate their relative speed. In this comparison, we include the cv.glm() function from the **boot** package, which takes the naive approach, and for which we have to fit the linear model as an equivalent Gaussian GLM. We use the microbenchmark() function from the package of the same name for the timings (Mersmann 2023):

```
R> m.auto.glm <- glm(mpg ~ poly(horsepower, 2), data=Auto)
R> boot::cv.glm(Auto, m.auto.glm)$delta

[1] 19.24821 19.24787

R> microbenchmark::microbenchmark(
+   hatvalues = cv(m.auto, k="loo"),
+   Woodbury = cv(m.auto, k="loo", method="Woodbury"),
+   naive = cv(m.auto, k="loo", method="naive"),
+   cv.glm = boot::cv.glm(Auto, m.auto.glm),
+   times=10
+ )

Warning in microbenchmark::microbenchmark(hatvalues = cv(m.auto, k = "loo"), :
less accurate nanosecond times to avoid potential integer overflows

Unit: microseconds
      expr        min         lq       mean     median         uq        max
 hatvalues    977.973    993.43   1143.433   1173.113   1202.981   1296.256
  Woodbury   9932.004  10178.21  11461.993  10363.201  10865.943  17762.266
     naive 215384.152 217809.02 224546.766 219116.505 221670.231 275518.278
    cv.glm 384357.616 388159.59 409612.546 390652.100 441741.913 443226.605
 neval cld
    10 a
    10 a
    10  b
    10   c
```

On our computer, using the hatvalues is about an order of magnitude faster than employing Woodbury matrix updates, and more than two orders of magnitude faster than refitting the model.[3]

Comparing competing models

[3]Out of impatience, we asked microbenchmark() to execute each command only 10 times rather than the default 100. With the exception of the last columns, the output is self-explanatory. The last column shows which methods have average timings that are statistically distinguishable. Because of the small number of repetitions (i.e., 10), the "hatvalues" and "Woodbury" methods aren't distinguishable, but the difference between these methods persists when we perform more repetitions—we invite the reader to redo this computation with the default times=100 repetitions.

The `cv()` function also has a method that can be applied to a list of regression models for the same data, composed using the `models()` function. For k-fold CV, the same folds are used for the competing models, which reduces random error in their comparison. This result can also be obtained by specifying a common seed for R's random-number generator while applying `cv()` separately to each model, but employing a list of models is more convenient for both k-fold and LOO CV (where there is no random component to the composition of the n folds).

We illustrate with the polynomial regression models of varying degree for the `Auto` data (discussed previously), beginning by fitting and saving the 10 models:

```
R> for (p in 1:10){
+   assign(paste0("m.", p),
+          lm(mpg ~ poly(horsepower, p), data=Auto))
+ }
R> objects(pattern="m\\.[0-9]")

 [1] "m.1"  "m.10" "m.2"  "m.3"  "m.4"  "m.5"  "m.6"  "m.7"  "m.8"  "m.9"

R> summary(m.2) # for example, the quadratic fit



Call:
lm(formula = mpg ~ poly(horsepower, p), data = Auto)

Residuals:
     Min       1Q   Median       3Q      Max
-14.7135  -2.5943  -0.0859   2.2868  15.8961

Coefficients:
                     Estimate Std. Error t value Pr(>|t|)
(Intercept)           23.4459     0.2209  106.13   <2e-16
poly(horsepower, p)1 -120.1377     4.3739  -27.47   <2e-16
poly(horsepower, p)2   44.0895     4.3739   10.08   <2e-16

Residual standard error: 4.374 on 389 degrees of freedom
Multiple R-squared:  0.6876,    Adjusted R-squared:  0.686
F-statistic:   428 on 2 and 389 DF,  p-value: < 2.2e-16
```

We then apply `cv()` to the list of 10 models (the `data` argument is required):

```
R> # 10-fold CV
R> cv.auto.10 <- cv(models(m.1, m.2, m.3, m.4, m.5,
+                      m.6, m.7, m.8, m.9, m.10),
+                data=Auto, seed=2120)
R> cv.auto.10[1:2] # for the linear and quadratic models
```

```
Model model.1:
10-Fold Cross Validation
method: Woodbury
cross-validation criterion = 24.24642
bias-adjusted cross-validation criterion = 24.23039
full-sample criterion = 23.94366

Model model.2:
10-Fold Cross Validation
method: Woodbury
cross-validation criterion = 19.34601
bias-adjusted cross-validation criterion = 19.32699
full-sample criterion = 18.98477
```

```
R> # LOO CV
R> cv.auto.loo <- cv(models(m.1, m.2, m.3, m.4, m.5,
+                           m.6, m.7, m.8, m.9, m.10),
+                    data=Auto, k="loo")
R> cv.auto.loo[1:2] # linear and quadratic models
```

```
Model model.1:
n-Fold Cross Validation
method: hatvalues
cross-validation criterion = 24.23151
Model model.2:
n-Fold Cross Validation
method: hatvalues
cross-validation criterion = 19.24821
```

Because we didn't supply names for the models in the calls to the `models()` function, the names `model.1`, `model.2`, etc., are generated by the function.

Finally, we extract and graph the adjusted MSEs for 10-fold CV and the MSEs for LOO CV:

```
R> cv.mse.10 <- sapply(cv.auto.10, function(x) x[["adj CV crit"]])
R> cv.mse.loo <- sapply(cv.auto.loo, function(x) x[["CV crit"]])
R> plot(c(1, 10), range(cv.mse.10, cv.mse.loo), type="n",
+      xlab="Degree of polynomial, p",
+      ylab="Cross-Validated MSE")
R> lines(1:10, cv.mse.10, lwd=2, lty=1, col=2, pch=16, type="b")
R> lines(1:10, cv.mse.loo, lwd=2, lty=2, col=3, pch=17, type="b")
R> legend("topright", inset=0.02,
+        legend=c("10-Fold CV", "LOO CV"),
+        lwd=2, lty=2:1, col=3:2, pch=17:16)
```

Alternatively, we can use the `plot()` method for `"cvModList"` objects to compare the models, though with separate graphs for 10-fold and LOO CV:

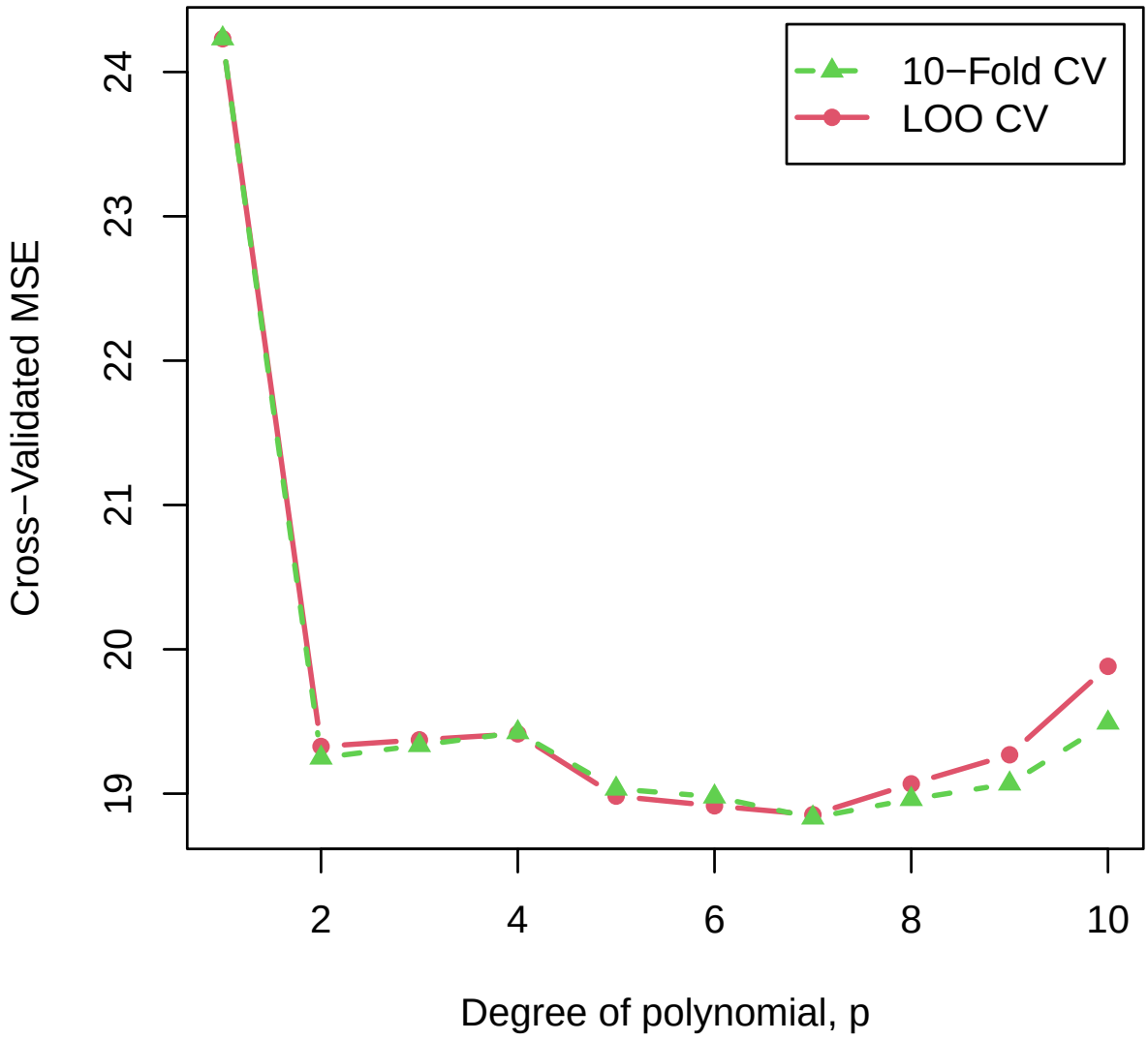


Figure 4: Cross-validated 10-fold and LOO MSE as a function of polynomial degree, p

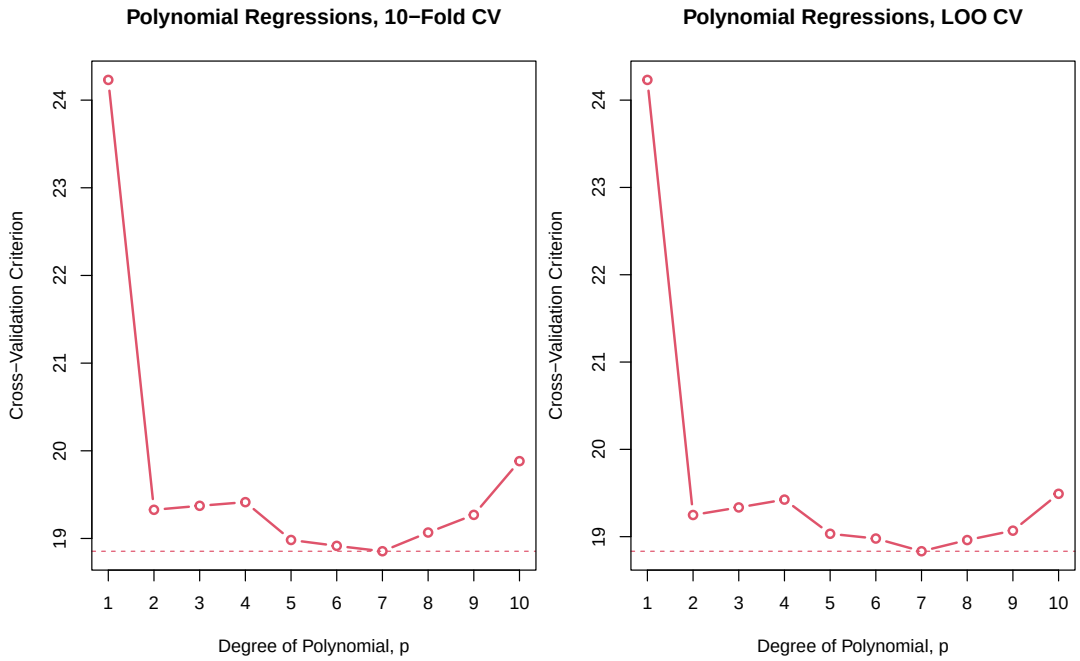


Figure 5: Cross-validated 10-fold and LOO MSE as a function of polynomial degree, p

```
R> plot(cv.auto.10, main="Polynomial Regressions, 10-Fold CV",
+      axis.args=list(labels=1:10), xlab="Degree of Polynomial, p")
R> plot(cv.auto.loo, main="Polynomial Regressions, LOO CV",
+      axis.args=list(labels=1:10), xlab="Degree of Polynomial, p")
```

In this example, 10-fold and LOO CV produce generally similar results, and also results that are similar to those produced by the estimated error variance $\widehat{\sigma}^2$ for each model, reported above (except for the highest-degree polynomials, where the CV results more clearly suggest over-fitting).

2.2. Logistic regression for the Mroz data

The `Mroz` data set from the **carData** package (associated with Fox and Weisberg 2019) has been used by several authors to illustrate binary logistic regression; see, in particular Fox and Weisberg (2019). The data were originally drawn from the U.S. Panel Study of Income Dynamics and pertain to married women. Here are a few cases in the data set:

```
R> data("Mroz", package="carData")
R> head(Mroz, 3)

  lfp k5 k618 age wc hc       lwg   inc
1 yes  1    0  32 no no 1.2101647 10.91
2 yes  0    2  30 no no 0.3285041 19.50
3 yes  1    3  35 no no 1.5141279 12.04

R> tail(Mroz, 3)
```

```
    lfp k5 k618 age wc hc       lwg    inc
751  no  0    0  43 no no 0.8881401  9.952
752  no  0    0  60 no no 1.2249736 24.984
753  no  0    3  39 no no 0.8532125 28.363
```

The response variable in the logistic regression is `lfp`, labor-force participation, a factor coded `"yes"` or `"no"`. The remaining variables are predictors:

- `k5`, number of children 5 years old of younger in the woman's household;
- `k618`, number of children between 6 and 18 years old;
- `age`, in years;
- `wc`, wife's college attendance, `"yes"` or `"no"`;
- `hc`, husband's college attendance;
- `lwg`, the woman's log wage rate if she is employed, or her *imputed* wage rate, if she is not (a variable that Fox and Weisberg 2019, show is problematically defined); and
- `inc`, family income, in $1000s, exclusive of wife's income.

We use the `glm()` function to fit a binary logistic regression to the `Mroz` data:

```
R> m.mroz <- glm(lfp ~ ., data=Mroz, family=binomial)
R> summary(m.mroz)


Call:
glm(formula = lfp ~ ., family = binomial, data = Mroz)

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  3.182140   0.644375   4.938 7.88e-07
k5          -1.462913   0.197001  -7.426 1.12e-13
k618        -0.064571   0.068001  -0.950 0.342337
age         -0.062871   0.012783  -4.918 8.73e-07
wcyes        0.807274   0.229980   3.510 0.000448
hcyes        0.111734   0.206040   0.542 0.587618
lwg          0.604693   0.150818   4.009 6.09e-05
inc         -0.034446   0.008208  -4.196 2.71e-05

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 1029.75  on 752  degrees of freedom
Residual deviance:  905.27  on 745  degrees of freedom
AIC: 921.27

Number of Fisher Scoring iterations: 4

R> BayesRule(ifelse(Mroz$lfp == "yes", 1, 0),
+           fitted(m.mroz, type="response"))
```

```
[1] 0.3067729
attr(,"casewise loss")
[1] "y != round(yhat)"
```

In addition to the usually summary output for a GLM, we show the result of applying the `BayesRule()` function from the **cv** package to predictions derived from the fitted model. Bayes rule, which predicts a "success" in a binary regression model when the fitted probability of success [i.e., $\phi = \Pr(y = 1)$] is $\widehat{\phi} \geq .5$ and a "failure" if $\widehat{\phi} < .5$.[4] The first argument to `BayesRule()` is the binary {0, 1} response, and the second argument is the predicted probability of success. `BayesRule()` returns the proportion of predictions that are *in error*, as appropriate for a "cost" function.

The value returned by `BayesRule()` is associated with an "attribute" named `"casewise loss"` and set to `"y != round(yhat)"`, signifying that the Bayes rule CV criterion is computed as the mean of casewise values, here 0 if the prediction for a case matches the observed value and 1 if it does not (signifying a prediction error). The `mse()` function for numeric responses is also calculated as a casewise average. Some other criteria, such as the median absolute error, computed by the `medAbsErr()` function in the **cv** package, aren't averages of casewise components. The distinction is important because, to our knowledge, the statistical theory of cross-validation, for example, in Davison and Hinkley (1997), Bates, Hastie, and Tibshirani (2023), and Arlot and Celisse (2010), is developed for CV criteria like MSE that are means of casewise components. As a consequence, we limit computation of bias adjustment and confidence intervals (see below) to criteria that are casewise averages.

In this example, the fitted logistic regression incorrectly predicts 31% of the responses; we expect this estimate to be optimistic given that the model is used to "predict" the data to which it is fit.

The `"glm"` method for `cv()` is largely similar to the `"lm"` method, although the default algorithm, selected explicitly by `method="exact"`, refits the model with each fold removed (and is thus equivalent to `method="naive"` for `"lm"` models). For generalized linear models, `method="Woodbury"` or (for LOO CV) `method="hatvalues"` provide approximate results (see the last section of the vignette for details):

```
R> cv(m.mroz, criterion=BayesRule, seed=248)

R RNG seed set to 248

10-Fold Cross Validation
method: exact
criterion: BayesRule
cross-validation criterion = 0.3240372
bias-adjusted cross-validation criterion = 0.3195223
95% CI for bias-adjusted CV criterion = (0.2860721, 0.3529724)
full-sample criterion = 0.3067729

R> cv(m.mroz, criterion=BayesRule, seed=248, method="Woodbury")
```

[4] `BayesRule()` does some error checking; `BayesRule2()` is similar, but omits the error checking, and so can be faster for large problems.

```
R RNG seed set to 248


10-Fold Cross Validation
method: Woodbury
criterion: BayesRule
cross-validation criterion = 0.3240372
bias-adjusted cross-validation criterion = 0.3192577
95% CI for bias-adjusted CV criterion = (0.2858076, 0.3527079)
full-sample criterion = 0.3067729
```

To ensure that the two methods use the same 10 folds, we specify the seed for R's random-number generator explicitly; here, and as is common in our experience, the `"exact"` and `"Woodbury"` algorithms produce nearly identical results. The CV estimates of prediction error are slightly higher than the estimate based on all of the cases.

The printed output includes a 95% confidence interval for the bias-adjusted Bayes rule CV criterion. Bates *et al.* (2023) show that these confidence intervals are unreliable for models fit to small samples, and by default `cv()` computes them only when the sample size is 400 or larger and when the CV criterion employed is an average of casewise components, as is the case for Bayes rule. See the final section of the vignette for details of the computation of confidence intervals for bias-adjusted CV criteria.

Here are results of applying LOO CV to the Mroz model, using both the exact and the approximate methods:

```
R> cv(m.mroz, k="loo", criterion=BayesRule)


n-Fold Cross Validation
method: exact
criterion: BayesRule
cross-validation criterion = 0.3200531
bias-adjusted cross-validation criterion = 0.3183001
95% CI for bias-adjusted CV criterion = (0.2849584, 0.3516418)
full-sample criterion = 0.3067729

R> cv(m.mroz, k="loo", criterion=BayesRule, method="Woodbury")


n-Fold Cross Validation
method: Woodbury
criterion: BayesRule
cross-validation criterion = 0.3200531
bias-adjusted cross-validation criterion = 0.3183001
95% CI for bias-adjusted CV criterion = (0.2849584, 0.3516418)
full-sample criterion = 0.3067729

R> cv(m.mroz, k="loo", criterion=BayesRule, method="hatvalues")
```

```
n-Fold Cross Validation
method: hatvalues
criterion: BayesRule
cross-validation criterion = 0.3200531
```

To the number of decimal digits shown, the three methods produce identical results for this example.

As for linear models, we report some timings for the various \code{cv()‘ methods of computation in LOO CV as well as for the `cv.glm()` function from the **boot** package (which, recall, refits the model with each case removed, and thus is comparable to `cv()` with `method="exact"`):

```
R> microbenchmark::microbenchmark(
+   hatvalues=cv(m.mroz, k="loo", criterion=BayesRule, method="hatvalues"),
+   Woodbury=cv(m.mroz, k="loo", criterion=BayesRule, method="Woodbury"),
+   exact=cv(m.mroz, k="loo", criterion=BayesRule),
+   cv.glm=boot::cv.glm(Mroz, m.mroz,
+                cost=BayesRule),
+   times=10)
```

```
Unit: milliseconds
      expr          min           lq         mean       median           uq
 hatvalues     1.316141     1.326842     1.654063     1.407571     1.442462
  Woodbury    37.127427    38.641639    39.368192    39.356904    40.562202
     exact  1757.625925  1827.861385  1905.072191  1911.421128  1951.049944
    cv.glm  2062.693354  2122.649130  2149.761134  2140.079440  2184.788525
          max neval cld
    4.022428    10 a
   41.060188    10 a
 2128.307540    10  b
 2299.544573    10   c
```

There is a substantial time penalty associated with exact computations.

3. Cross-validating mixed-effects models

The fundamental analogy for cross-validation is to the collection of new data. That is, predicting the response in each fold from the model fit to data in the other folds is like using the model fit to all of the data to predict the response for new cases from the values of the predictors for those new cases. As we explained, the application of this idea to independently sampled cases is straightforward—simply partition the data into random folds of equal size and leave each fold out in turn, or, in the case of LOO CV, simply omit each case in turn.

In contrast, mixed-effects models are fit to *dependent* data, in which cases as clustered, such as hierarchical data, where the clusters comprise higher-level units (e.g., students clustered in schools), or longitudinal data, where the clusters are individuals and the cases repeated

observations on the individuals over time.[5]

We can think of two approaches to applying cross-validation to clustered data:[6]

1. Treat CV as analogous to predicting the response for one or more cases in a *newly observed cluster*. In this instance, the folds comprise one or more whole clusters; we refit the model with all of the cases in clusters in the current fold removed; and then we predict the response for the cases in clusters in the current fold. These predictions are based only on fixed effects because the random effects for the omitted clusters are presumably unknown, as they would be for data on cases in newly observed clusters.

2. Treat CV as analogous to predicting the response for a newly observed case in an *existing cluster*. In this instance, the folds comprise one or more individual cases, and the predictions can use both the fixed and random effects.

3.1. Example: The High-School and Beyond data

Following their use by Raudenbush and Bryk (2002), data from the 1982 *High School and Beyond* (HSB) survey have become a staple of the literature on mixed-effects models. The HSB data are used by Fox and Weisberg (2019, Sec. 7.2.2) to illustrate the application of linear mixed models to hierarchical data, and we'll closely follow their example here.

The HSB data are included in the `MathAchieve` and `MathAchSchool` data sets in the **nlme** package (Pinheiro and Bates 2000). `MathAchieve` includes individual-level data on 7185 students in 160 high schools, and `MathAchSchool` includes school-level data:

```
R> data("MathAchieve", package="nlme")
R> dim(MathAchieve)

[1] 7185    6

R> head(MathAchieve, 3)

Grouped Data: MathAch ~ SES | School
  School Minority    Sex    SES MathAch MEANSES
1   1224       No Female -1.528   5.876  -0.428
2   1224       No Female -0.588  19.708  -0.428
3   1224       No   Male -0.528  20.349  -0.428

R> tail(MathAchieve, 3)
```

[5] There are, however, more complex situations that give rise to so-called *crossed* (rather than *nested*) random effects. For example, consider students within classes within schools. In primary schools, students typically are in a single class, and so classes are nested within schools. In secondary schools, however, students typically take several classes and students who are together in a particular class may not be together in other classes; consequently, random effects based on classes within schools are crossed. The `lmer()` function in the **lme4** package is capable of modeling both nested and crossed random effects, and the `cv()` methods for mixed models in the **cv** package pertain to both nested and crossed random effects. We present an example of the latter later in the vignette.

[6] We subsequently discovered that Vehtari (2023, Section 8) makes similar points.

```
Grouped Data: MathAch ~ SES | School
     School Minority    Sex    SES MathAch MEANSES
7183   9586       No Female  1.332  19.641   0.627
7184   9586       No Female -0.008  16.241   0.627
7185   9586       No Female  0.792  22.733   0.627

R> data("MathAchSchool", package="nlme")
R> dim(MathAchSchool)

[1] 160   7

R> head(MathAchSchool, 2)

     School Size Sector PRACAD DISCLIM HIMINTY MEANSES
1224   1224  842 Public   0.35   1.597       0  -0.428
1288   1288 1855 Public   0.27   0.174       0   0.128

R> tail(MathAchSchool, 2)

     School Size   Sector PRACAD DISCLIM HIMINTY MEANSES
9550   9550 1532   Public   0.45   0.791       0   0.059
9586   9586  262 Catholic   1.00  -2.416       0   0.627
```

The first few students are in school number 1224 and the last few in school 9586.

We'll use only the `School`, `SES` (students' socioeconomic status), and `MathAch` (their score on a standardized math-achievement test) variables in the `MathAchieve` data set, and `Sector` (`"Catholic"` or `"Public"`) in the `MathAchSchool` data set.

Some data-management is required before fitting a mixed-effects model to the HSB data, for which we use the **dplyr** package (Wickham, François, Henry, Müller, and Vaughan 2023):

```
R> library("dplyr")


Attaching package: 'dplyr'

The following objects are masked from 'package:stats':

    filter, lag

The following objects are masked from 'package:base':

    intersect, setdiff, setequal, union

R> MathAchieve %>% group_by(School) %>%
+   summarize(mean.ses = mean(SES)) -> Temp
R> Temp <- merge(MathAchSchool, Temp, by="School")
```

```
R> HSB <- merge(Temp[, c("School", "Sector", "mean.ses")],
+               MathAchieve[, c("School", "SES", "MathAch")], by="School")
R> names(HSB) <- tolower(names(HSB))
R>
R> HSB$cses <- with(HSB, ses - mean.ses)
```

In the process, we created two new school-level variables: `meanses`, which is the average SES for students in each school; and `cses`, which is school-average SES centered at its mean. For details, see Fox and Weisberg (2019, Sec. 7.2.2).

Still following Fox and Weisberg, we proceed to use the `lmer()` function in the **lme4** package (Bates, Mächler, Bolker, and Walker 2015) to fit a mixed model for math achievement to the HSB data:

```
R> library("lme4")

Loading required package: Matrix

R> hsb.lmer <- lmer(mathach ~ mean.ses*cses + sector*cses
+                     + (cses | school), data=HSB)
R> summary(hsb.lmer, correlation=FALSE)

Linear mixed model fit by REML ['lmerMod']
Formula: mathach ~ mean.ses * cses + sector * cses + (cses | school)
   Data: HSB

REML criterion at convergence: 46503.7

Scaled residuals:
     Min       1Q   Median       3Q      Max
-3.15926 -0.72319  0.01704  0.75444  2.95822

Random effects:
 Groups   Name        Variance Std.Dev. Corr
 school   (Intercept)  2.380   1.5426
          cses         0.101   0.3179   0.39
 Residual             36.721   6.0598
Number of obs: 7185, groups:  school, 160

Fixed effects:
                    Estimate Std. Error t value
(Intercept)          12.1279     0.1993  60.856
mean.ses              5.3329     0.3692  14.446
cses                  2.9450     0.1556  18.928
sectorCatholic        1.2266     0.3063   4.005
mean.ses:cses         1.0393     0.2989   3.477
cses:sectorCatholic  -1.6427     0.2398  -6.851
```

We can then cross-validate at the cluster (i.e., school) level,

```
R> cv(hsb.lmer, k=10, clusterVariables="school", seed=5240)

R RNG seed set to 5240

10-Fold Cross Validation based on 160 {school} clusters
cross-validation criterion = 39.15662
bias-adjusted cross-validation criterion = 39.14844
95% CI for bias-adjusted CV criterion = (38.06554, 40.23135)
full-sample criterion = 39.00599
```

or at the case (i.e., student) level,

```
R> cv(hsb.lmer, seed=1575)

R RNG seed set to 1575

Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
Model failed to converge with max|grad| = 0.00587228 (tol = 0.002, component 1)

boundary (singular) fit: see help('isSingular')

10-Fold Cross Validation
cross-validation criterion = 37.44473
bias-adjusted cross-validation criterion = 37.33801
95% CI for bias-adjusted CV criterion = (36.28761, 38.38841)
full-sample criterion = 36.06767
```

For cluster-level CV, the `clusterVariables` argument tells `cv()` how the clusters are defined. Were there more than one clustering variable, say classes within schools, these would be provided as a character vector of variable names: `clusterVariables = c("school", "class")`. For cluster-level CV, the default is `k = "loo"`, that is, leave one cluster out at a time; we instead specify `k = 10` folds of clusters, each fold therefore comprising $160/10 = 16$ schools.

If the `clusterVariables` argument is omitted, then case-level CV is employed, with `k = 10` folds as the default, here each with $7185/10 \approx 719$ students. Notice that one of the 10 models refit with a fold removed failed to converge. Convergence problems are common in mixed-effects modeling. The apparent issue here is that an estimated variance component is close to or equal to 0, which is at a boundary of the parameter space. That shouldn't disqualify the fitted model for the kind of prediction required for cross-validation.

There is also a `cv()` method for linear mixed models fit by the `lme()` function in the **nlme** package, and the arguments for `cv()` in this case are the same as for a model fit by `lmer()` or `glmer()`. We illustrate with the mixed model fit to the HSB data:

```
R> library(nlme)
R> hsb.lme <- lme(mathach ~ mean.ses*cses + sector*cses,
+                  random = ~ cses | school, data=HSB,
+                control=list(opt="optim"))
R> summary(hsb.lme)

Linear mixed-effects model fit by REML
  Data: HSB
       AIC      BIC    logLik
  46524.78 46593.57 -23252.39

Random effects:
 Formula: ~cses | school
 Structure: General positive-definite, Log-Cholesky parametrization
            StdDev     Corr
(Intercept) 1.54117685 (Intr)
cses        0.01817364 0.006
Residual    6.06349216

Fixed effects:  mathach ~ mean.ses * cses + sector * cses
                       Value Std.Error   DF  t-value p-value
(Intercept)         12.128207 0.1991964 7022 60.88567   0e+00
mean.ses             5.336665 0.3689784  157 14.46335   0e+00
cses                 2.942145 0.1512240 7022 19.45554   0e+00
sectorCatholic       1.224531 0.3061139  157  4.00025   1e-04
mean.ses:cses        1.044406 0.2910747 7022  3.58810   3e-04
cses:sectorCatholic -1.642148 0.2331162 7022 -7.04433   0e+00
 Correlation:
                    (Intr) men.ss cses   sctrCt mn.ss:
mean.ses             0.256
cses                 0.000  0.000
sectorCatholic      -0.699 -0.356  0.000
mean.ses:cses        0.000  0.000  0.295  0.000
cses:sectorCatholic  0.000  0.000 -0.696  0.000 -0.351

Standardized Within-Group Residuals:
        Min          Q1         Med          Q3         Max
-3.17010624 -0.72487654  0.01489162  0.75426269  2.96549829

Number of Observations: 7185
Number of Groups: 160

R> cv(hsb.lme, k=10, clusterVariables="school", seed=5240)

R RNG seed set to 5240

10-Fold Cross Validation based on 160 {school} clusters
cross-validation criterion = 39.1569
```

```
bias-adjusted cross-validation criterion = 39.14881
95% CI for bias-adjusted CV criterion = (38.06591, 40.23171)
full-sample criterion = 39.0062
```

```
R> cv(hsb.lme, seed=1575)
```

```
R RNG seed set to 1575
```

```
10-Fold Cross Validation
cross-validation criterion = 37.44163
bias-adjusted cross-validation criterion = 37.40222
95% CI for bias-adjusted CV criterion = (36.35136, 38.45309)
full-sample criterion = 36.14707
```

We used the same random-number generator seeds as in the previous example cross-validating the model fit by `lmer()`, and so the same folds are employed in both cases.[7] The estimated covariance components and fixed effects in the summary output differ slightly between the `lmer()` and `lme()` solutions, although both functions seek to maximize the REML criterion. This is, of course, to be expected when different algorithms are used for numerical optimization. To the precision reported, the cluster-level CV results for the `lmer()` and `lme()` models are identical, while the case-level CV results are very similar but not identical.

3.2. Example: Contrived hierarchical data

We introduce an artificial data set that exemplifies aspects of cross-validation particular to hierarchical models. Using this data set, we show that model comparisons employing cluster-based and those employing case-based cross-validation may not agree on a "best" model. Furthermore, commonly used measures of fit, such as mean-squared error, do not necessarily become smaller as models become larger, even when the models are nested, and even when the measure of fit is computed for the whole data set.

Consider a researcher studying improvement in a skill, yodeling, for example, among students enrolled in a four-year yodeling program. The plan is to measure each student's skill level at the beginning of the program and every year thereafter until the end of the program, resulting in five annual measurements for each student. It turns out that yodeling appeals to students of all ages, and students enrolling in the program range in age from 20 to 70. Moreover, participants' untrained yodeling skill is similar at all ages, as is their rate of progress with training. All students complete the four-year program.

The researcher, who has more expertise in yodeling than in modeling, decides to model the response, y, yodeling skill, as a function of age, x, reasoning that students get older during their stay in the program, and (incorrectly) that age can serve as a proxy for elapsed time. The researcher knows that a mixed model should be used to account for clustering due to the expected similarity of measurements taken from each student.

[7] The observant reader will notice that we set the argument `control=list(opt="optim")` in the call to `lme()`, changing the optimizer employed from the default `"nlminb"`. We did this because with the default optimizer, `lme()` encountered the same convergence issue as `lmer()`, but rather than issuing a warning, `lme()` failed, reporting an error. As it turns out, setting the optimizer to `"optim"` avoids this problem.

We start by generating the data, using parameters consistent with the description above and meant to highlight the issues that arise in cross-validating mixed-effects models:[8]

```
R> # Parameters:
R> set.seed(9693)
R> Nb <- 100     # number of groups
R> Nw <- 5       # number of individuals within groups
R> Bb <- 0       # between-group regression coefficient on group mean
R> SDre <- 2.0   # between-group SD of random level relative to group mean of x
R> SDwithin <- 0.5  # within group SD
R> Bw <- 1          # within group effect of x
R> Ay <- 10         # intercept for response
R> Ax <- 20         # starting level of x
R> Nx <- Nw*10      # number of distinct x values
R>
R> Data <- data.frame(
+   group = factor(rep(1:Nb, each=Nw)),
+   x = Ax + rep(1:Nx, length.out = Nw*Nb)
+ ) |>
+   within(
+     {
+       xm  <- ave(x, group, FUN = mean) # within-group mean
+       y <- Ay +
+         Bb * xm +                    # contextual effect
+         Bw * (x - xm) +              # within-group effect
+         rnorm(Nb, sd=SDre)[group] +  # random level by group
+         rnorm(Nb*Nw, sd=SDwithin)    # random error within groups
+     }
+   )
```

Here is a scatterplot of the data for a representative group of 10 (without loss of generality, the first 10) of 100 students, showing the 95% concentration ellipse for each cluster:[9]

```
R> library("lattice")
R> library("latticeExtra")
R> plot <- xyplot(y ~ x, data=Data[1:Nx, ], group=group,
+                 ylim=c(4, 16),
+                 par.settings=list(superpose.symbol=list(pch=1, cex=0.7))) +
+     layer(panel.ellipse(..., center.cex=0))
R> plot # display graph
```

[8] The `regsubsets()` function computes several measures of model predictive performance, including the R^2 and R^2 adjusted for degrees of freedom, the residual sums of squares, Mallows's C_p, and the BIC. Several of these are suitable for comparing models with differing numbers of coefficients—we use the BIC below—but all necessarily agree when comparing models with the *same* number of coefficients.

[9] We find it convenient to use the **lattice** (Sarkar 2008) and **latticeExtra** (Sarkar and Andrews 2022) packages for this and other graphs in this section.

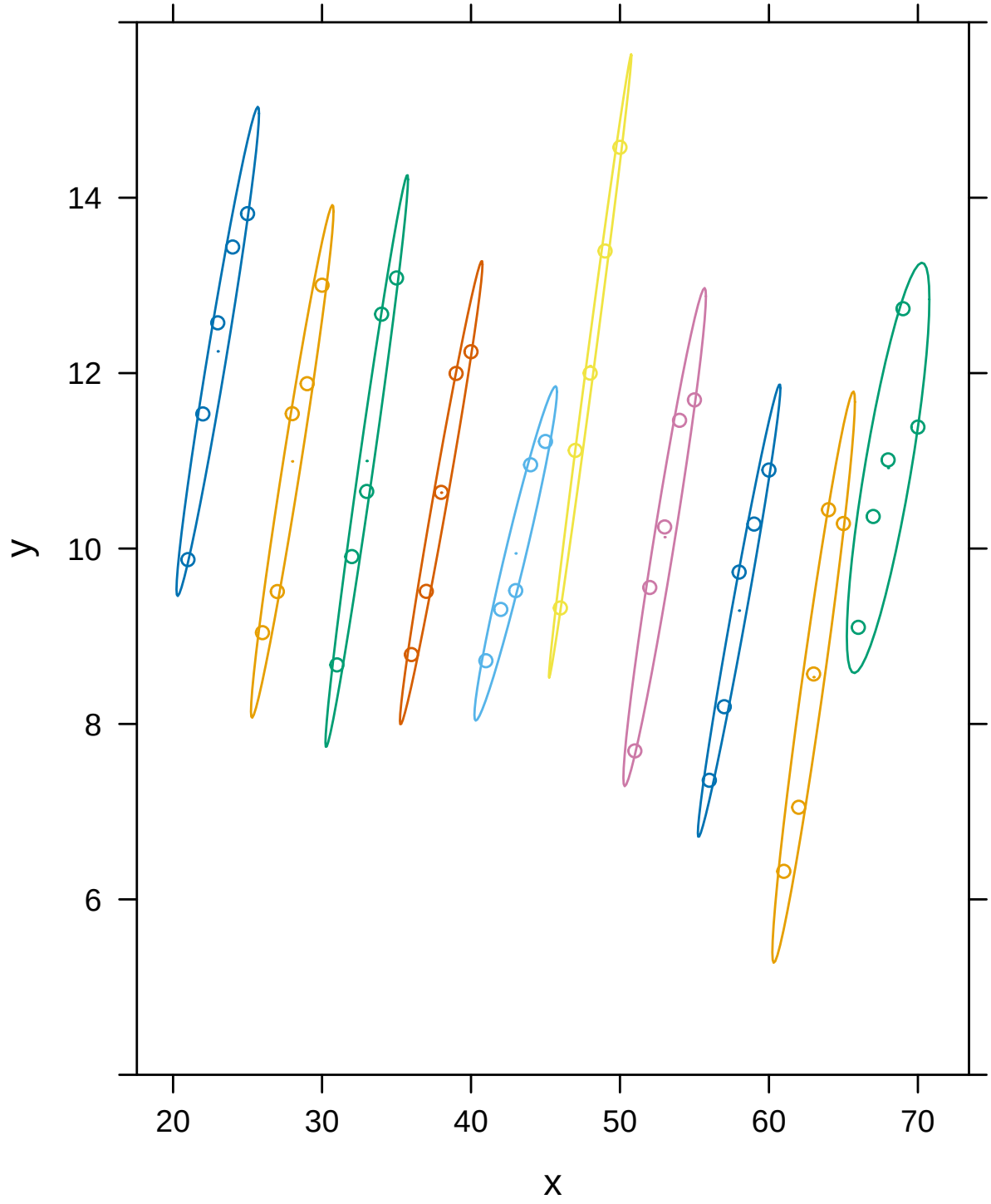


Figure 6: Hierarchical data set, showing the first 10 of 100 students.

The between-student effect of age is 0 but the within-student effect is 1. Due to the large variation in ages between students, the least-squares regression of yodeling skill on age (for the 500 observations among all 100 students) produces an estimated slope close to 0 (though with a small p-value), because the slope is heavily weighted toward the between-student effect:

```
R> summary(lm(y ~ x, data=Data))


Call:
lm(formula = y ~ x, data = Data)

Residuals:
    Min      1Q  Median      3Q     Max
-5.7713 -1.6583 -0.0894  1.5520  7.6240

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 9.050430   0.347189  26.068  < 2e-16
x           0.020908   0.007273   2.875  0.00422

Residual standard error: 2.347 on 498 degrees of freedom
Multiple R-squared:  0.01632,   Adjusted R-squared:  0.01435
F-statistic: 8.263 on 1 and 498 DF,  p-value: 0.004219
```

The initial mixed-effects model that we fit to the data is a simple random-intercepts model:

```
R> # random intercept only:
R> mod.0 <- lmer(y ~ 1 + (1 | group), Data)
R> summary(mod.0)

Linear mixed model fit by REML ['lmerMod']
Formula: y ~ 1 + (1 | group)
   Data: Data

REML criterion at convergence: 2103.1

Scaled residuals:
     Min       1Q   Median       3Q      Max
-2.03514 -0.72645 -0.01169  0.78477  2.04377

Random effects:
 Groups   Name        Variance Std.Dev.
 group    (Intercept) 2.900    1.703
 Residual             2.712    1.647
Number of obs: 500, groups:  group, 100
```

```
Fixed effects:
            Estimate Std. Error t value
(Intercept)  10.0018     0.1855   53.91
```

We will shortly consider three other, more complex, mixed models; because of data-management considerations, it is convenient to fit them now, but we defer discussion of these models:

```
R> # effect of x and random intercept:
R> mod.1 <- lmer(y ~ x + (1 | group), Data)
R>
R> # effect of x, contextual (student) mean of x, and random intercept:
R> mod.2 <- lmer(y ~ x + xm + (1 | group), Data)
R>         # equivalent to y ~ I(x - xm) + xm + (1 | group)
R>
R> # model generating the data (where Bb = 0)
R> mod.3 <- lmer(y ~ I(x - xm) + (1 | group), Data)
```

We proceed to obtain predictions from the random-intercept model (`mod.0`) and the other models (`mod.1`, `mod.2`, and `mod.3`) based on fixed effects alone, as would be used for cross-validation based on clusters (i.e., students), and for fixed and random effects—so-called best linear unbiased predictions or BLUPs—as would be used for cross-validation based on cases (i.e., occasions within students):

```
R> Data <- within(Data, {
+   fit_mod0.fe <- predict(mod.0, re.form = ~ 0) # fixed effects only
+   fit_mod0.re <- predict(mod.0) # fixed and random effects (BLUPs)
+   fit_mod1.fe <- predict(mod.1, re.form = ~ 0)
+   fit_mod1.re <- predict(mod.1)
+   fit_mod2.fe <- predict(mod.2, re.form = ~ 0)
+   fit_mod2.re <- predict(mod.2)
+   fit_mod3.fe <- predict(mod.3, re.form = ~ 0)
+   fit_mod3.re <- predict(mod.3)
+ })
```

We then prepare the data for plotting:

```
R> Data_long <- reshape(Data[1:Nx, ], direction = "long", sep = ".",
+                timevar = "effect", varying = grep("\\.", names(Data[1:Nx, ])))
R> Data_long$id <- 1:nrow(Data_long)
R> Data_long <- reshape(Data_long, direction = "long", sep = "_",
+                timevar = "modelcode",  varying = grep("_", names(Data_long)))
R> Data_long$model <- factor(
+   c("~ 1", "~ 1 + x", "~ 1 + x + xm", "~ 1 + I(x - xm)")
+   [match(Data_long$modelcode, c("mod0", "mod1", "mod2", "mod3"))]
+ )
```

Predictions based on the random-intercept model `mod.0` for the first 10 students are shown in the following graph:

```
R> (plot +
+   xyplot(fit ~ x, subset(Data_long, modelcode == "mod0" & effect == "fe"),
+          groups=group, type="l", lwd=2) +
+   xyplot(fit ~ x, subset(Data_long, modelcode == "mod0" &  effect == "re"),
+          groups=group, type="l", lwd=2, lty=3)
+ ) |> update(
+   main="Model: y ~ 1 + (1 | group)",
+   key=list(
+     corner=c(0.05, 0.05),
+     text=list(c("fixed effects only","fixed and random")),
+     lines=list(lty=c(1, 3))))
```

The fixed-effect predictions for the various individuals are identical—the estimated fixed-effects intercept or estimated general mean of y—while the BLUPs are the sums of the fixed-effects intercept and the random intercepts, and are only slightly shrunken towards the general mean. Because in our artificial data there is no population relationship between age and skill, the fixed-effect-only predictions and the BLUPs are not very different.

Our next model, `mod.1`, includes a fixed intercept and fixed effect of `x` along with a random intercept:

```
R> summary(mod.1)

Linear mixed model fit by REML ['lmerMod']
Formula: y ~ x + (1 | group)
   Data: Data

REML criterion at convergence: 1564.5

Scaled residuals:
     Min       1Q   Median       3Q      Max
-2.90160 -0.63501  0.01879  0.55407  2.82932

Random effects:
 Groups   Name        Variance Std.Dev.
 group    (Intercept) 192.9406 13.8903
 Residual               0.2569  0.5068
Number of obs: 500, groups:  group, 100

Fixed effects:
             Estimate Std. Error t value
(Intercept) -33.91892    1.56446  -21.68
x             0.96529    0.01581   61.05

Correlation of Fixed Effects:
  (Intr)
x -0.460
```

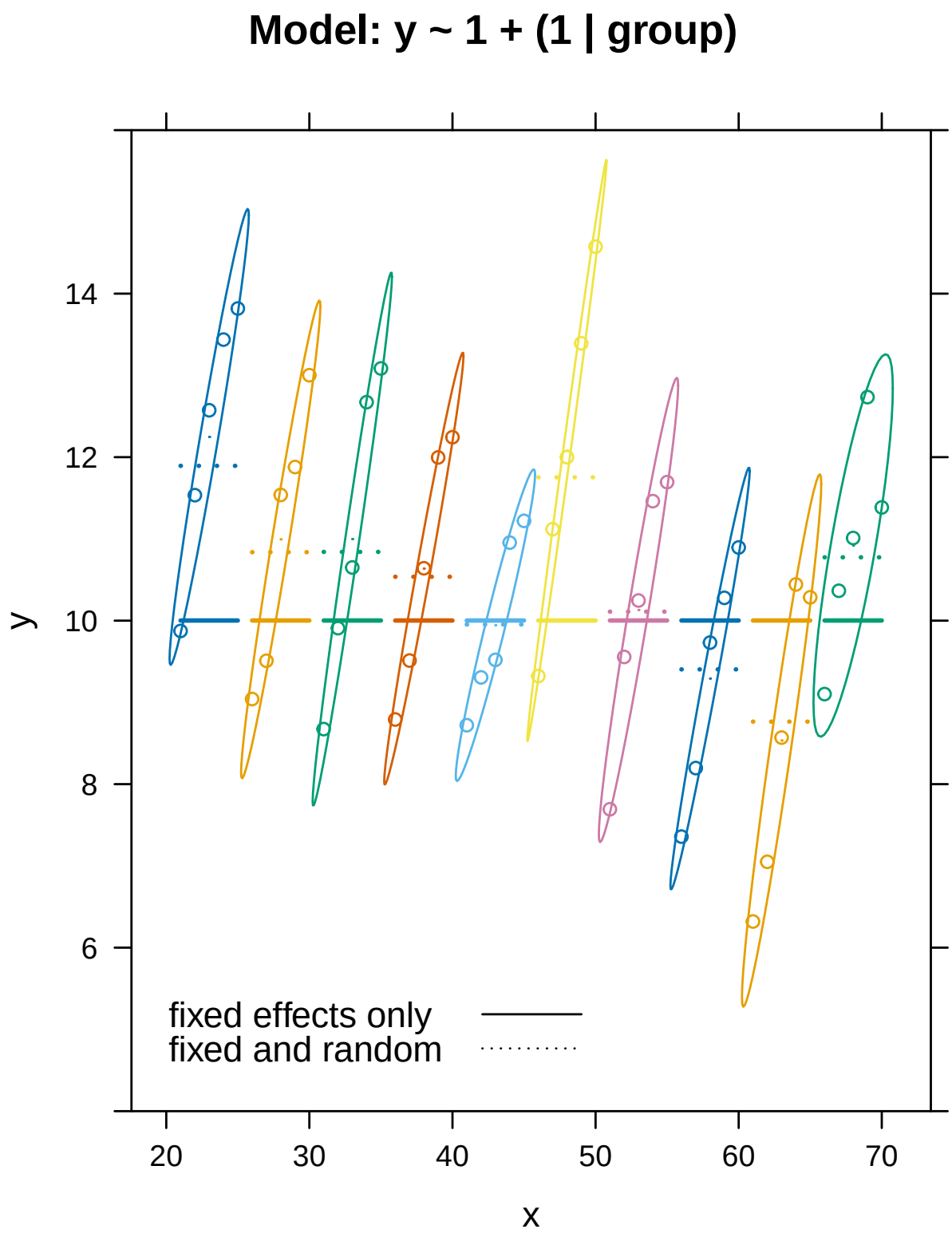


Figure 7: Predictions from the random intercept model.

Predictions from this model appear in the following graph:

```
R> (plot +
+   xyplot(fit ~ x, subset(Data_long, modelcode == "mod1" & effect == "fe"),
+          groups=group, type="l", lwd=2) +
+   xyplot(fit ~ x, subset(Data_long, modelcode == "mod1" & effect == "re"),
+          groups=group, type="l", lwd=2, lty=3)
+ ) |> update(
+   main="Model: y ~ 1 + x + (1 | group)",
+   ylim=c(-15, 35),
+   key=list(
+     corner=c(0.95, 0.05),
+     text=list(c("fixed effects only","fixed and random")),
+     lines=list(lty=c(1, 3))))
```

The BLUPs fit the observed data very closely, but predictions based on the fixed effects alone, with a common intercept and slope for all clusters, are very poor—indeed, much worse than the fixed-effects-only predictions based on the simpler random-intercept model, `mod.0`. We therefore anticipate (and show later in this section) that case-based cross-validation will prefer `mod1` to `mod0`, but that cluster-based cross-validation will prefer `mod0` to `mod1`.

Our third model, `mod.2`, includes the contextual effect of x—that is, the cluster mean \code{xm]—along with x and the intercept in the fixed-effect part of the model, and a random intercept:

```
R> summary(mod.2)

Linear mixed model fit by REML ['lmerMod']
Formula: y ~ x + xm + (1 | group)
   Data: Data

REML criterion at convergence: 1169.2

Scaled residuals:
     Min       1Q   Median       3Q      Max
-2.98466 -0.63750  0.00191  0.55682  2.73246

Random effects:
 Groups   Name        Variance Std.Dev.
 group    (Intercept) 3.3986   1.8435
 Residual             0.2552   0.5052
Number of obs: 500, groups:  group, 100

Fixed effects:
            Estimate Std. Error t value
(Intercept)  9.47866    0.61705   15.36
x            0.99147    0.01597   62.07
```

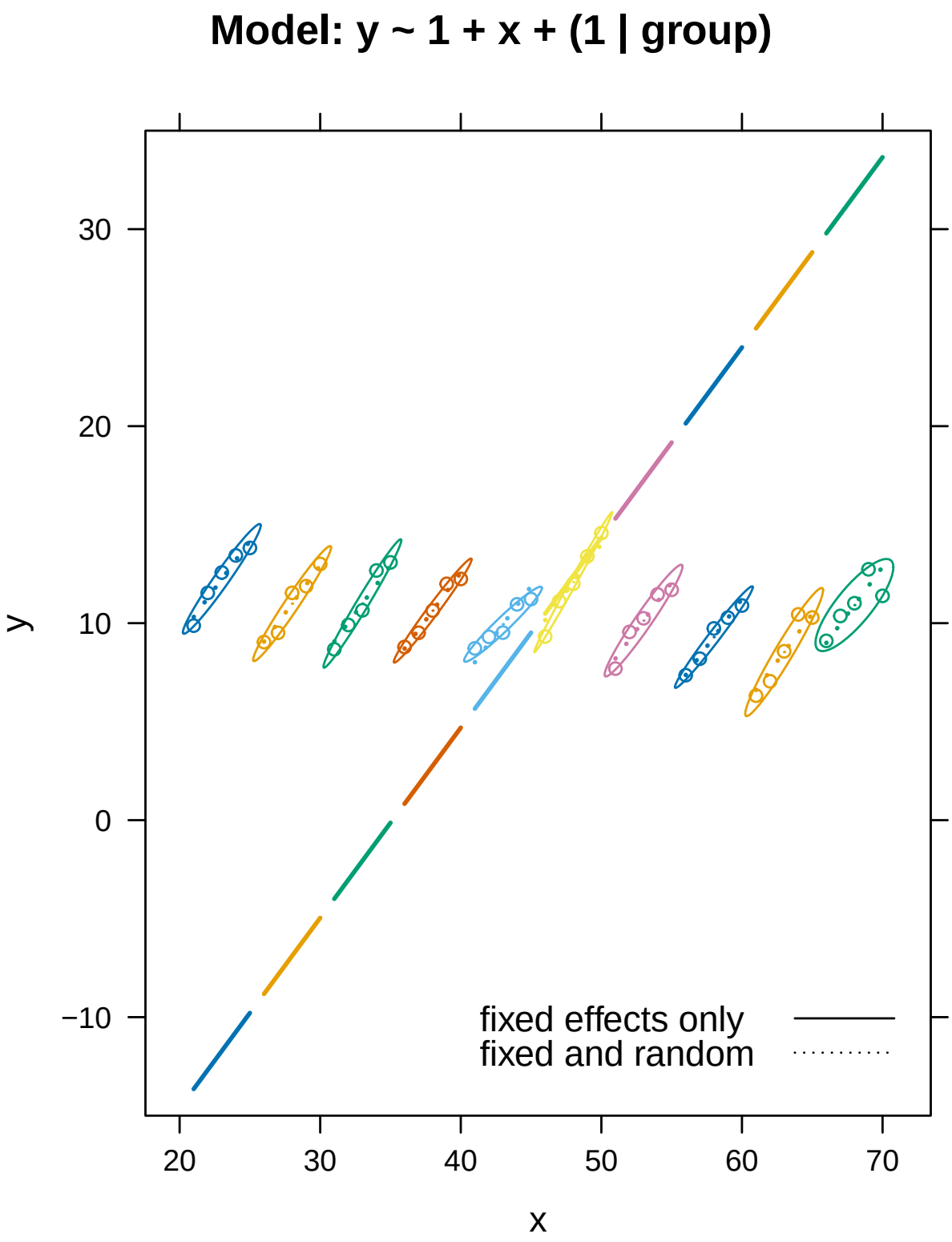


Figure 8: Predictions from the model with random intercepts and x as a fixed-effect predictor.

```
xm          -0.97998    0.02055  -47.68

Correlation of Fixed Effects:
   (Intr) x
x   0.000
xm -0.600 -0.777
```

This model is equivalent to fitting `y ~ I(x - xm) + xm + (1 | group)`, which is the model that generated the data once the coefficient of the contextual predictor `xm` is set to 0 (as it is in \code{mod.3], discussed below).

Predictions from model `mod.2` appear in the following graph:

```
R> (plot +
+   xyplot(fit ~ x, subset(Data_long, modelcode == "mod2" & effect == "fe"),
+          groups=group, type="l", lwd=2) +
+   xyplot(fit ~ x, subset(Data_long, modelcode == "mod2" & effect == "re"),
+          groups=group, type="l", lwd=2, lty=3)
+ ) |> update(
+   main="Model: y ~ 1 + x + xm + (1 | group)",
+   ylim=c(4, 16),
+   key=list(
+     corner=c(0.05, 0.05),
+     text=list(c("fixed effects only","fixed and random")),
+     lines=list(lty=c(1, 3))))
```

Depending on the estimated variance parameters of the model, a mixed model like `mod.2` will apply varying degrees of shrinkage to the random-intercept BLUPs that correspond to variation in the heights of the parallel fitted lines for the individual students. In our contrived data, the `mod.2` applies little shrinkage, allowing substantial variability in the heights of the fitted lines, which closely approach the observed values for each student. The fit of the mixed model `mod.2` is consequently similar to that of a fixed-effects model with age and a categorical predictor for individual students (i.e., treating students as a factor, and not shown here).

The mixed model `mod.2` therefore fits individual observations well, and we anticipate a favorable assessment using individual-based cross-validation. In contrast, the large variability in the BLUPs results in larger residuals for predictions based on fixed effects alone, and so we expect that cluster-based cross-validation won't show an advantage for model `mod.2` compared to the smaller model `mod.0`, which includes only fixed and random intercepts.

Had the mixed model applied considerable shrinkage, then neither cluster-based nor case-based cross-validation would show much improvement over the random-intercept-only model. In our experience, the degree of shrinkage does not vary smoothly as parameters are changed but tends to be "all or nothing," and near the tipping point, the behavior of estimates can be affected considerably by the choice of algorithm used to fit the model.

Finally, `mod.3` directly estimates the model used to generate the data. As mentioned, it is a constrained version of `mod.2`, with the coefficient of `xm` set to 0, and with `x` expressed as a deviation from the cluster mean `xm`:

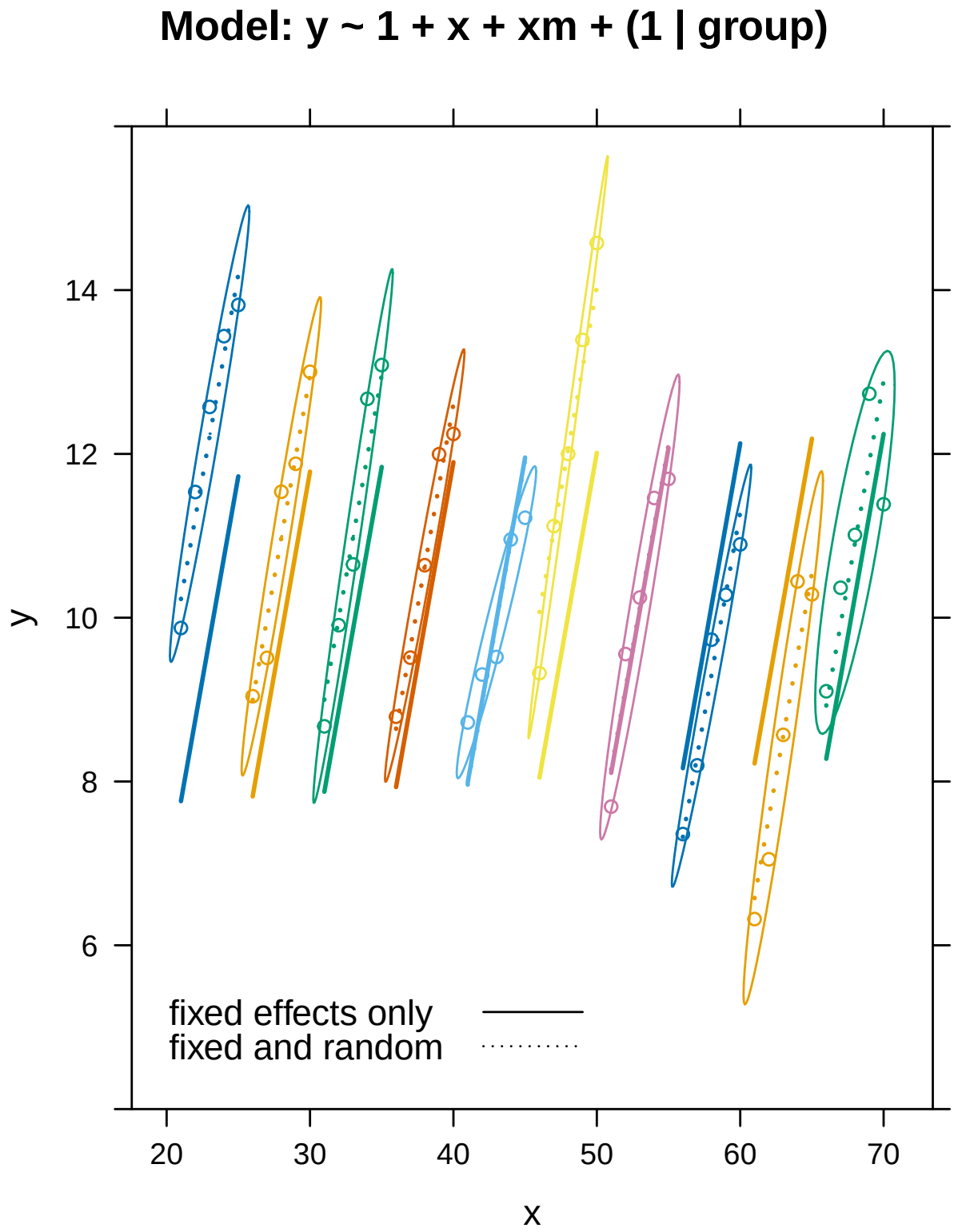


Figure 9: Predictors from the model with random intercepts, x, and the group (student) mean of x as predictors.

```
R> summary(mod.3)

Linear mixed model fit by REML ['lmerMod']
Formula: y ~ I(x - xm) + (1 | group)
   Data: Data

REML criterion at convergence: 1163.2

Scaled residuals:
     Min       1Q   Median       3Q      Max
-2.97703 -0.63204  0.00627  0.56032  2.72489

Random effects:
 Groups   Name        Variance Std.Dev.
 group    (Intercept) 3.3913   1.8415
 Residual             0.2552   0.5052
Number of obs: 500, groups:  group, 100

Fixed effects:
            Estimate Std. Error t value
(Intercept) 10.00176    0.18553   53.91
I(x - xm)    0.99147    0.01597   62.07

Correlation of Fixed Effects:
          (Intr)
I(x - xm) 0.000
```

The predictions from `mod.3` are therefore similar to those from `mod.2`:

```
R> (plot +
+   xyplot(fit ~ x, subset(Data_long, modelcode == "mod3" & effect == "fe"),
+          groups=group, type="l", lwd=2) +
+   xyplot(fit ~ x, subset(Data_long, modelcode == "mod3" & effect == "re"),
+          groups=group, type="l", lwd=2, lty=3)
+ ) |> update(
+   main="Model: y ~ 1 + I(x - xm) + (1 | group)",
+   ylim=c(4, 16),
+   key=list(
+     corner=c(0.05, 0.05),
+     text=list(c("fixed effects only","fixed and random")),
+     lines=list(lty=c(1, 3))))
```

We next carry out case-based cross-validation, which, as we have explained, is based on both fixed and predicted random effects (i.e., BLUPs), and cluster-based cross-validation, which is based on fixed effects only. In order to reduce between-model random variability in comparisons of models, we apply `cv()` to the list of models created by the `models()` function (introduced previously), performing cross-validation with the same folds for each model:

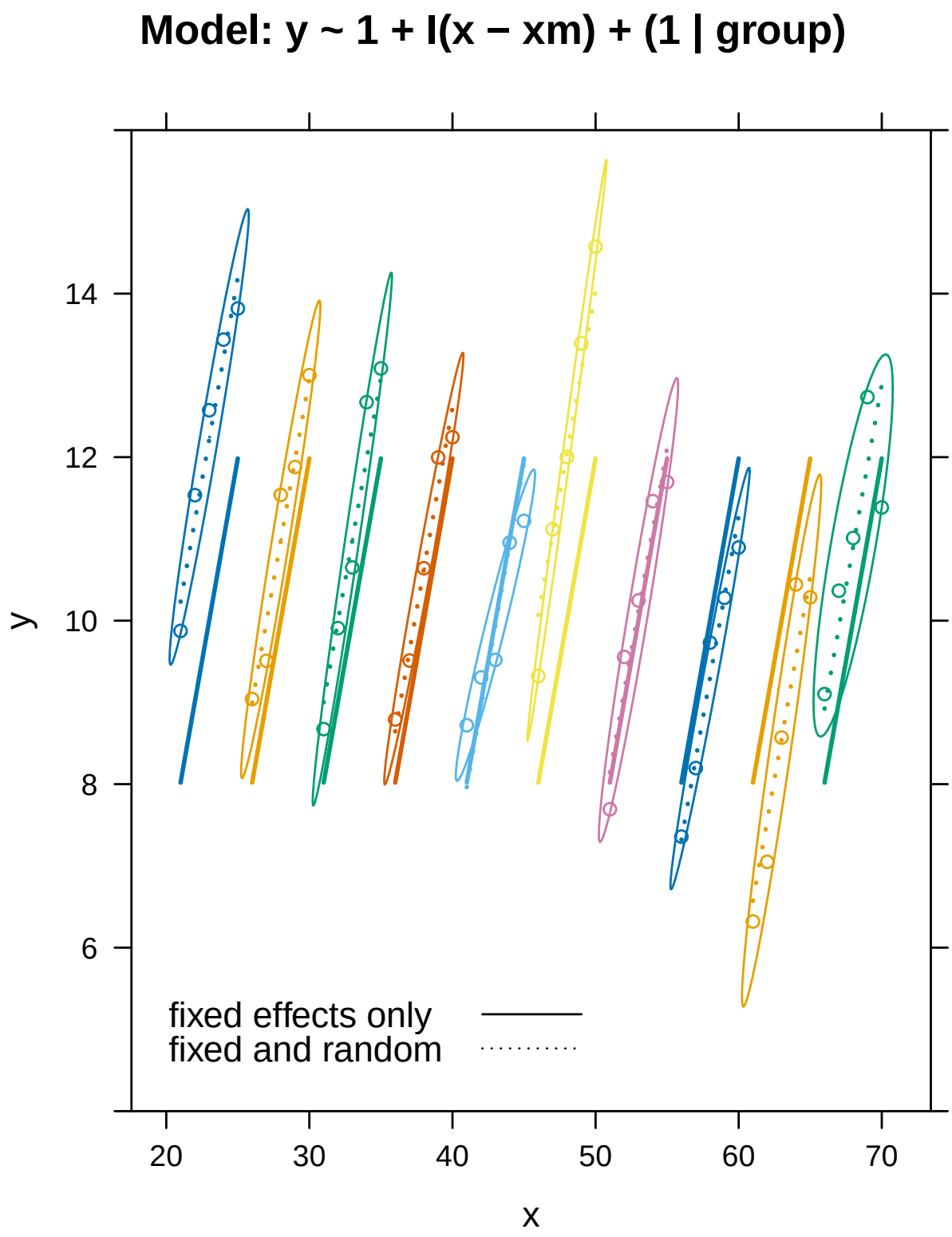


Figure 10: Predictions from the estimated model generating the data.

```
R> modlist <- models("~ 1"=mod.0, "~ 1 + x"=mod.1,
+                    "~ 1 + x + xm"=mod.2, "~ 1 + I(x - xm)"=mod.3)
R> cvs_clusters <- cv(modlist, data=Data, cluster="group", k=10, seed=6449)
R> plot(cvs_clusters, main="Model Comparison, Cluster-Based CV")

R> cvs_cases <- cv(modlist, data=Data, seed=9693)
R> plot(cvs_cases, main="Model Comparison, Case-Based CV")
```

In summary, model `mod.1`, with x alone and without the contextual mean of x, is assessed as fitting very poorly by cluster-based CV, but relatively much better by case-based CV. Model `mod.2`, which includes both x and its contextual mean, produces better results using both cluster-based and case-based CV. The data-generating model, `mod.3`, which includes the fixed effect of `x - xm` in place of separate terms in `x` and `xm`, isn't distinguishable from model `mod.2`, which includes `x` and `xm` separately, even though `mod.2` has an unnecessary parameter (recall that the population coefficient of `xm` is 0 when `x` is expressed as deviations from the contextual mean). These conclusions are consistent with our observations based on graphing predictions from the various models, and they illustrate the desirability of assessing mixed-effect models at different hierarchical levels.

3.3. Example: Crossed random effects

Crossed random effects arise when the structure of the data aren't strictly hierarchical. Nevertheless, crossed and nested random effects can be handled in much the same manner, by refitting the mixed-effects model to the data with a fold of clusters or cases removed and using the refitted model to predict the response in the removed fold.

We'll illustrate with data on pig growth, introduced by Diggle, Liang, and Zeger (1994, Table 3.1). The data are in the `Pigs` data frame in the **cv** package:

```
R> head(Pigs, 9)

  id week weight
1  1    1   24.0
2  1    2   32.0
3  1    3   39.0
4  1    4   42.5
5  1    5   48.0
6  1    6   54.5
7  1    7   61.0
8  1    8   65.0
9  1    9   72.0

R> head(xtabs(~ id + week, data=Pigs), 3)

   week
id  1 2 3 4 5 6 7 8 9
  1 1 1 1 1 1 1 1 1 1
  2 1 1 1 1 1 1 1 1 1
  3 1 1 1 1 1 1 1 1 1
```

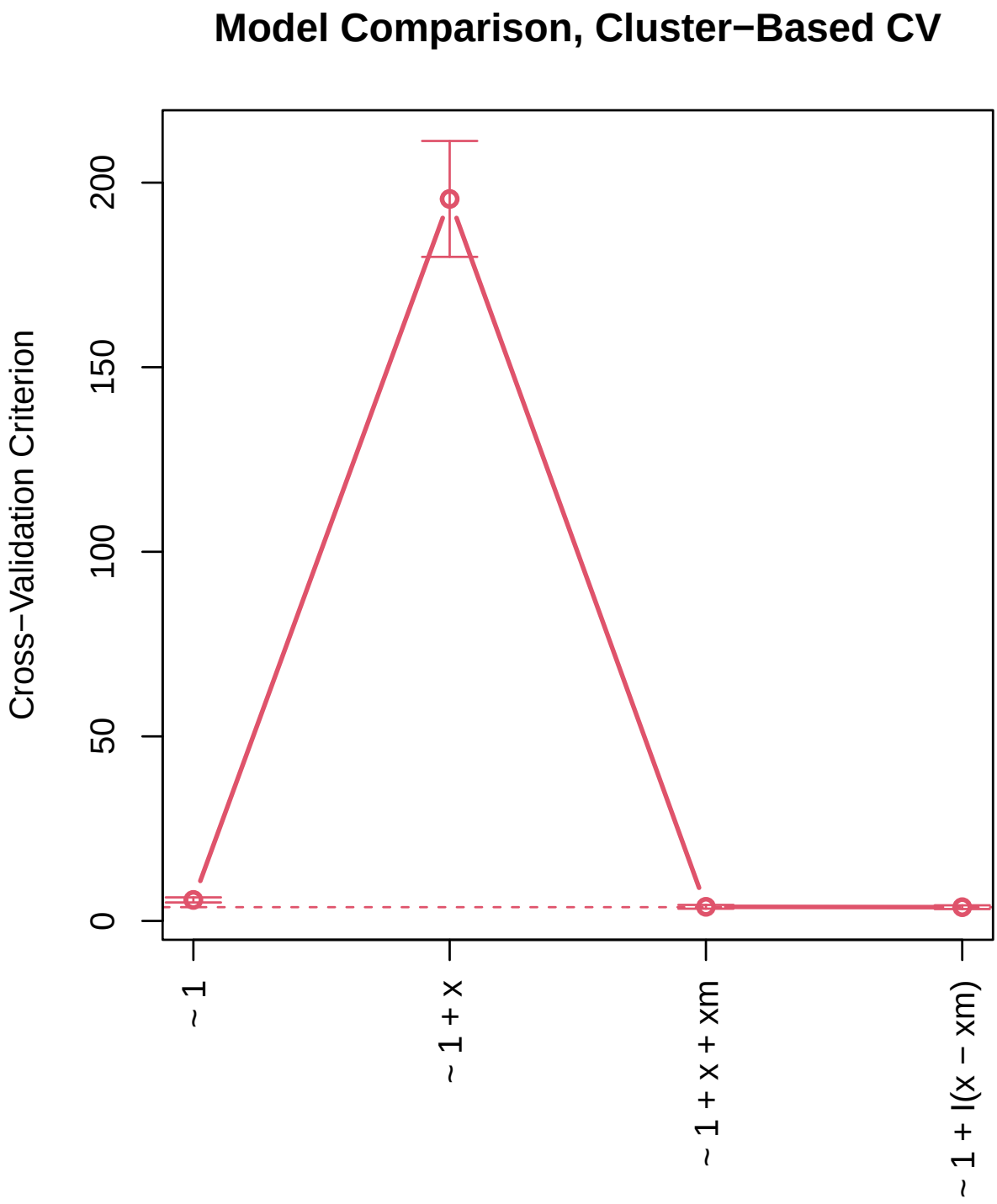


Figure 11: 10-fold cluster-based cross-validation comparing random intercept models with varying fixed effects. The error bars show the 95% confidence interval around the CV estimate of the MSE for each model.

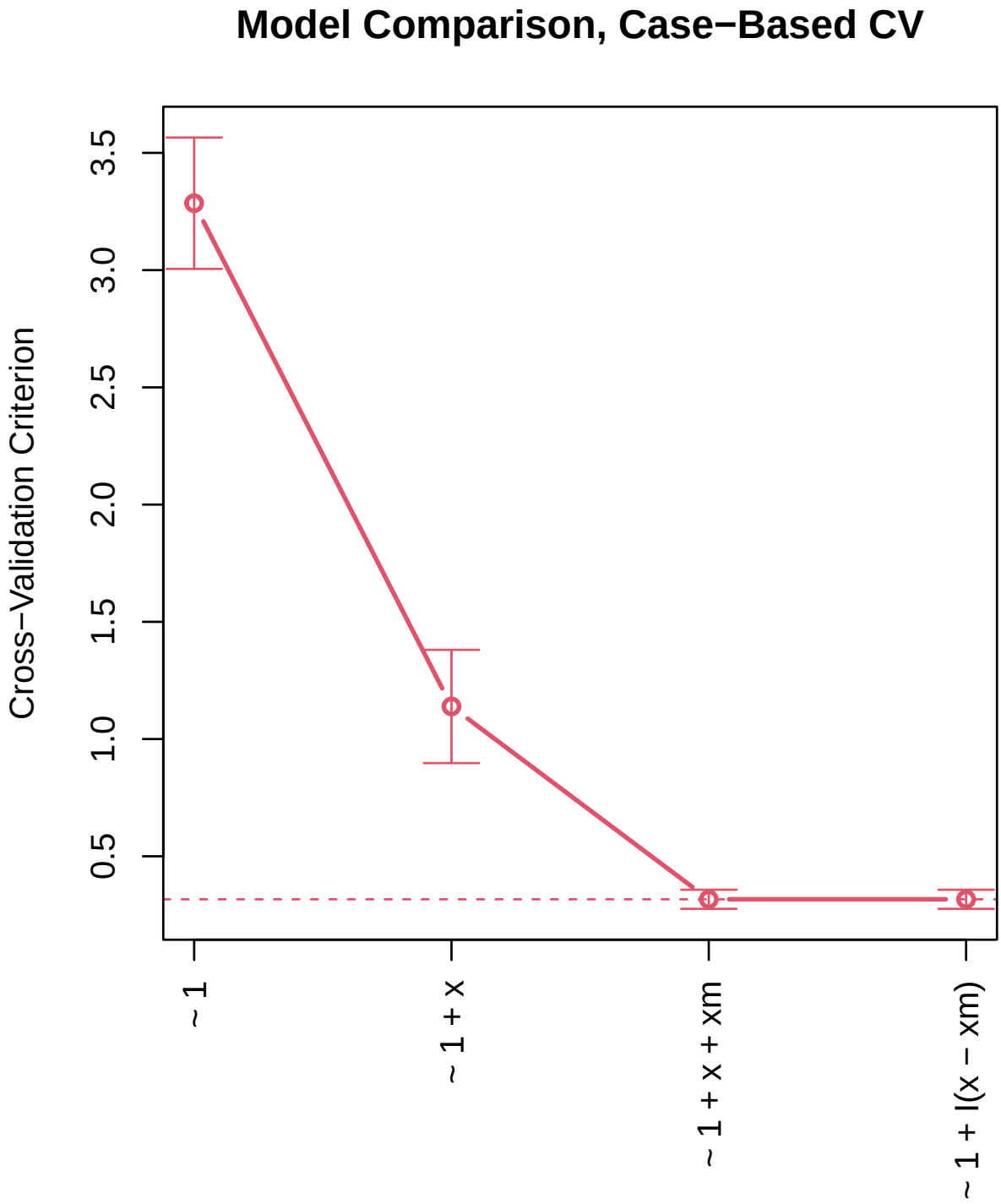


Figure 12: 10-fold case-based cross-validation comparing random intercept models with varying fixed effects.

```
R> tail(xtabs(~ id + week, data=Pigs), 3)

    week
id   1 2 3 4 5 6 7 8 9
  46 1 1 1 1 1 1 1 1 1
  47 1 1 1 1 1 1 1 1 1
  48 1 1 1 1 1 1 1 1 1
```

Each of 48 pigs is observed weekly over a period of 9 weeks, with the weight of the pig recorded in kg. The data are in "long" format, as is appropriate for use with the `lmer()` function in the **lme4** package. The data are very regular, with no missing cases.

The following graph, showing the growth trajectories of the pigs, is similar to Figure 3.1 in Diggle *et al.* (1994); we add an overall least-squares line and a loess smooth, which are nearly indistinguishable:

```
R> plot(weight ~ week, data=Pigs, type="n")
R> for (i in unique(Pigs$id)){
+   with(Pigs, lines(x=1:9, y=Pigs[id == i, "weight"],
+                    col="gray"))
+ }
R> abline(lm(weight ~ week, data=Pigs), col="blue", lwd=2)
R> lines(with(Pigs, loess.smooth(week, weight, span=0.5)),
+       col="magenta", lty=2, lwd=2)
```

The individual "growth curves" and the overall trend are generally linear, with some tendency for variability of pig weight to increase over weeks (a feature of the data that we ignore in the mixed model that we fit to the data below).

The Stata mixed-effects models manual proposes a model with crossed random effects for the `Pigs` data (StataCorp LLC 2023, page 37):

> [S]uppose that we wish to fit
>
> $$\text{weight}_{ij} = \beta_0 + \beta_1 \text{week}_{ij} + u_i + v_j + \varepsilon_{ij}$$
>
> for the $i = 1, \ldots, 9$ weeks and $j = 1, \ldots, 48$ pigs and
>
> $$u_i \sim N(0, \sigma_u^2); v_j \sim N(0, \sigma_v^2); \varepsilon_{ij} \sim N(0, \sigma_\varepsilon^2)$$
>
> all independently. That is, we assume an overall population-average growth curve $\beta_0 + \beta_1$week and a random pig-specific shift. In other words, the effect due to week, u_i, is systematic to that week and common to all pigs. The rationale behind [this model] could be that, assuming that the pigs were measured contemporaneously, we might be concerned that week-specific random factors such as weather and feeding patterns had significant systematic effects on all pigs.

Although we might prefer an alternative model,[10] we think that this is a reasonable specification.

[10] These are repeated-measures data, which would be more conventionally modeled with autocorrelated errors within pigs. The `lme()` function in the **nlme** package, for example, is capable of fitting a mixed-model of this form.

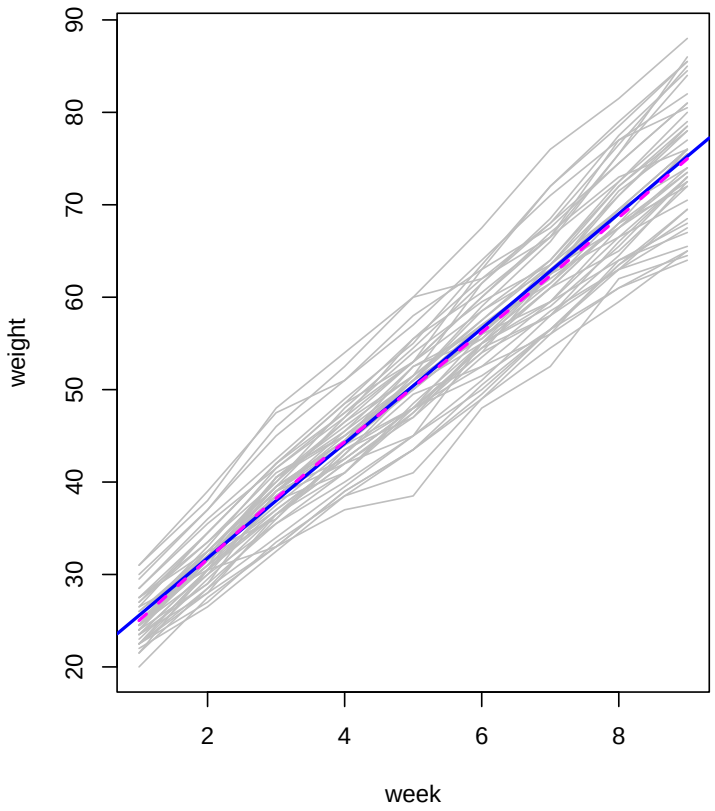


Figure 13: Growth trajectories for 48 pigs, with overall least-squares line (sold blue) and loess line (broken magenta).

The Stata manual fits the mixed model by maximum likelihood (rather than REML), and we duplicate the results reported there using `lmer()`:

```
R> m.p <- lmer(weight ~ week + (1 | id) + (1 | week),
+              data=Pigs, REML=FALSE, # i.e., ML
+              control=lmerControl(optimizer="bobyqa"))
R> summary(m.p)

Linear mixed model fit by maximum likelihood  ['lmerMod']
Formula: weight ~ week + (1 | id) + (1 | week)
   Data: Pigs
Control: lmerControl(optimizer = "bobyqa")

     AIC      BIC   logLik deviance df.resid
  2037.6   2058.0  -1013.8   2027.6      427

Scaled residuals:
    Min      1Q  Median      3Q     Max
-3.7750 -0.5418  0.0054  0.4762  3.9816

Random effects:
 Groups   Name        Variance Std.Dev.
 id       (Intercept) 14.83622 3.8518
 week     (Intercept)  0.08499 0.2915
 Residual              4.29733 2.0730
Number of obs: 432, groups:  id, 48; week, 9

Fixed effects:
            Estimate Std. Error t value
(Intercept) 19.35561    0.63340   30.56
week         6.20990    0.05393  115.14

Correlation of Fixed Effects:
     (Intr)
week -0.426
```

We opt for the non-default `"bobyqa"` optimizer because it provides more numerically stable results for subsequent cross-validation in this example.

We can then cross-validate the model by omitting folds composed of pigs, folds composed of weeks, or folds composed of pig-weeks (which in the `Pigs` data set correspond to individual cases, using only the fixed effects):

```
R> cv(m.p, clusterVariables="id")

n-Fold Cross Validation based on 48 {id} clusters
cross-validation criterion = 19.97309
```

```
bias-adjusted cross-validation criterion = 19.96496
95% CI for bias-adjusted CV criterion = (17.1249, 22.80502)
full-sample criterion = 19.20076
```

```
R> cv(m.p, clusterVariables="week")
```

```
boundary (singular) fit: see help('isSingular')

n-Fold Cross Validation based on 9 {week} clusters
cross-validation criterion = 19.31219
bias-adjusted cross-validation criterion = 19.30499
95% CI for bias-adjusted CV criterion = (16.56624, 22.04373)
full-sample criterion = 19.20076
```

```
R> cv(m.p, clusterVariables=c("id", "week"), k=10, seed=8469)
```

```
R RNG seed set to 8469

10-Fold Cross Validation based on 432 {id, week} clusters
cross-validation criterion = 19.2352
bias-adjusted cross-validation criterion = 19.23294
95% CI for bias-adjusted CV criterion = (16.49263, 21.97325)
full-sample criterion = 19.20076
```

We can also cross-validate the individual cases taking account of the random effects (employing the same 10 folds):

```
R> cv(m.p, k=10, seed=8469)
```

```
R RNG seed set to 8469

10-Fold Cross Validation
cross-validation criterion = 5.15835
bias-adjusted cross-validation criterion = 5.072933
95% CI for bias-adjusted CV criterion = (4.122952, 6.022913)
full-sample criterion = 3.795972
```

Because these predictions are based on BLUPs, they are more accurate than the predictions based only on fixed effects.[11] As well, the difference between the MSE computed for the model

[11] Even though there is only one observation per combination of pigs and weeks, we can use the BLUP for the omitted case because of the crossed structure of the random effects; that is each pig-week has a pig random effect and a week random effect. Although it probably isn't sensible, we can imagine a mixed model for the pig data that employs nested random effects, which would be specified by `lmer(weight  week + (1 | id/week), data=Pigs)`—that is, a random intercept that varies by combinations of `id` (pig) and `week`. This model can't be fit, however: With only one case per combination of `id` and `week`, the nested random-effect variance is indistinguishable from the case-level variance.

fit to the full data and the CV estimates of the MSE is greater here than for cluster-based predictions.

4. Replicating cross-validation

Assuming that the number of cases n is a multiple of the number of folds k—a slightly simplifying assumption—the number of possible partitions of cases into folds is $\frac{n!}{[(n/k)!]^k}$, a number that grows very large very quickly. For example, for $n = 10$ and $k = 5$, so that the folds are each of size $n/k = 2$, there are $113,400$ possible partitions; for $n = 100$ and $k = 5$, where $n/k = 20$, still a small problem, the number of possible partitions is truly astronomical, 1.09×10^{66}.

Because the partition into folds that's employed is selected randomly, the resulting CV criterion estimates are subject to sampling error. (An exception is LOO cross-validation, which is not at all random.) To get a sense of the magnitude of the sampling error, we can repeat the CV procedure with different randomly selected partitions into folds. All of the CV functions in the **cv** package are capable of repeated cross-validation, with the number of repetitions controlled by the `reps` argument, which defaults to `1`.

Here, for example, is 10-fold CV for the Mroz logistic regression, repeated 5 times:

```
R> cv(m.mroz, criterion=BayesRule, seed=248, reps=5,
+    method="Woodbury")

R RNG seed set to 248

R RNG seed set to 68134

R RNG seed set to 767359

R RNG seed set to 556270

R RNG seed set to 882966


Replicate 1:
10-Fold Cross Validation
method: Woodbury
criterion: BayesRule
cross-validation criterion = 0.3200531
bias-adjusted cross-validation criterion = 0.3130109
95% CI for bias-adjusted CV criterion = (0.2796692, 0.3463526)
full-sample criterion = 0.3067729

Replicate 2:
10-Fold Cross Validation
method: Woodbury
```

```
criterion: BayesRule
cross-validation criterion = 0.3160691
bias-adjusted cross-validation criterion = 0.311697
95% CI for bias-adjusted CV criterion = (0.2784665, 0.3449274)
full-sample criterion = 0.3067729

Replicate 3:
10-Fold Cross Validation
method: Woodbury
criterion: BayesRule
cross-validation criterion = 0.314741
bias-adjusted cross-validation criterion = 0.3086212
95% CI for bias-adjusted CV criterion = (0.2754285, 0.341814)
full-sample criterion = 0.3067729

Replicate 4:
10-Fold Cross Validation
method: Woodbury
criterion: BayesRule
cross-validation criterion = 0.3240372
bias-adjusted cross-validation criterion = 0.318069
95% CI for bias-adjusted CV criterion = (0.2846189, 0.3515192)
full-sample criterion = 0.3067729

Replicate 5:
10-Fold Cross Validation
method: Woodbury
criterion: BayesRule
cross-validation criterion = 0.3240372
bias-adjusted cross-validation criterion = 0.3192577
95% CI for bias-adjusted CV criterion = (0.2858076, 0.3527079)
full-sample criterion = 0.3067729

Average:
10-Fold Cross Validation
method: Woodbury
criterion: BayesRule
cross-validation criterion = 0.3198318 (0.003886968)
bias-adjusted cross-validation criterion = 0.3139445 (0.004009339)
full-sample criterion = 0.3067729
```

When `reps` > 1, the result returned by `cv()` is an object of class `"cvList"`—literally a list of `"cv"` objects. The results are reported for each repetition and then averaged across repetitions, with the standard deviations of the CV criterion and the biased-adjusted CV criterion given in parentheses. In this example, there is therefore little variation across repetitions, increasing our confidence in the reliability of the results.

Notice that the seed that's set in the `cv()` command pertains to the first repetition and the

seeds for the remaining repetitions are then selected pseudo-randomly.[12] Setting the first seed, however, makes the entire process easily replicable, and the seed for each repetition is stored in the corresponding element of the "cvList" object (which isn't, however, saved in the example).

It's also possible to replicate CV when comparing competing models via the cv() method for "modList" objects. Recall our comparison of polynomial regressions of varying degree fit to the Auto data; we performed 10-fold CV for each of 10 models. Here, we replicate that process 5 times for each model and graph the results:

```
R> cv.auto.reps <- cv(models(m.1, m.2, m.3, m.4, m.5,
+                            m.6, m.7, m.8, m.9, m.10),
+                     data=Auto, seed=8004, reps=5)
R> plot(cv.auto.reps)
```

The graph shows both the average CV criterion and its range for each of the competing models.

5. Cross-validating model selection

5.1. A preliminary example

As Hastie, Tibshirani, and Friedman (2009, Sec. 7.10.2: "The Wrong and Right Way to Do Cross-validation") explain, if the whole data are used to select or fine-tune a statistical model, subsequent cross-validation of the model is intrinsically misleading, because the model is selected to fit the whole data, including the part of the data that remains when each fold is removed.

The following example is similar in spirit to one employed by Hastie *et al.* (2009). Suppose that we randomly generate $n = 1000$ independent observations for a response variable variable $y \sim N(\mu = 10, \sigma^2 = 0)$, and independently sample 1000 observations for $p = 100$ "predictors," $x_1, \ldots, x_{100}$, each from $x_j \sim N(0, 1)$. The response has nothing to do with the predictors and so the population linear-regression model $y_i = \alpha + \beta_1 x_{i1} + \cdots + \beta_{100} x_{i,100} + \varepsilon_i$ has $\alpha = 10$ and all $\beta_j = 0$.

```
R> set.seed(24361) # for reproducibility
R> D <- data.frame(
+   y = rnorm(1000, mean=10),
+   X = matrix(rnorm(1000*100), 1000, 100)
+ )
R> head(D[, 1:6])
```

[12] Because of the manner in which the computation is performed, the order of the replicates in the "cvList" object returned by cv() isn't the same as the order in which the replicates are computed. Each element of the result, however, is a "cv" object with the correct random-number seed saved, and so this technical detail can be safely ignored. The individual "cv" objects are printed in the order in which they are stored rather than the order in which they are computed.

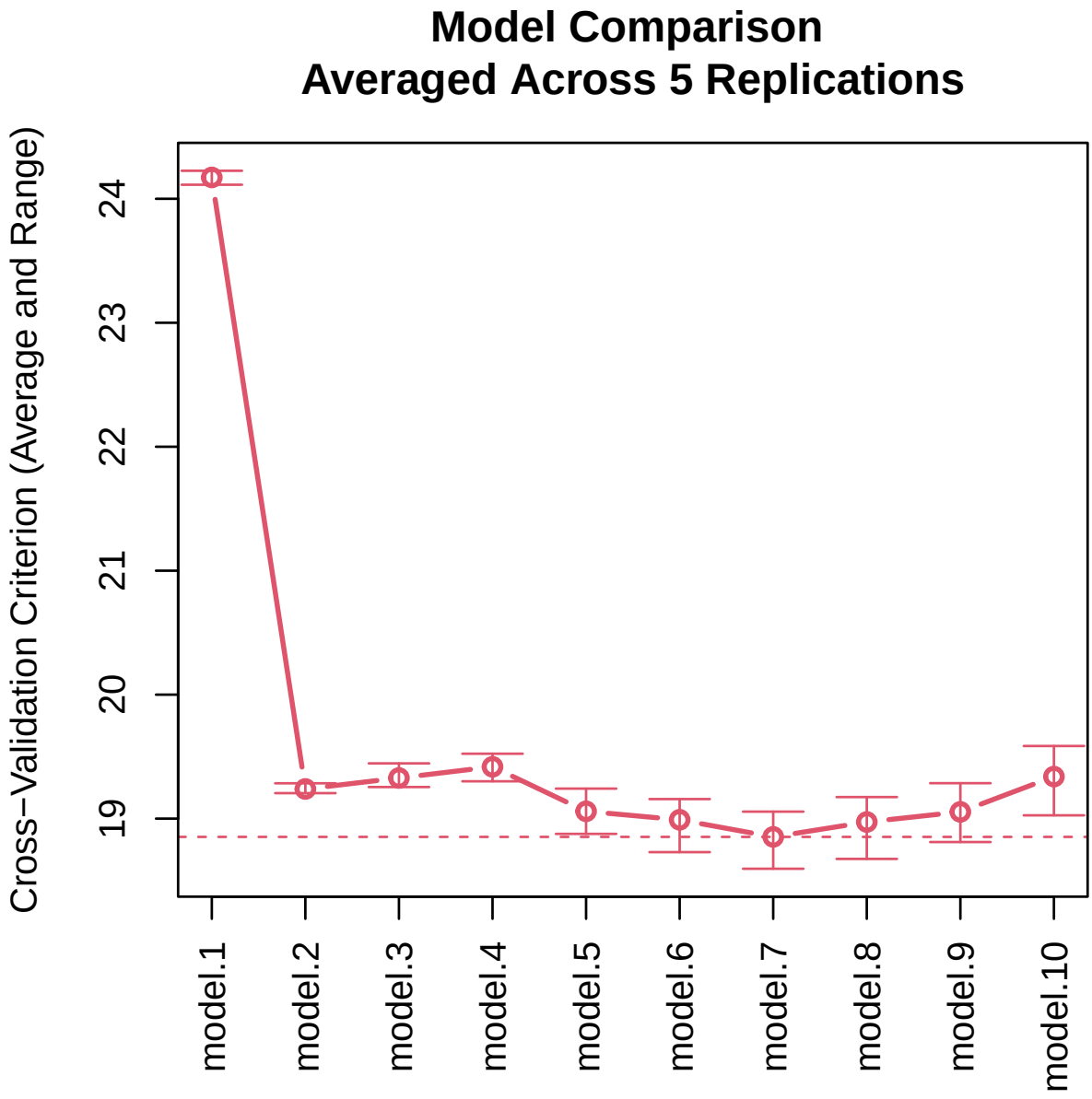


Figure 14: Replicated cross-validated 10-fold CV as a function of polynomial degree, p

```
          y        X.1        X.2         X.3         X.4         X.5
1 10.031647 -1.2388628 -0.2648705 -0.03539048 -2.57697337  0.81104761
2  9.664989  0.1228689 -0.1774440  0.37290421 -0.93513788  0.62867324
3 10.023249 -0.9505172 -0.7348667 -1.05978180  0.88294443  0.02391808
4  8.990969  1.1357103  0.3241085  0.11036901  1.37630285 -0.42211426
5  9.071249  1.4947403  1.8753802  0.10574793  0.29213991 -0.18456833
6 11.349283 -0.1845331 -0.7803709 -1.23803778 -0.01094861  0.69103395
```

Least-squares provides accurate estimates of the regression constant $\alpha = 10$ and the error variance $\sigma^2 = 1$ for the "null model" including only the regression constant; moreover, the omnibus F-test of the correct null hypothesis that all of the βs are 0 for the "full model" with all 100 xs is associated with a large p-value:

```
R> m.full <- lm(y ~ ., data=D)
R> m.null <- lm(y ~ 1, data=D)
R> anova(m.null, m.full)

Analysis of Variance Table

Model 1: y ~ 1
Model 2: y ~ X.1 + X.2 + X.3 + X.4 + X.5 + X.6 + X.7 + X.8 + X.9 + X.10 +
    X.11 + X.12 + X.13 + X.14 + X.15 + X.16 + X.17 + X.18 + X.19 +
    X.20 + X.21 + X.22 + X.23 + X.24 + X.25 + X.26 + X.27 + X.28 +
    X.29 + X.30 + X.31 + X.32 + X.33 + X.34 + X.35 + X.36 + X.37 +
    X.38 + X.39 + X.40 + X.41 + X.42 + X.43 + X.44 + X.45 + X.46 +
    X.47 + X.48 + X.49 + X.50 + X.51 + X.52 + X.53 + X.54 + X.55 +
    X.56 + X.57 + X.58 + X.59 + X.60 + X.61 + X.62 + X.63 + X.64 +
    X.65 + X.66 + X.67 + X.68 + X.69 + X.70 + X.71 + X.72 + X.73 +
    X.74 + X.75 + X.76 + X.77 + X.78 + X.79 + X.80 + X.81 + X.82 +
    X.83 + X.84 + X.85 + X.86 + X.87 + X.88 + X.89 + X.90 + X.91 +
    X.92 + X.93 + X.94 + X.95 + X.96 + X.97 + X.98 + X.99 + X.100
  Res.Df    RSS  Df Sum of Sq      F Pr(>F)
1    999 973.65
2    899 888.44 100    85.208 0.8622  0.825

R> summary(m.null)


Call:
lm(formula = y ~ 1, data = D)

Residuals:
    Min      1Q  Median      3Q     Max
-3.4585 -0.6809  0.0190  0.6365  2.9346

Coefficients:
```

```
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  9.93704    0.03122   318.3   <2e-16

Residual standard error: 0.9872 on 999 degrees of freedom
```

Next, using the `stepAIC()` function in the **MASS** package (Venables and Ripley 2002), let us perform a forward stepwise regression to select a "best" model, starting with the null model, and using AIC as the model-selection criterion (see the help page for `stepAIC()` for details):[13]

```
R> library("MASS")  # for stepAIC()
R> m.select <- stepAIC(m.null,
+                      direction="forward", trace=FALSE,
+                      scope=list(lower=~1, upper=formula(m.full)))
R> summary(m.select)


Call:
lm(formula = y ~ X.99 + X.90 + X.87 + X.40 + X.65 + X.91 + X.53 +
    X.45 + X.31 + X.56 + X.61 + X.60 + X.46 + X.35 + X.92, data = D)

Residuals:
    Min      1Q  Median      3Q     Max
-3.2620 -0.6446  0.0236  0.6406  3.1180

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  9.93716    0.03098 320.803  < 2e-16
X.99        -0.09103    0.03082  -2.953  0.00322
X.90        -0.08205    0.03135  -2.617  0.00901
X.87        -0.06942    0.03105  -2.235  0.02561
X.40        -0.04759    0.03076  -1.547  0.12211
X.65        -0.05523    0.03147  -1.755  0.07952
X.91         0.05245    0.03084   1.700  0.08937
X.53        -0.04921    0.03048  -1.615  0.10672
X.45         0.05543    0.03182   1.742  0.08183
X.31         0.04525    0.03108   1.456  0.14570
X.56         0.05433    0.03273   1.660  0.09723
X.61        -0.05085    0.03170  -1.604  0.10908
X.60        -0.05133    0.03194  -1.607  0.10832
X.46         0.05158    0.03272   1.576  0.11529
X.35         0.04696    0.03146   1.493  0.13584
X.92         0.04430    0.03100   1.429  0.15329

Residual standard error: 0.9725 on 984 degrees of freedom
```

[13] It's generally advantageous to start with the largest model, here the one with 100 predictors, and proceed by backward elimination. In this demonstration, however, where all of the βs are really 0, the selected model will be small, and so we proceed by forward selection from the null model to save computing time.

```
Multiple R-squared:  0.04419,   Adjusted R-squared:  0.02962
F-statistic: 3.033 on 15 and 984 DF,  p-value: 8.338e-05
```

```
R> mse(D$y, fitted(m.select))
```

```
[1] 0.9306254
attr(,"casewise loss")
[1] "(y - yhat)^2"
```

The resulting model has 15 predictors, a very modest $R^2 = .044$, but a small p-value for its omnibus F-test (which, of course, is entirely spurious because the same data were used to select and test the model). The MSE for the selected model is smaller than the true error variance $\sigma^2 = 1$, as is the estimated error variance for the selected model, $\widehat{\sigma}^2 = 0.973^2 = 0.947$.

If we cross-validate the selected model, we also obtain an optimistic estimate of its predictive power (although the confidence interval for the bias-adjusted MSE includes 1):

```
R> cv(m.select, seed=2529)
```

```
R RNG seed set to 2529

10-Fold Cross Validation
method: Woodbury
criterion: mse
cross-validation criterion = 0.9593695
bias-adjusted cross-validation criterion = 0.9578478
95% CI for bias-adjusted CV criterion = (0.8766138, 1.039082)
full-sample criterion = 0.9306254
```

The `cvSelect()` function in the **cv** package allows us to cross-validate the whole model-selection procedure. The first argument to `cvSelect()` is a model-selection function capable of refitting the model with a fold omitted and returning a CV criterion. The `selectStepAIC()` function, also in **cv** and based on `stepAIC()`, is suitable for use with `cvSelect()`:

```
R> cv.select <- cvSelect(selectStepAIC, data=D, seed=3791,
+                        model=m.null, direction="forward",
+                        scope=list(lower=~1,
+                                   upper=formula(m.full)))
```

```
R RNG seed set to 3791
```

```
R> cv.select
```

```
10-Fold Cross Validation
cross-validation criterion = 1.06873
bias-adjusted cross-validation criterion = 1.061183
95% CI for bias-adjusted CV criterion = (0.9717229, 1.150642)
full-sample criterion = 0.9306254
```

The other arguments to `cvSelect()` are:

- `data`, the data set to which the model is fit;
- `seed`, an optional seed for R's pseudo-random-number generator; as for `cv()`, if the seed isn't supplied by the user, a seed is randomly selected and saved;
- additional arguments required by the model-selection function, here the starting `model` argument, the `direction` of model selection, and the `scope` of models considered (from the model with only a regression constant to the model with all 100 predictors).

By default, `cvSelect()` performs 10-fold CV, and produces an estimate of MSE for the model-selection procedure even *larger* than the true error variance, $\sigma^2 = 1$.

Also by default, when the number of folds is 10 or fewer, `cvSelect()` saves the coefficients of the selected models. In this example, the `compareFolds()` function reveals that the variables retained by the model-selection process in the several folds are quite different:

```
R> compareFolds(cv.select)
```

```
        (Intercept)    X.87    X.90    X.99    X.91    X.54    X.53    X.56
Fold 1       9.9187 -0.0615 -0.0994 -0.0942  0.0512  0.0516
Fold 2       9.9451 -0.0745 -0.0899 -0.0614          0.0587          0.0673
Fold 3       9.9423 -0.0783 -0.0718 -0.0987  0.0601                  0.0512
Fold 4       9.9410 -0.0860 -0.0831 -0.0867  0.0570         -0.0508
Fold 5       9.9421 -0.0659 -0.0849 -0.1004  0.0701  0.0511 -0.0487  0.0537
Fold 6       9.9633 -0.0733 -0.0874 -0.0960  0.0555  0.0629 -0.0478
Fold 7       9.9279 -0.0618 -0.0960 -0.0838  0.0533         -0.0464
Fold 8       9.9453 -0.0610 -0.0811 -0.0818          0.0497 -0.0612  0.0560
Fold 9       9.9173 -0.0663 -0.0894 -0.1100  0.0504  0.0524          0.0747
Fold 10      9.9449 -0.0745 -0.0906 -0.0891  0.0535  0.0482 -0.0583  0.0642
           X.40    X.45    X.65    X.68    X.92    X.15    X.26    X.46    X.60
Fold 1                  -0.0590                 -0.0456  0.0658  0.0608
Fold 2                                  0.0607          0.0487
Fold 3  -0.0496         -0.0664         0.0494
Fold 4  -0.0597  0.0579 -0.0531         0.0519 -0.0566                  -0.0519
Fold 5                          0.0587                          0.0527 -0.0603
Fold 6  -0.0596  0.0552         0.0474
Fold 7           0.0572         0.0595
Fold 8           0.0547 -0.0617  0.0453  0.0493 -0.0613  0.0591  0.0703 -0.0588
Fold 9  -0.0552  0.0573 -0.0635  0.0492         -0.0513  0.0484         -0.0507
Fold 10 -0.0558                         0.0529                  0.0710
           X.61     X.8    X.28    X.29    X.31    X.35    X.70    X.89    X.17
Fold 1  -0.0490          0.0616 -0.0537                  0.0638
Fold 2           0.0671                 0.0568                  0.0523
Fold 3  -0.0631          0.0616
Fold 4           0.0659         -0.0549          0.0527                  0.0527
Fold 5           0.0425                 0.0672  0.0613          0.0493
Fold 6           0.0559         -0.0629  0.0498          0.0487
```

```
Fold 7                                                          0.0611  0.0472
Fold 8  -0.0719                                         0.0586
Fold 9                    0.0525
Fold 10 -0.0580                                 0.0603
          X.25     X.4    X.64    X.81    X.97    X.11     X.2    X.33    X.47
Fold 1                                    0.0604          0.0575
Fold 2   0.0478          0.0532  0.0518
Fold 3                           0.0574                           0.0473
Fold 4                    0.0628
Fold 5   0.0518
Fold 6                                          0.0521
Fold 7           0.0550
Fold 8
Fold 9                                    0.0556                          0.0447
Fold 10          0.0516
            X.6    X.72    X.73    X.77    X.79 X.88
Fold 1   0.0476
Fold 2                    0.0514
Fold 3
Fold 4                                  -0.0473
Fold 5           0.0586                         0.07
Fold 6                           -0.0489
Fold 7
Fold 8
Fold 9
Fold 10
```

5.2. Mroz's logistic regression revisited

For a contrasting example we apply model selection to Mroz's logistic regression for married women's labor-force participation. First, recall the logistic regression model that we fit to the `Mroz` data:

```
R> summary(m.mroz)


Call:
glm(formula = lfp ~ ., family = binomial, data = Mroz)

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  3.182140   0.644375   4.938 7.88e-07
k5          -1.462913   0.197001  -7.426 1.12e-13
k618        -0.064571   0.068001  -0.950 0.342337
age         -0.062871   0.012783  -4.918 8.73e-07
wcyes        0.807274   0.229980   3.510 0.000448
```

```
hcyes        0.111734   0.206040   0.542 0.587618
lwg          0.604693   0.150818   4.009 6.09e-05
inc         -0.034446   0.008208  -4.196 2.71e-05

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 1029.75  on 752  degrees of freedom
Residual deviance:  905.27  on 745  degrees of freedom
AIC: 921.27

Number of Fisher Scoring iterations: 4
```

Applying stepwise model selection Mroz's logistic regression, using BIC as the model-selection criterion (via the argument `k=log(nrow(Mroz))` to `stepAIC()`) selects 5 of the 7 original predictors:

```
R> m.mroz.sel <- stepAIC(m.mroz, k=log(nrow(Mroz)),
+                        trace=FALSE)
R> summary(m.mroz.sel)


Call:
glm(formula = lfp ~ k5 + age + wc + lwg + inc, family = binomial,
    data = Mroz)

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  2.90193    0.54290   5.345 9.03e-08
k5          -1.43180    0.19320  -7.411 1.25e-13
age         -0.05853    0.01142  -5.127 2.94e-07
wcyes        0.87237    0.20639   4.227 2.37e-05
lwg          0.61568    0.15014   4.101 4.12e-05
inc         -0.03367    0.00780  -4.317 1.58e-05

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 1029.75  on 752  degrees of freedom
Residual deviance:  906.46  on 747  degrees of freedom
AIC: 918.46

Number of Fisher Scoring iterations: 3

R> BayesRule(Mroz$lfp == "yes",
+           predict(m.mroz.sel, type="response"))

[1] 0.3187251
attr(,"casewise loss")
[1] "y != round(yhat)"
```

Bayes rule applied to the selected model misclassifies 32% of the cases in the `Mroz` data.

Cross-validating the selected model produces a similar, slightly larger, estimate of misclassification, about 33%:

```
R> cv(m.mroz.sel, criterion=BayesRule, seed=345266)

R RNG seed set to 345266

10-Fold Cross Validation
method: exact
criterion: BayesRule
cross-validation criterion = 0.3306773
bias-adjusted cross-validation criterion = 0.3333245
95% CI for bias-adjusted CV criterion = (0.2996998, 0.3669493)
full-sample criterion = 0.3187251
```

Is this estimate of predictive performance optimistic?

We proceed to apply the model-selection procedure by cross-validation, producing more or less the same result:

```
R> m.mroz.sel.cv <- cvSelect(selectStepAIC, Mroz,
+                            seed=6681,
+                            criterion=BayesRule,
+                            model=m.mroz,
+                            AIC=FALSE)

R RNG seed set to 6681

R> m.mroz.sel.cv

10-Fold Cross Validation
cross-validation criterion = 0.3306773
bias-adjusted cross-validation criterion = 0.3345203
95% CI for bias-adjusted CV criterion = (0.3008955, 0.368145)
full-sample criterion = 0.3187251
```

Setting `AIC=FALSE` in the call to `cvSelect()` uses the BIC rather than the AIC as the model-selection criterion. As it turns out, exactly the same predictors are selected when each of the 10 folds are omitted, and the several coefficient estimates are very similar, as we show using `compareFolds()`:

```
R> compareFolds(m.mroz.sel.cv)

        (Intercept)     age     inc      k5     lwg wcyes
Fold 1       2.5014 -0.0454 -0.0388 -1.3613  0.5653  0.85
Fold 2       3.0789 -0.0659 -0.0306 -1.5335  0.6923  0.79
```

```
Fold 3       3.0141 -0.0595 -0.0305 -1.3994  0.5428  0.86
Fold 4       2.7251 -0.0543 -0.0354 -1.4474  0.6298  1.09
Fold 5       2.7617 -0.0566 -0.0320 -1.4752  0.6324  0.74
Fold 6       3.0234 -0.0621 -0.0348 -1.4537  0.6618  0.94
Fold 7       2.9615 -0.0600 -0.0351 -1.4127  0.5835  0.97
Fold 8       2.9598 -0.0603 -0.0329 -1.3865  0.6210  0.69
Fold 9       3.2481 -0.0650 -0.0381 -1.4138  0.6093  0.94
Fold 10      2.7724 -0.0569 -0.0295 -1.4503  0.6347  0.85
```

In this example, therefore, we appear to obtain a realistic estimate of model performance directly from the selected model, because there is little added uncertainty induced by model selection.

5.3. Cross-validating choice of transformations in regression

The **cv** package also provides a `cvSelect()` procedure, `selectTrans()`, for choosing transformations of the predictors and the response in regression.

Some background: As Weisberg (2014, Sec. 8.2) explains, there are technical advantages to having (numeric) predictors in linear regression analysis that are themselves linearly related. If the predictors *aren't* linearly related, then the relationships between them can often be straightened by power transformations. Transformations can be selected after graphical examination of the data, or by analytic methods. Once the relationships between the predictors are linearized, it can be advantageous similarly to transform the response variable towards normality.

Selecting transformations analytically raises the possibility of automating the process, as would be required for cross-validation. One could, in principle, apply graphical methods to select transformations for each fold, but because a data analyst couldn't forget the choices made for previous folds, the process wouldn't really be applied independently to the folds.

To illustrate, we adapt an example appearing in several places in Fox and Weisberg (2019) (for example in Chapter 3 on transforming data), using data on the prestige and other characteristics of 102 Canadian occupations circa 1970. The data are in the `Prestige` data frame in the **carData** package:

```
R> data("Prestige", package="carData")
R> head(Prestige)
```

```
                    education income women prestige census type
gov.administrators      13.11  12351 11.16     68.8   1113 prof
general.managers        12.26  25879  4.02     69.1   1130 prof
accountants             12.77   9271 15.70     63.4   1171 prof
purchasing.officers     11.42   8865  9.11     56.8   1175 prof
chemists                14.62   8403 11.68     73.5   2111 prof
physicists              15.64  11030  5.13     77.6   2113 prof
```

```
R> summary(Prestige)
```

```
   education          income          women          prestige
 Min.   : 6.380   Min.   :  611   Min.   : 0.000   Min.   :14.80
 1st Qu.: 8.445   1st Qu.: 4106   1st Qu.: 3.592   1st Qu.:35.23
 Median :10.540   Median : 5930   Median :13.600   Median :43.60
 Mean   :10.738   Mean   : 6798   Mean   :28.979   Mean   :46.83
 3rd Qu.:12.648   3rd Qu.: 8187   3rd Qu.:52.203   3rd Qu.:59.27
 Max.   :15.970   Max.   :25879   Max.   :97.510   Max.   :87.20
     census       type
 Min.   :1113   bc  :44
 1st Qu.:3120   prof:31
 Median :5135   wc  :23
 Mean   :5402   NA's: 4
 3rd Qu.:8312
 Max.   :9517
```

The variables in the `Prestige` data set are:

- `education`: average years of education for incumbents in the occupation, from the 1971 Canadian Census.
- `income`: average dollars of annual income for the occupation, from the Census.
- `women`: percentage of occupational incumbents who were women, also from the Census.
- `prestige`: the average prestige rating of the occupation on a 0–100 "thermometer" scale, in a Canadian social survey conducted around the same time.
- `type`, type of occupation, and `census`, the Census occupational code, which are not used in our example.

The object of a regression analysis for the `Prestige` data (and their original purpose) is to predict occupational prestige from the other variables in the data set.

A scatterplot matrix (using the `scatterplotMatrix()` function in the **car** package) of the numeric variables in the data reveals that the distributions of `income` and `women` are positively skewed, and that some of the relationships among the three predictors, and between the predictors and the response (i.e., `prestige`), are nonlinear:

```
R> library("car")

Loading required package: carData

R> scatterplotMatrix(~ prestige + income + education + women,
+                    data=Prestige, smooth=list(spread=FALSE))
```

The `powerTransform()` function in the **car** package transforms variables towards multivariate normality by a generalization of Box and Cox's maximum-likelihood-like approach (Box and Cox 1964). Several "families" of power transformations can be used, including the original Box-Cox family, simple powers (and roots), and two adaptations of the Box-Cox family to data that may include negative values and zeros: the Box-Cox-with-negatives family and the Yeo-Johnson family; see Weisberg (2014, Chap. 8), and Fox and Weisberg (2019, Chap. 3) for details. Because `women` has some 0 values, we use the Yeo-Johnson family:

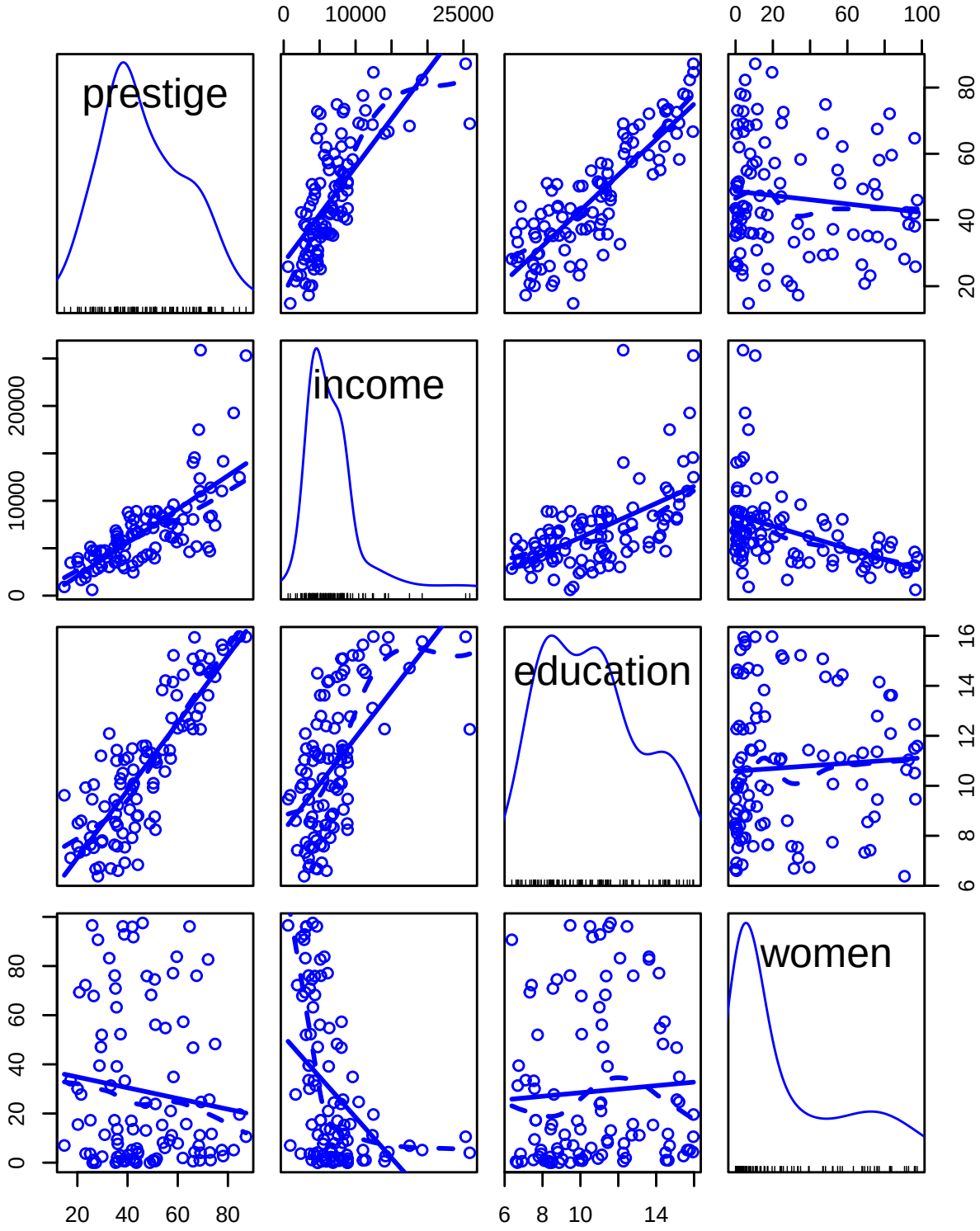


Figure 15: Scatterplot matrix for the ‘Prestige‘ data.

```
R> trans <- powerTransform( cbind(income, education, women) ~ 1,
+                           data=Prestige, family="yjPower")
R> summary(trans)

yjPower Transformations to Multinormality
          Est Power Rounded Pwr Wald Lwr Bnd Wald Upr Bnd
income       0.2678        0.33       0.1051       0.4304
education    0.5162        1.00      -0.2822       1.3145
women        0.1630        0.16       0.0112       0.3149

 Likelihood ratio test that all transformation parameters are equal to 0
                                LRT df      pval
LR test, lambda = (0 0 0) 15.73879  3 0.0012827
```

We thus have evidence of the desirability of transforming `income` (by the 1/3 power) and `women` (by the 0.16 power—which is close to the "0" power, i.e., the log transformation), but not `education`. Applying the "rounded" power transformations makes the predictors better-behaved:

```
R> P <- Prestige[, c("prestige", "income", "education", "women")]
R> (lambdas <- trans$roundlam)

   income education     women
0.3300000 1.0000000 0.1630182

R> names(lambdas) <- c("income", "education", "women")
R> for (var in c("income", "education", "women")){
+   P[, var] <- yjPower(P[, var], lambda=lambdas[var])
+ }
R> summary(P)

    prestige         income        education          women
 Min.   :14.80   Min.   :22.15   Min.   : 6.380   Min.   :0.000
 1st Qu.:35.23   1st Qu.:44.17   1st Qu.: 8.445   1st Qu.:1.731
 Median :43.60   Median :50.26   Median :10.540   Median :3.362
 Mean   :46.83   Mean   :50.76   Mean   :10.738   Mean   :3.502
 3rd Qu.:59.27   3rd Qu.:56.24   3rd Qu.:12.648   3rd Qu.:5.591
 Max.   :87.20   Max.   :83.62   Max.   :15.970   Max.   :6.830

R> scatterplotMatrix(~ prestige + income + education + women,
+                    data=P, smooth=list(spread=FALSE))
```

Comparing the MSE for the regressions with the original and transformed predictors shows a advantage to the latter:

```
R> m.pres <- lm(prestige ~ income + education + women, data=Prestige)
R> m.pres.trans <- lm(prestige ~ income + education + women, data=P)
R> mse(Prestige$prestige, fitted(m.pres))
```

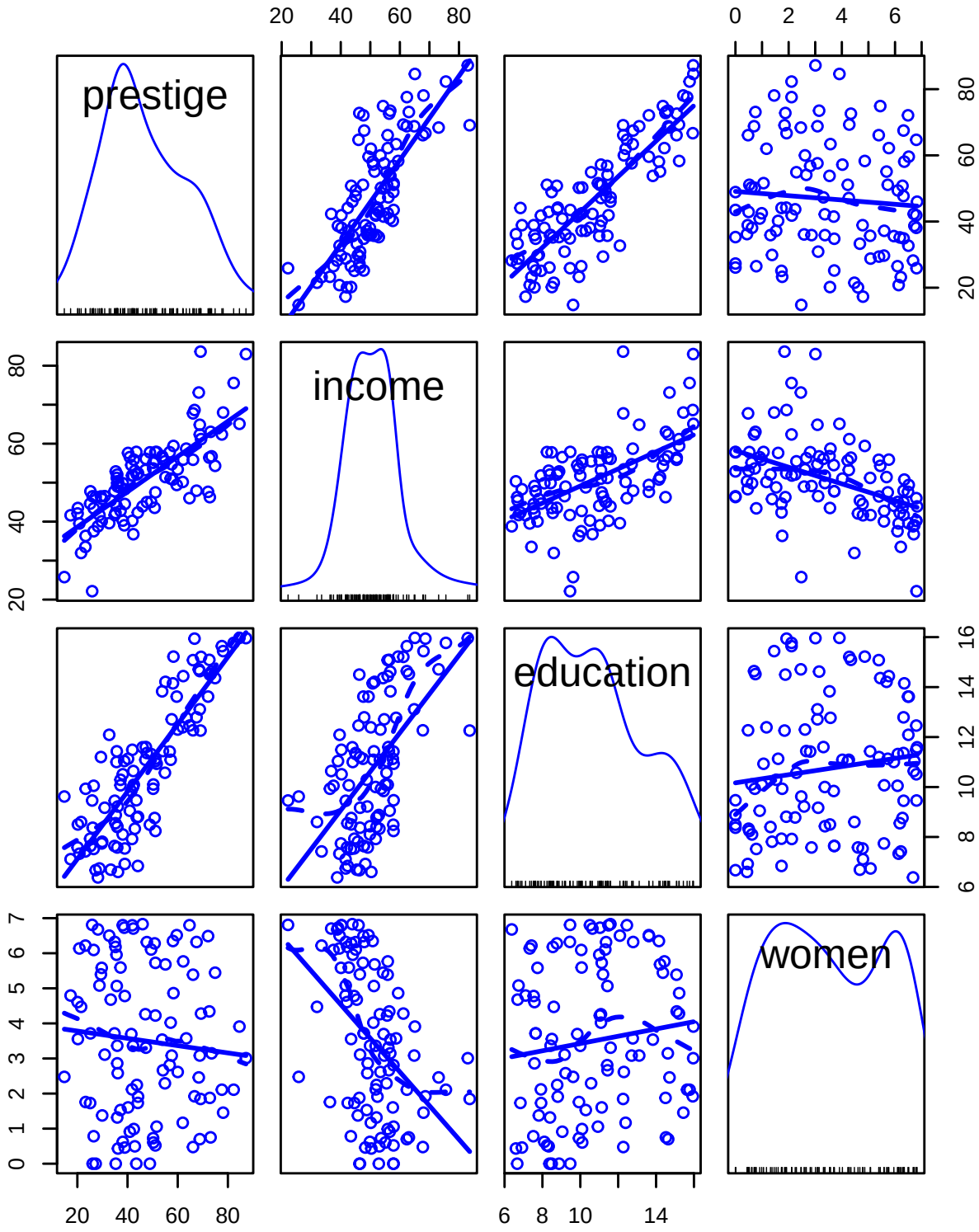


Figure 16: Scatterplot matrix for the ‘Prestige‘ data with the predictors transformed.

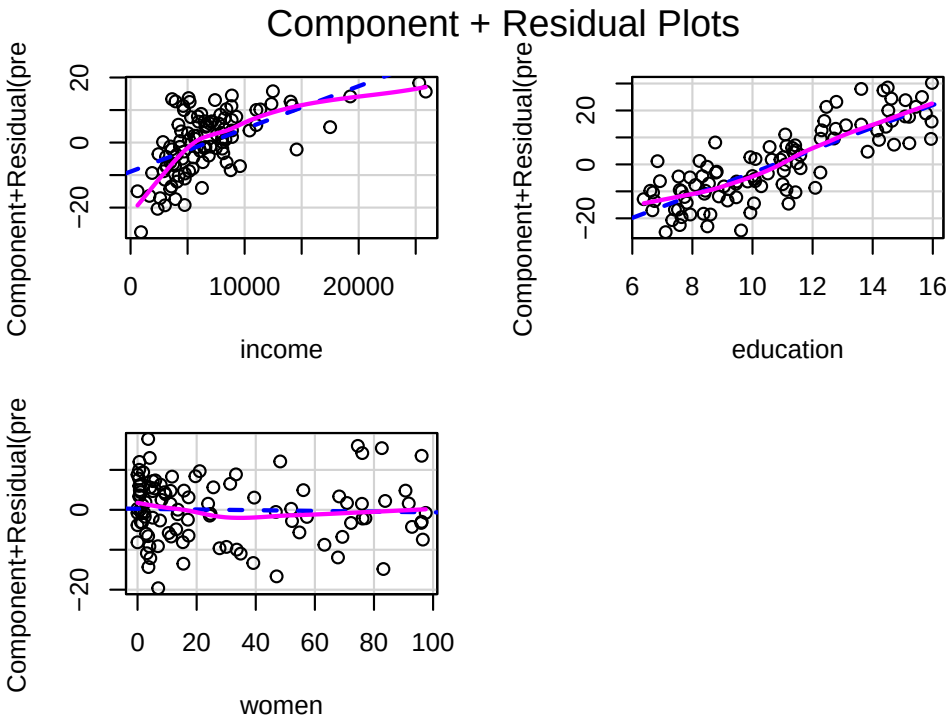


Figure 17: Component+residual plots for the 'Prestige' regression with the original predictors.

```
[1] 59.15265
attr(,"casewise loss")
[1] "(y - yhat)^2"
```

```
R> mse(P$prestige, fitted(m.pres.trans))
```

```
[1] 50.60016
attr(,"casewise loss")
[1] "(y - yhat)^2"
```

Similarly, component+residual plots for the two regressions, produced by the `crPlots()` function in the **car** package, suggest that the partial relationship of `prestige` to `income` is more nearly linear in the transformed data, but the transformation of \code{women] fails to capture what appears to be a slight quadratic partial relationship; the partial relationship of `prestige` to `education` is close to linear in both regressions:

```
R> crPlots(m.pres)
```

```
R> crPlots(m.pres.trans)
```

Having transformed the predictors towards multinormality, we now consider whether there's evidence for transforming the response (using `powerTransform()` for Box and Cox's original method), and we discover that there's not:

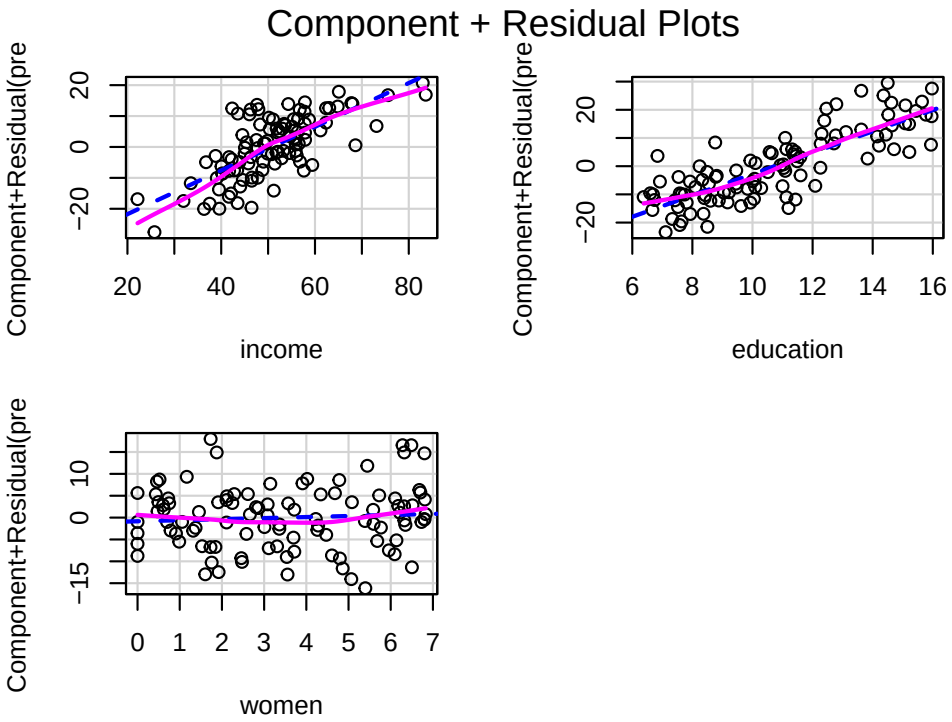


Figure 18: Component+residual plots for the 'Prestige' regression with transformed predictors.

```
R> summary(powerTransform(m.pres.trans))

bcPower Transformation to Normality
   Est Power Rounded Pwr Wald Lwr Bnd Wald Upr Bnd
Y1    1.0194           1       0.6773       1.3615

Likelihood ratio test that transformation parameter is equal to 0
 (log transformation)
                           LRT df       pval
LR test, lambda = (0) 32.2174  1 1.3785e-08

Likelihood ratio test that no transformation is needed
                              LRT df    pval
LR test, lambda = (1) 0.01238421  1 0.91139
```

The `selectTrans()` function in the **cv** package automates the process of selecting predictor and response transformations. The function takes a `data` set and "working" `model` as arguments, along with the candidate `predictors` and `response` for transformation, and the transformation `family` to employ. If the `predictors` argument is missing then only the response is transformed, and if the `response` argument is missing, only the supplied predictors are transformed. The default `family` for transforming the predictors is `"bcPower"`—the original Box-Cox family—as is the default `family.y` for transforming the response; here we specify `family="yjPower` because of the 0s in `women`. `selectTrans()` returns the result of

applying a lack-of-fit criterion to the model after the selected transformation is applied, with the default `criterion=mse`:

```
R> selectTrans(data=Prestige, model=m.pres,
+             predictors=c("income", "education", "women"),
+             response="prestige", family="yjPower")

[1] 50.60016
attr(,"casewise loss")
[1] "(y - yhat)^2"
```

`selectTrans()` also takes an optional `indices` argument, making it suitable for doing computations on a subset of the data (i.e., a CV fold), and hence for use with `cvSelect()` (see `?selectTrans` for details):

```
R> cvs <- cvSelect(selectTrans, data=Prestige, model=m.pres, seed=1463,
+                 predictors=c("income", "education", "women"),
+                 response="prestige",
+                 family="yjPower")

R RNG seed set to 1463

R> cvs

10-Fold Cross Validation
cross-validation criterion = 54.4871
bias-adjusted cross-validation criterion = 54.30824
full-sample criterion = 50.60016

R> cv(m.pres, seed=1463) # untransformed model with same folds

R RNG seed set to 1463

10-Fold Cross Validation
method: Woodbury
criterion: mse
cross-validation criterion = 63.2926
bias-adjusted cross-validation criterion = 63.07251
full-sample criterion = 59.15265

R> compareFolds(cvs)

        lam.education lam.income lam.women lambda
Fold 1          1.000      0.330     0.330      1
Fold 2          1.000      0.330     0.169      1
Fold 3          1.000      0.330     0.330      1
```

```
Fold 4          1.000      0.330      0.330      1
Fold 5          1.000      0.330      0.000      1
Fold 6          1.000      0.330      0.330      1
Fold 7          1.000      0.330      0.330      1
Fold 8          1.000      0.330      0.000      1
Fold 9          1.000      0.330      0.000      1
Fold 10         1.000      0.330      0.000      1
```

The results suggest that the predictive power of the transformed regression is reliably greater than that of the untransformed regression (though in both case, the cross-validated MSE is considerably higher than the MSE computed for the whole data). Examining the selected transformations for each fold reveals that the predictor `education` and the response `prestige` are never transformed; that the 1/3 power is selected for `income` in all of the folds; and that the transformation selected for `women` varies narrowly across the folds between the 0th power (i.e., log) and the 1/3 power.

5.4. Selecting both transformations and predictors[14]

As we mentioned, Hastie *et al.* (2009, Sec. 7.10.2: "The Wrong and Right Way to Do Cross-validation") explain that honest cross-validation has to take account of model specification and selection. Statistical modeling is at least partly a craft, and one could imagine applying that craft to successive partial data sets, each with a fold removed. The resulting procedure would be tedious, though possibly worth the effort, but it would also be difficult to realize in practice: After all, we can hardly erase our memory of statistical modeling choices between analyzing partial data sets.

Alternatively, if we're able to automate the process of model selection, then we can more realistically apply CV mechanically. That's what we did in the preceding two sections, first for predictor selection and then for selection of transformations in regression. In this section, we consider the case where we both select variable transformations and then proceed to select predictors. It's insufficient to apply these steps sequentially, first, for example, using `cvSelect()` with `selectTrans()` and then with `selectStepAIC()`; rather we should apply the whole model-selection procedure with each fold omitted. The `selectTransAndStepAIC()` function, also supplied by the **cv** package, does exactly that.

To illustrate this process, we return to the `Auto` data set:

```
R> summary(Auto)
```

```
      mpg          cylinders      displacement     horsepower        weight
 Min.   : 9.00   Min.   :3.000   Min.   : 68.0   Min.   : 46.0   Min.   :1613
 1st Qu.:17.00   1st Qu.:4.000   1st Qu.:105.0   1st Qu.: 75.0   1st Qu.:2225
 Median :22.75   Median :4.000   Median :151.0   Median : 93.5   Median :2804
 Mean   :23.45   Mean   :5.472   Mean   :194.4   Mean   :104.5   Mean   :2978
 3rd Qu.:29.00   3rd Qu.:8.000   3rd Qu.:275.8   3rd Qu.:126.0   3rd Qu.:3615
 Max.   :46.60   Max.   :8.000   Max.   :455.0   Max.   :230.0   Max.   :5140
```

[14] The presentation in the section benefits from an email conversation with Bill Venables, who of course isn't responsible for the use to which we've put his insightful remarks.

```
  acceleration        year           origin                      name
 Min.   : 8.00   Min.   :70.00   Min.   :1.000   amc matador       :  5
 1st Qu.:13.78   1st Qu.:73.00   1st Qu.:1.000   ford pinto        :  5
 Median :15.50   Median :76.00   Median :1.000   toyota corolla    :  5
 Mean   :15.54   Mean   :75.98   Mean   :1.577   amc gremlin       :  4
 3rd Qu.:17.02   3rd Qu.:79.00   3rd Qu.:2.000   amc hornet        :  4
 Max.   :24.80   Max.   :82.00   Max.   :3.000   chevrolet chevette:  4
                                                 (Other)           :365
```

```
R> xtabs(~ year, data=Auto)
```

```
year
70 71 72 73 74 75 76 77 78 79 80 81 82
29 27 28 40 26 30 34 28 36 29 27 28 30
```

```
R> xtabs(~ origin, data=Auto)
```

```
origin
  1   2   3
245  68  79
```

```
R> xtabs(~ cylinders, data=Auto)
```

```
cylinders
  3   4   5   6   8
  4 199   3  83 103
```

We previously used the `Auto` here in a preliminary example where we employed CV to inform the selection of the order of a polynomial regression of `mpg` on `horsepower`. Here, we consider more generally the problem of predicting `mpg` from the other variables in the `Auto` data. We begin with a bit of data management, and then examine the pairwise relationships among the numeric variables in the data set:

```
R> Auto$cylinders <- factor(Auto$cylinders,
+                           labels=c("3.4", "3.4", "5.6", "5.6", "8"))
R> Auto$year <- as.factor(Auto$year)
R> Auto$origin <- factor(Auto$origin,
+                        labels=c("America", "Europe", "Japan"))
R> rownames(Auto) <- make.names(Auto$name, unique=TRUE)
R> Auto$name <- NULL
R>
R> scatterplotMatrix(~ mpg + displacement + horsepower + weight + acceleration,
+                    smooth=list(spread=FALSE), data=Auto)
```

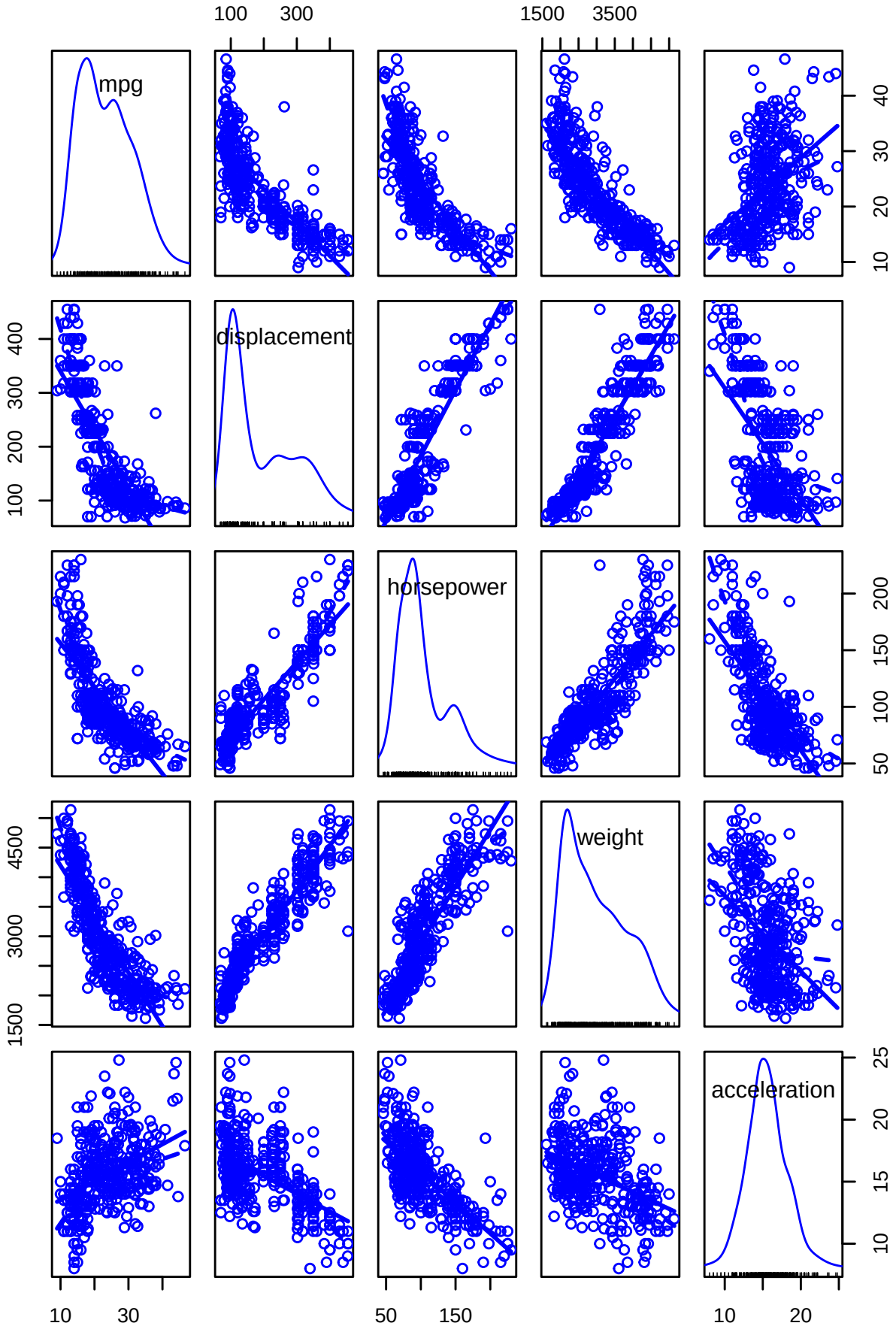


Figure 19: Scatterplot matrix for the numeric variables in the 'Auto' data

A comment before we proceed: `origin` is clearly categorical and so converting it to a factor is natural, but we could imagine treating `cylinders` and `year` as numeric predictors. There are, however, only 5 distinct values of `cylinders` (ranging from 3 to 8), but cars with 3 or 5 cylinders are rare. and none of the cars has 7 cylinders. There are similarly only 13 distinct years between 1970 and 1982 in the data, and the relationship between `mpg` and `year` is difficult to characterize.[15] It's apparent that most these variables are positively skewed and that many of the pairwise relationships among them are nonlinear.

We begin with a "working model" that specifies linear partial relationships of the response to the numeric predictors:

```
R> m.auto <- lm(mpg ~ ., data = Auto)
R> summary(m.auto)


Call:
lm(formula = mpg ~ ., data = Auto)

Residuals:
    Min      1Q  Median      3Q     Max
-9.0064 -1.7450 -0.0917  1.5251 10.9504

Coefficients:
               Estimate Std. Error t value Pr(>|t|)
(Intercept)  37.0341323  1.9693933  18.805  < 2e-16
cylinders5.6 -2.6029412  0.6552000  -3.973 8.54e-05
cylinders8   -0.5824578  1.1714516  -0.497 0.619335
displacement  0.0174253  0.0067340   2.588 0.010043
horsepower   -0.0413534  0.0133786  -3.091 0.002145
weight       -0.0055479  0.0006323  -8.774  < 2e-16
acceleration  0.0615272  0.0883132   0.697 0.486431
year71        0.9680584  0.8373899   1.156 0.248408
year72       -0.6014345  0.8251155  -0.729 0.466517
year73       -0.6876890  0.7402723  -0.929 0.353510
year74        1.3755758  0.8765000   1.569 0.117408
year75        0.9299288  0.8590716   1.082 0.279742
year76        1.5598929  0.8225051   1.897 0.058669
year77        2.9094161  0.8417285   3.456 0.000611
year78        3.1751976  0.7989396   3.974 8.48e-05
year79        5.0192987  0.8457587   5.935 6.76e-09
year80        9.0997634  0.8972933  10.141  < 2e-16
year81        6.6886597  0.8852181   7.556 3.28e-13
year82        8.0711248  0.8706683   9.270  < 2e-16
```

[15] Of course, making the decision to treat `year` as a factor on this basis could be construed as cheating in the current context, which illustrates the difficulty of automating the whole model-selection process. It's rarely desirable, in our opinion, to forgo exploration of the data to ensure the purity of model validation. We believe, however, that it's still useful to automate as much of the process as we can to obtain a more realistic, if still biased, estimate of the predictive power of a model.

```
originEurope  2.0466642  0.5171236   3.958 9.07e-05
originJapan   2.1448874  0.5077169   4.225 3.02e-05

Residual standard error: 2.924 on 371 degrees of freedom
Multiple R-squared:  0.8668,    Adjusted R-squared:  0.8596
F-statistic: 120.7 on 20 and 371 DF,  p-value: < 2.2e-16
```

```
R> Anova(m.auto)
```

```
Anova Table (Type II tests)

Response: mpg
             Sum Sq  Df F value    Pr(>F)
cylinders     292.3   2 17.0915 7.935e-08
displacement   57.3   1  6.6959  0.010043
horsepower     81.7   1  9.5544  0.002145
weight        658.3   1 76.9801 < 2.2e-16
acceleration    4.2   1  0.4854  0.486431
year         3016.8  12 29.3987 < 2.2e-16
origin        190.3   2 11.1287 2.024e-05
Residuals    3172.5 371
```

```
R> crPlots(m.auto)
```

The component+residual plots, created with the `crPlots()` function in the previously loaded **car** package, clearly reveal the inadequacy of the model.

We proceed to transform the numeric predictors towards multi-normality:

```
R> num.predictors <- c("displacement", "horsepower", "weight", "acceleration")
R> tr.x <- powerTransform(Auto[, num.predictors])
R> summary(tr.x)
```

```
bcPower Transformations to Multinormality
             Est Power Rounded Pwr Wald Lwr Bnd Wald Upr Bnd
displacement   -0.0509           0      -0.2082       0.1065
horsepower     -0.1249           0      -0.2693       0.0194
weight         -0.0870           0      -0.2948       0.1208
acceleration    0.3061           0      -0.0255       0.6376

Likelihood ratio test that transformation parameters are equal to 0
 (all log transformations)
                                  LRT df    pval
LR test, lambda = (0 0 0 0) 4.872911  4 0.30059

Likelihood ratio test that no transformations are needed
                                  LRT df       pval
LR test, lambda = (1 1 1 1) 390.0777  4 < 2.22e-16
```

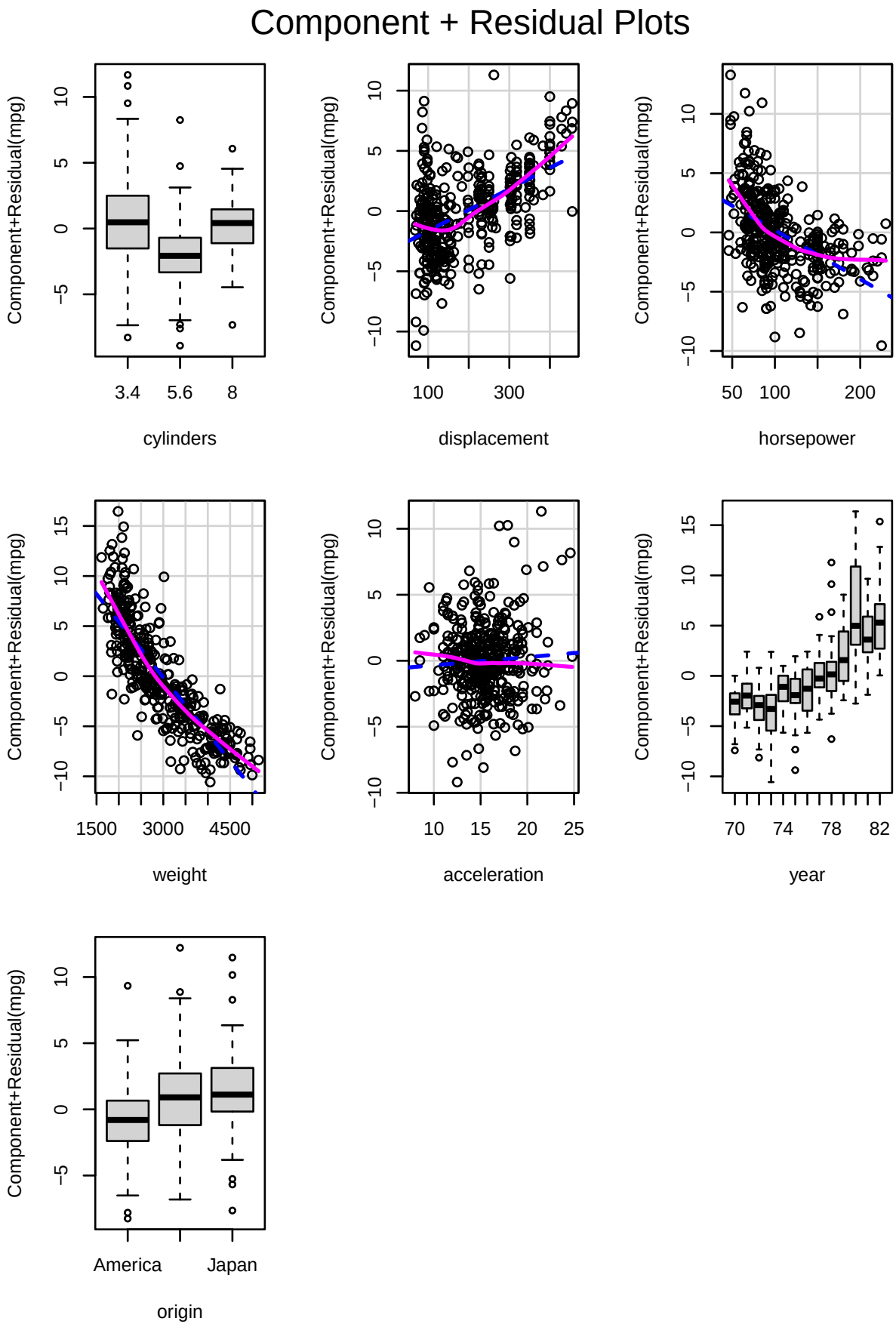


Figure 20: Component+residual plots for the working model fit to the ‘Auto‘ data

We then apply the (rounded) transformations—all, as it turns out, logs—to the data and re-estimate the model:

```
R> A <- Auto
R> powers <- tr.x$roundlam
R> for (pred in num.predictors){
+   A[, pred] <- bcPower(A[, pred], lambda=powers[pred])
+ }
R> head(A)

                          mpg cylinders displacement horsepower   weight
chevrolet.chevelle.malibu  18         8     5.726848   4.867534 8.161660
buick.skylark.320          15         8     5.857933   5.105945 8.214194
plymouth.satellite         18         8     5.762051   5.010635 8.142063
amc.rebel.sst              16         8     5.717028   5.010635 8.141190
ford.torino                17         8     5.710427   4.941642 8.145840
ford.galaxie.500           15         8     6.061457   5.288267 8.375860
                          acceleration year  origin
chevrolet.chevelle.malibu     2.484907   70 America
buick.skylark.320             2.442347   70 America
plymouth.satellite            2.397895   70 America
amc.rebel.sst                 2.484907   70 America
ford.torino                   2.351375   70 America
ford.galaxie.500              2.302585   70 America

R> m <- update(m.auto, data=A)
```

Finally, we perform Box-Cox regression to transform the response (also obtaining a log transformation):

```
R> summary(powerTransform(m))

bcPower Transformation to Normality
   Est Power Rounded Pwr Wald Lwr Bnd Wald Upr Bnd
Y1    0.0024           0      -0.1607       0.1654

Likelihood ratio test that transformation parameter is equal to 0
 (log transformation)
                              LRT df    pval
LR test, lambda = (0) 0.0008015428  1 0.97741

Likelihood ratio test that no transformation is needed
                            LRT df       pval
LR test, lambda = (1) 124.1307  1 < 2.22e-16

R> m <- update(m, log(mpg) ~ .)
R> summary(m)
```

```
Call:
lm(formula = log(mpg) ~ cylinders + displacement + horsepower +
    weight + acceleration + year + origin, data = A)

Residuals:
     Min       1Q   Median       3Q      Max
-0.33412 -0.05774  0.00410  0.06072  0.38081

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)   8.89652    0.35822  24.835  < 2e-16
cylinders5.6 -0.06355    0.02574  -2.469   0.0140
cylinders8   -0.07691    0.03900  -1.972   0.0493
displacement  0.02799    0.05146   0.544   0.5868
horsepower   -0.29010    0.05631  -5.152 4.20e-07
weight       -0.54274    0.08193  -6.624 1.23e-10
acceleration -0.14214    0.05630  -2.525   0.0120
year71        0.02505    0.02891   0.866   0.3869
year72       -0.01680    0.02894  -0.580   0.5620
year73       -0.04257    0.02602  -1.636   0.1026
year74        0.04932    0.03041   1.622   0.1056
year75        0.04715    0.02959   1.594   0.1118
year76        0.07087    0.02845   2.491   0.0132
year77        0.13241    0.02927   4.523 8.21e-06
year78        0.14472    0.02777   5.211 3.13e-07
year79        0.23354    0.02921   7.994 1.67e-14
year80        0.32381    0.03170  10.216  < 2e-16
year81        0.25655    0.03094   8.291 2.10e-15
year82        0.30756    0.03036  10.131  < 2e-16
originEurope  0.04921    0.01955   2.518   0.0122
originJapan   0.04409    0.01947   2.265   0.0241

Residual standard error: 0.1043 on 371 degrees of freedom
Multiple R-squared:  0.9108,    Adjusted R-squared:  0.906
F-statistic: 189.4 on 20 and 371 DF,  p-value: < 2.2e-16

R> Anova(m)

Anova Table (Type II tests)

Response: log(mpg)
             Sum Sq  Df F value    Pr(>F)
cylinders    0.0663   2  3.0521   0.04845
displacement 0.0032   1  0.2959   0.58679
horsepower   0.2885   1 26.5420 4.198e-07
weight       0.4769   1 43.8805 1.229e-10
```

```
acceleration 0.0693   1  6.3745   0.01199
year         4.4521  12 34.1339 < 2.2e-16
origin       0.0807   2  3.7128   0.02532
Residuals    4.0325 371
```

The transformed numeric variables are much better-behaved:

```
R> scatterplotMatrix(~ log(mpg) + displacement + horsepower + weight
+                    + acceleration,
+                    smooth=list(spread=FALSE), data=A)
```

And the partial relationships in the model fit to the transformed data are much more nearly linear:

```
R> crPlots(m)
```

Having transformed both the numeric predictors and the response, we proceed to use the `stepAIC()` function in the **MASS** package to perform predictor selection, employing the BIC model-selection criterion (by setting the `k` argument of `stepAIC()` to $\log(n)$):

```
R> m.step <- stepAIC(m, k=log(nrow(A)), trace=FALSE)
R> summary(m.step)


Call:
lm(formula = log(mpg) ~ horsepower + weight + acceleration +
    year + origin, data = A)

Residuals:
     Min       1Q   Median       3Q      Max
-0.35230 -0.05682  0.00677  0.06741  0.35861

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)   9.434594   0.261529  36.075  < 2e-16
horsepower   -0.276254   0.056143  -4.921 1.30e-06
weight       -0.609071   0.056003 -10.876  < 2e-16
acceleration -0.131380   0.053195  -2.470  0.01397
year71        0.027984   0.028936   0.967  0.33412
year72       -0.007111   0.028446  -0.250  0.80274
year73       -0.039529   0.026014  -1.520  0.12947
year74        0.052752   0.029986   1.759  0.07936
year75        0.053199   0.029280   1.817  0.07004
year76        0.074317   0.028212   2.634  0.00878
year77        0.137931   0.028875   4.777 2.56e-06
year78        0.145876   0.027529   5.299 1.99e-07
```

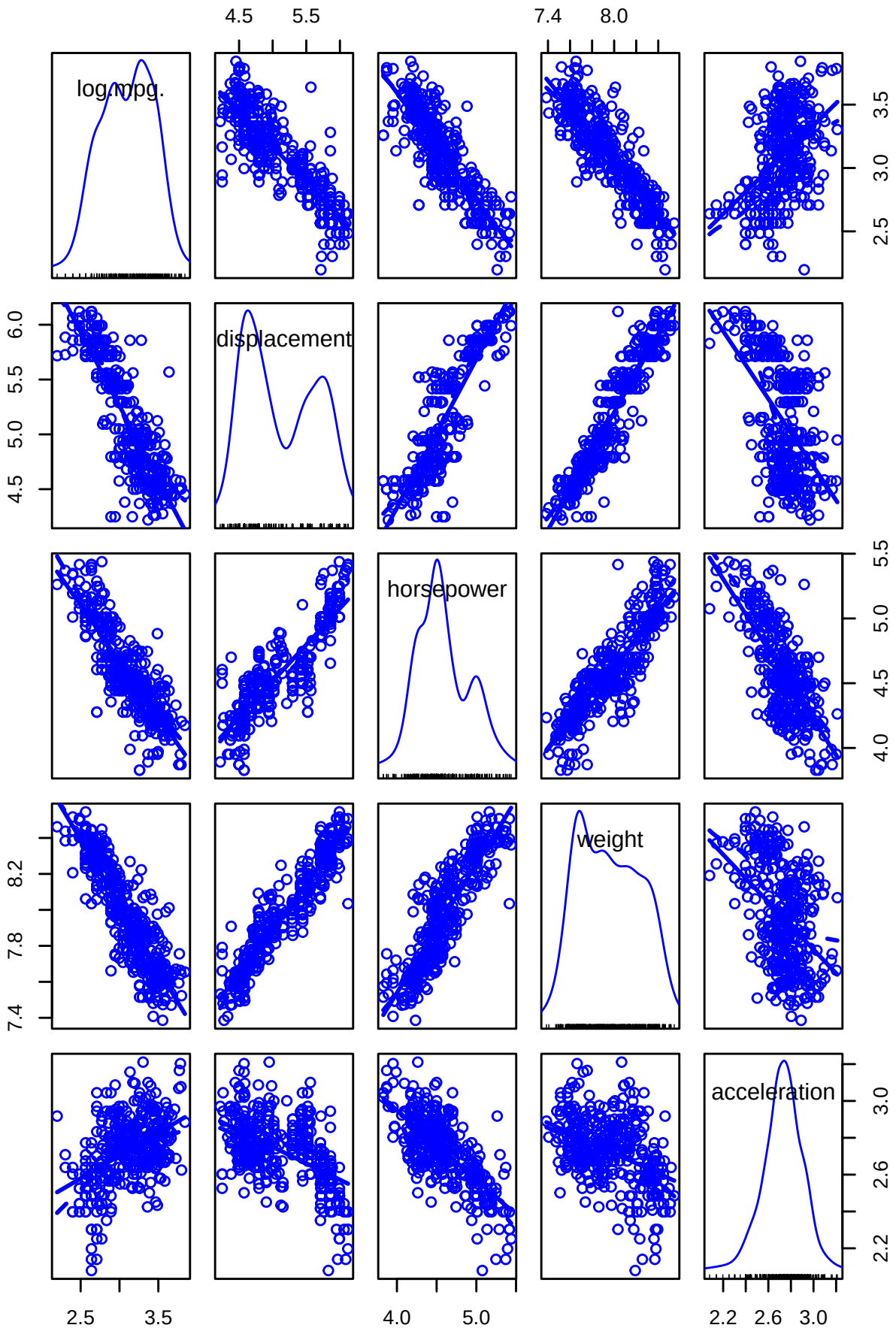


Figure 21: Scatterplot matrix for the transformed numeric variables in the 'Auto' data

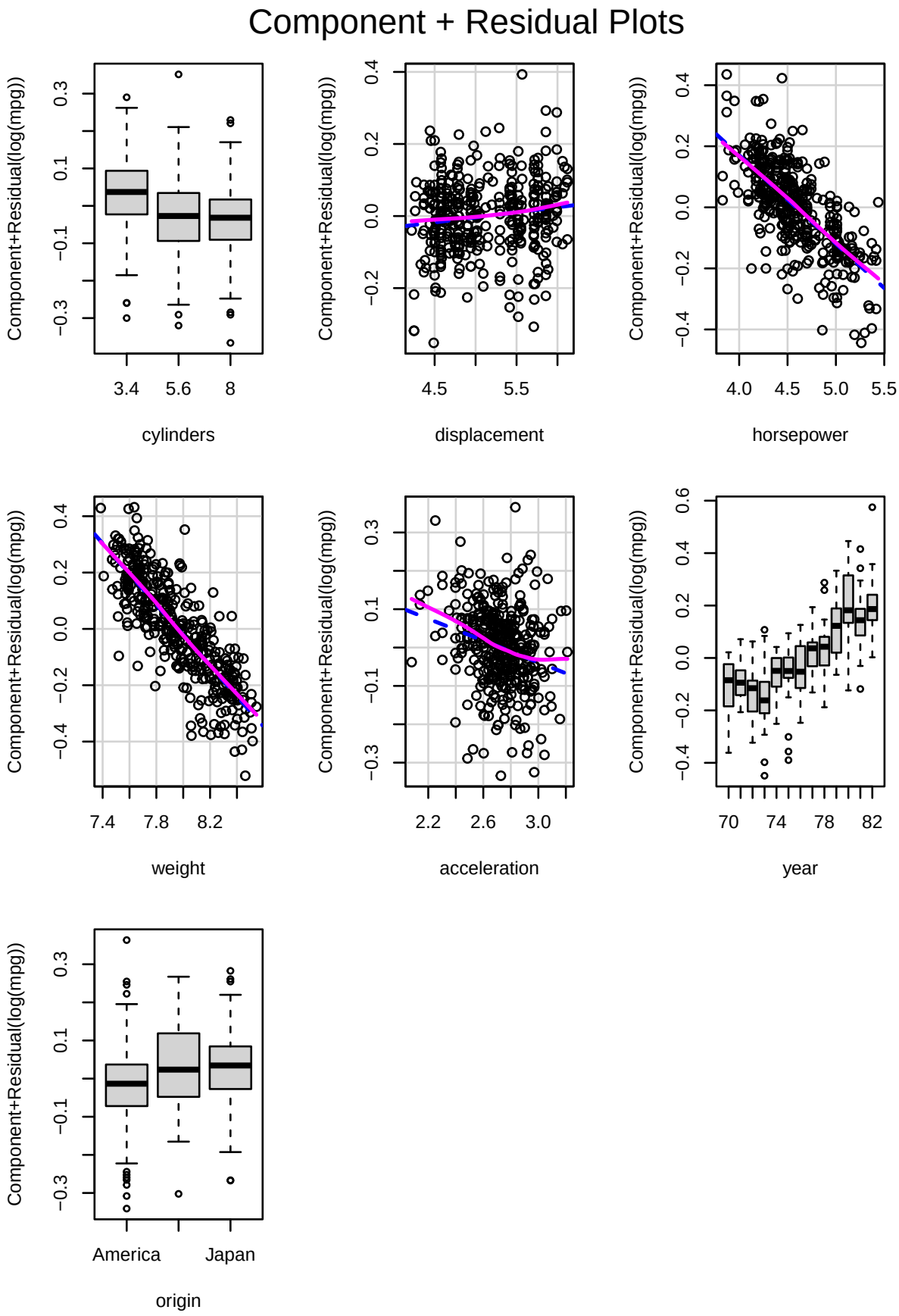


Figure 22: Component+residual plots for the model fit to the transformed ‘Auto‘ data

```
year79        0.236036   0.029080   8.117 6.99e-15
year80        0.335274   0.031148  10.764  < 2e-16
year81        0.262872   0.030555   8.603  < 2e-16
year82        0.323391   0.029608  10.922  < 2e-16
originEurope  0.055818   0.016785   3.326  0.00097
originJapan   0.043554   0.017479   2.492  0.01314

Residual standard error: 0.1049 on 374 degrees of freedom
Multiple R-squared:  0.909, Adjusted R-squared:  0.9049
F-statistic: 219.8 on 17 and 374 DF,  p-value: < 2.2e-16
```

```
R> Anova(m.step)

Anova Table (Type II tests)

Response: log(mpg)
             Sum Sq  Df  F value    Pr(>F)
horsepower   0.2663   1  24.2120 1.296e-06
weight       1.3010   1 118.2805 < 2.2e-16
acceleration 0.0671   1   6.0998  0.013965
year         4.7589  12  36.0549 < 2.2e-16
origin       0.1366   2   6.2090  0.002225
Residuals    4.1137 374
```

The selected model includes three of the numeric predictors, `horsepower`, `weight`, and `acceleration`, along with the factors `year` and `origin`. We can calculate the MSE for this model, but we expect that the result will be optimistic because we used the whole data to help specify the model

```
R> mse(Auto$mpg, exp(fitted(m.step)))

[1] 6.512144
attr(,"casewise loss")
[1] "(y - yhat)^2"
```

This is considerably smaller than the MSE for the original working model:

```
R> mse(Auto$mpg, fitted(m.auto))

[1] 8.093171
attr(,"casewise loss")
[1] "(y - yhat)^2"
```

A perhaps subtle point is that we compute the MSE for the selected model on the original `mpg` response scale rather than the log scale, so as to make the selected model comparable to the working model. That's slightly uncomfortable given the skewed distribution of `mpg`. An alternative is to use the median absolute error instead of the mean-squared error, employing the `medAbsErr()` function from the **cv** package:

```
R> medAbsErr(Auto$mpg, exp(fitted(m.step)))

[1] 1.339604

R> medAbsErr(Auto$mpg, fitted(m.auto))

[1] 1.666121
```

Now let's use `cvSelect()` with `selectTransAndStepAIC()` to automate and cross-validate the whole model-specification process:

```
R> num.predictors

[1] "displacement" "horsepower"   "weight"       "acceleration"

R> cvs <- cvSelect(selectTransStepAIC, data=Auto, seed=76692, model=m.auto,
+                  predictors=num.predictors,
+                  response="mpg", AIC=FALSE, criterion=medAbsErr)

R RNG seed set to 76692

R> cvs

10-Fold Cross Validation
cross-validation criterion = 1.495075
full-sample criterion = 1.339604

R> compareFolds(cvs)

        (Intercept) horsepower lam.acceleration lam.displacement lam.horsepower
Fold 1      9.71384   -0.17408          0.50000          0.00000        0.00000
Fold 2      9.21713   -0.31480          0.00000          0.00000        0.00000
Fold 3      9.61824   -0.19248          0.00000          0.00000        0.00000
Fold 4      8.69910   -0.25523          0.50000          0.00000        0.00000
Fold 5      9.14403   -0.14934          0.00000          0.00000        0.00000
Fold 6      9.63481   -0.16739          0.50000          0.00000        0.00000
Fold 7      9.98933   -0.36847          0.00000          0.00000       -0.15447
Fold 8      9.06301   -0.29721          0.00000          0.00000        0.00000
Fold 9      8.88315   -0.22684          0.00000          0.00000        0.00000
Fold 10     9.61727   -0.17086          0.00000          0.00000        0.00000
        lam.weight   lambda   weight   year71   year72   year73   year74
Fold 1     0.00000  0.00000 -0.74636  0.03764 -0.00327 -0.02477  0.05606
Fold 2     0.00000  0.00000 -0.47728  0.02173 -0.01488 -0.03770  0.04312
Fold 3     0.00000  0.00000 -0.72085  0.01128 -0.02569 -0.03872  0.05187
Fold 4     0.00000  0.00000 -0.53846  0.02153 -0.02922 -0.05181  0.04136
Fold 5     0.00000  0.00000 -0.69081  0.02531 -0.01062 -0.04625  0.05039
```

```
Fold 6     0.00000  0.00000 -0.74049  0.02456  0.00759 -0.03412  0.06266
Fold 7     0.00000  0.00000 -0.72843  0.02532 -0.01271 -0.04144  0.04568
Fold 8     0.00000  0.00000 -0.46392  0.02702 -0.02041 -0.05605  0.04437
Fold 9     0.00000  0.00000 -0.47136  0.00860 -0.03620 -0.04835  0.01906
Fold 10    0.00000  0.00000 -0.73550  0.02937 -0.00899 -0.03814  0.05408
          year75   year76   year77   year78   year79   year80   year81   year82
Fold 1   0.07080  0.07250  0.14420  0.14281  0.23266  0.35127  0.25635  0.30546
Fold 2   0.04031  0.06718  0.13094  0.14917  0.21871  0.33192  0.26196  0.30943
Fold 3   0.03837  0.06399  0.11593  0.12601  0.20499  0.32821  0.24478  0.29204
Fold 4   0.04072  0.05537  0.12292  0.14083  0.22878  0.32947  0.25140  0.27248
Fold 5   0.05596  0.07044  0.13356  0.14724  0.24675  0.33331  0.26938  0.32594
Fold 6   0.06940  0.07769  0.14211  0.14647  0.23532  0.34761  0.26737  0.33062
Fold 7   0.03614  0.07385  0.12976  0.14040  0.23976  0.33998  0.27652  0.30659
Fold 8   0.06573  0.08135  0.13158  0.13987  0.23011  0.32880  0.25886  0.30538
Fold 9   0.03018  0.05846  0.10536  0.11722  0.20665  0.31533  0.23352  0.29375
Fold 10  0.04881  0.07862  0.14101  0.14313  0.23258  0.35649  0.26214  0.32421
        acceleration displacement cylinders5.6 cylinders8 originEurope
Fold 1
Fold 2      -0.18909     -0.09197
Fold 3
Fold 4      -0.03484                 -0.09080   -0.10909
Fold 5                                                        0.06261
Fold 6
Fold 7
Fold 8      -0.17676     -0.10542
Fold 9      -0.14514     -0.13452
Fold 10
        originJapan
Fold 1
Fold 2
Fold 3
Fold 4
Fold 5         0.04
Fold 6
Fold 7
Fold 8
Fold 9
Fold 10
```

Here, as for `selectTrans()`, the `predictors` and `response` arguments specify candidate variables for transformation, and `AIC=FALSE` uses the BIC for model selection. The starting model, `m.auto`, is the working model fit to the `Auto` data. The CV criterion isn't bias-adjusted because median absolute error isn't a mean of casewise error components.

Some noteworthy points:

- `selectTransStepAIC()` automatically computes CV cost criteria, here the median absolute error, on the untransformed response scale.

- The estimate of the median absolute error that we obtain by cross-validating the whole model-specification process is a little larger than the median absolute error computed for the model we fit to the `Auto` data separately selecting transformations of the predictors and the response and then selecting predictors for the whole data set.
- When we look at the transformations and predictors selected with each of the 10 folds omitted (i.e., the output of `compareFolds()`), we see that there is little uncertainty in choosing variable transformations (the `lam.*`s for the xs and `lambda` for y in the output), but considerably more uncertainty in subsequently selecting predictors: `horsepower`, `weight`, and `year` are always included among the selected predictors; `acceleration` and `displacement` are each included respectively in 4 and 3 of 10 selected models; and `cylinders` and `origin` are each included in only 1 of 10 models. Recall that when we selected predictors for the full data, we obtained a model with `horsepower`, `weight`, `acceleration`, `year`, and `origin`.

6. Parallel computations

The CV functions in the **cv** package are all capable of performing parallel computations by setting the `ncores` argument (specifying the number of computer cores to be used) to a number $>$ `1` (which is the default). Parallel computation can be advantageous for large problems, reducing the execution time of the program.

To illustrate, let's time model selection in Mroz's logistic regression, repeating the computation as performed previously and then doing it in parallel using 2 cores:

```
R> system.time(m.mroz.sel.cv <- cvSelect(selectStepAIC, Mroz,
+                            seed=6681,
+                            criterion=BayesRule,
+                            model=m.mroz,
+                            AIC=FALSE))

R RNG seed set to 6681

   user  system elapsed
  0.241   0.010   0.253

R> system.time(m.mroz.sel.cv.p <- cvSelect(selectStepAIC, Mroz,
+                            seed=6681,
+                            criterion=BayesRule,
+                            model=m.mroz,
+                            AIC=FALSE,
+                            ncores=2))

R RNG seed set to 6681

   user  system elapsed
  0.035   0.004   0.894
```

```
R> all.equal(m.mroz.sel.cv, m.mroz.sel.cv.p)
```

```
[1] TRUE
```

In this small problem, the parallel computation is actually *slower*, because there is an overhead cost to parallelization, but we can see that it produces the same result as before.

7. Extending the cv package

The **cv** package is designed to be extensible in several directions. In this vignette, we discuss three kinds of extensions, ordered by increasing general complexity: (1) adding a cross-validation cost criterion; (2) adding a model class that's not directly accommodated by the `cv()` default method or by another directly inherited method, with separate consideration of mixed-effects models; and (3) adding a new model-selection procedure suitable for use with `selectModel()`.

7.1. Adding a cost criterion

A cost criterion suitable for use with `cv()` or `cvSelect()` should take two arguments, `y` (the observed response vector) and `yhat` (a vector of fitted or predicted response values), and return a numeric index of lack of fit. The **cv** package supplies several such criteria: `mse(y, yhat)`, which returns the mean-squared prediction error for a numeric response; `rmse(y, yhat)`, which returns the (square-)root mean-squared error; `medAbsErr(y, yhat)`, which returns the median absolute error; and `BayesRule(y, yhat)` (and its non-error-checking version, `BayesRule2(y, yhat)`), suitable for use with a binary regression model, where \code{y‘ is the binary response coded `0` for a "failure" or `1` for a "success"; where `yhat` is the predicted probability of success; and where the proportion of *incorrectly* classified cases is returned.

To illustrate using a different prediction cost criterion, we'll base a cost criterion on the area under the receiver operating characteristic ("ROC") curve for a logistic regression. The ROC curve is a graphical representation of the classification power of a binary regression model, and the area under the ROC curve ("AUC"), which varies from 0 to 1, is a common summary measure based on the ROC (see "Receiver operating characteristic" 2023). The **Metrics** package (Hamner and Frasco 2018) includes a variety of measures useful for model selection, including an `auc()` function. We convert the AUC into a cost measure by taking its complement:

```
R> AUCcomp <- function(y, yhat) 1 - Metrics::auc(y, yhat)
```

We then apply `AUCcomp()` to the the Mroz logistic regression discussed in the main **cv** package vignette, which we reproduce here, using the `Mroz` data frame from the **carData** package (Fox and Weisberg 2019):

```
R> data("Mroz", package="carData")
R> m.mroz <- glm(lfp ~ ., data=Mroz, family=binomial)
R> summary(m.mroz)
```

```
Call:
glm(formula = lfp ~ ., family = binomial, data = Mroz)

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  3.182140   0.644375   4.938 7.88e-07
k5          -1.462913   0.197001  -7.426 1.12e-13
k618        -0.064571   0.068001  -0.950 0.342337
age         -0.062871   0.012783  -4.918 8.73e-07
wcyes        0.807274   0.229980   3.510 0.000448
hcyes        0.111734   0.206040   0.542 0.587618
lwg          0.604693   0.150818   4.009 6.09e-05
inc         -0.034446   0.008208  -4.196 2.71e-05

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 1029.75  on 752  degrees of freedom
Residual deviance:  905.27  on 745  degrees of freedom
AIC: 921.27

Number of Fisher Scoring iterations: 4

R> AUCcomp(with(Mroz, as.numeric(lfp == "yes")), fitted(m.mroz))

[1] 0.2636161
```

Cross-validating this cost measure is straightforward:

```
R> library("cv")
R> cv(m.mroz, criterion=AUCcomp, seed=3639)

R RNG seed set to 3639

10-Fold Cross Validation
method: exact
criterion: AUCcomp
cross-validation criterion = 0.2747088
full-sample criterion = 0.2636161
```

As expected, the cross-validated complement to the AUC is somewhat less optimistic than the criterion computed from the model fit to the whole data set.

As we explain in the vignette "Cross-validation of regression models," the `cv()` function differentiates between CV criteria that are averages of casewise components and criteria that are not. Computation of bias corrections and confidence intervals is limited to the former. We show in the appendix to this vignette that the AUC, and hence its complement, cannot be expressed as averages of casewise components.

`cv()` looks for a `"casewise loss"` attribute of the value returned by a CV criterion function. If this attribute exists, then the criterion is treated as the mean of casewise components, and `cv()` uses the unexported function `getLossFn()` to construct a function that returns the casewise components of the criterion.

We illustrate with the `mse()`:

```
R> mse

 [1] 23.94366 18.98477 18.94499 18.87633 18.42697 18.24065 18.07817 18.06613
 [9] 18.02697 18.00953

R> cv:::getLossFn(mse(rnorm(100), rnorm(100)))

function (y, yhat)
{
    (y - yhat)^2
}
<environment: 0x12f694d48>
```

For this scheme to work, the "casewise loss" attribute must be a character string (or vector of character strings), here `"(y - yhat)^2"`, that evaluates to an expression that is a function of `y` and `yhat`, and that computes the vector of casewise components of the CV criterion.

7.2. Adding a model class not covered by the default cv() method

Independently sampled cases

Suppose that we want to cross-validate a multinomial logistic regression model fit by the `multinom()` function in the **nnet** package (Venables and Ripley 2002). We borrow an example from Fox (2016, Sec. 14.2.1), with data from the British Election Panel Study on vote choice in the 2001 British election. Data for the example are in the `BEPS` data frame in the **carData** package:

```
R> data("BEPS", package="carData")
R> head(BEPS)

              vote age economic.cond.national economic.cond.household Blair
1 Liberal Democrat  43                       3                       3     4
2           Labour  36                       4                       4     4
3           Labour  35                       4                       4     5
4           Labour  24                       4                       2     2
5           Labour  41                       2                       2     1
6           Labour  47                       3                       4     4
  Hague Kennedy Europe political.knowledge gender
1     1       4      2                   2 female
2     4       4      5                   2   male
```

```
3     2       3      3                    2   male
4     1       3      4                    0 female
5     1       4      6                    2   male
6     4       2      4                    2   male
```

The polytomous (multi-category) response variable is `vote`, a factor with levels `"Conservative"`, `"Labour"`, and `"Liberal Democrat"`. The predictors of `vote` are:

- `age`, in years;
- `econ.cond.national` and `econ.cond.household`, the respondent's ratings of the state of the economy, on 1 to 5 scales.
- `Blair`, `Hague`, and `Kennedy`, ratings of the leaders of the Labour, Conservative, and Liberal Democratic parties, on 1 to 5 scales.
- `Europe`, an 11-point scale on attitude towards European integration, with high scores representing "Euro-skepticism."
- `political.knowledge`, knowledge of the parties' positions on European integration, with scores from 0 to 3.
- `gender`, `"female"` or `"male"`.

The model fit to the data includes an interaction between `Europe` and `political.knowledge`; the other predictors enter the model additively:

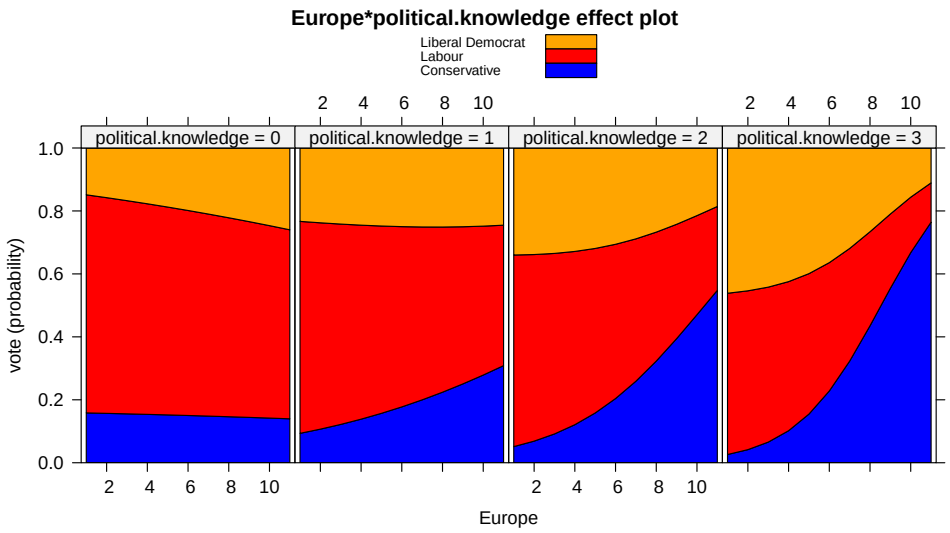
```
R> library("nnet")
R> m.beps <- multinom(vote ~ age + gender + economic.cond.national +
+                         economic.cond.household + Blair + Hague + Kennedy +
+                         Europe*political.knowledge, data=BEPS)

# weights:  36 (22 variable)
initial  value 1675.383740
iter  10 value 1240.047788
iter  20 value 1163.199642
iter  30 value 1116.519687
final  value 1116.519666
converged

R> car::Anova(m.beps)

Analysis of Deviance Table (Type II tests)

Response: vote
                          LR Chisq Df Pr(>Chisq)
age                         13.872  2  0.0009721
gender                       0.453  2  0.7972568
economic.cond.national      30.604  2  2.262e-07
economic.cond.household      5.652  2  0.0592570
Blair                      135.369  2  < 2.2e-16
```

```
Hague                          166.770  2  < 2.2e-16
Kennedy                         68.878  2  1.105e-15
Europe                          78.033  2  < 2.2e-16
political.knowledge             55.568  2  8.582e-13
Europe:political.knowledge      50.804  2  9.291e-12
```

Most of the predictors, including the `Europe` × `political.knowledge` interaction, are associated with very small p-values; the `Anova()` function is from the **car** package (Fox and Weisberg 2019).

Here's an "effect plot", using the the **effects** package (Fox and Weisberg 2019) to visualize the `Europe` × `political.knowledge` interaction in a "stacked-area" graph:

```
R> plot(effects::Effect(c("Europe", "political.knowledge"), m.beps,
+             xlevels=list(Europe=1:11, political.knowledge=0:3),
+             fixed.predictors=list(given.values=c(gendermale=0.5))),
+      lines=list(col=c("blue", "red", "orange")),
+      axes=list(x=list(rug=FALSE), y=list(style="stacked")))
```



To cross-validate this multinomial-logit model we need an appropriate cost criterion. None of the criteria supplied by the **cv** package—for example, neither `mse()`, which is appropriate for a numeric response, nor `BayesRule()`, which is appropriate for a binary response—will do. One possibility is to adapt Bayes rule to a polytomous response:

```
R> head(BEPS$vote)

[1] Liberal Democrat Labour           Labour           Labour
[5] Labour           Labour
Levels: Conservative Labour Liberal Democrat

R> yhat <- predict(m.beps, type="class")
R> head(yhat)
```

```
[1] Labour           Labour           Labour           Labour
[5] Liberal Democrat Labour
Levels: Conservative Labour Liberal Democrat
```

```
R> BayesRuleMulti <- function(y, yhat){
+   result <- mean(y != yhat)
+   attr(result, "casewise loss") <- "y != yhat"
+   result
+ }
R>
R> BayesRuleMulti(BEPS$vote, yhat)
```

```
[1] 0.3186885
attr(,"casewise loss")
[1] "y != yhat"
```

The `predict()` method for `"multinom"` models called with argument `type="class"` reports the Bayes-rule prediction for each case—that is, the response category with the highest predicted probability. Our `BayesRuleMulti()` function calculates the proportion of misclassified cases. Because this value is the mean of casewise components, we attach a `"casewise loss"` attribute to the result (as explained in the preceding section).

The marginal proportions for the response categories are

```
R> xtabs(~ vote, data=BEPS)/nrow(BEPS)
```

```
vote
    Conservative           Labour Liberal Democrat
       0.3029508        0.4721311        0.2249180
```

and so the marginal Bayes-rule prediction, that everyone will vote Labour, produces an error rate of $1 - 0.47213 = 0.52787$. The multinomial-logit model appears to do substantially better than that, but does its performance hold up to cross-validation?

We check first whether the default `cv()` method works "out-of-the-box" for the `"multinom"` model:

```
R> cv(m.beps, seed=3465, criterion=BayesRuleMulti)
```

```
Error in GetResponse.default(model): non-vector response
```

The default method of `GetResponse()` (a function supplied by the **cv** package—see `?GetResponse`) fails for a `"multinom"` object. A straightforward solution is to supply a `GetResponse.multinom()` method that returns the factor response (using the `get_response()` function from the **insight** package, Lüdecke, Waggoner, and Makowski 2019),

```
R> GetResponse.multinom <- function(model, ...) {
+   insight::get_response(model)
+ }
R>
R> head(GetResponse(m.beps))
```

```
[1] Liberal Democrat Labour           Labour           Labour
[5] Labour           Labour
Levels: Conservative Labour Liberal Democrat
```

and to try again:

```
R> cv(m.beps, seed=3465, criterion=BayesRuleMulti)

R RNG seed set to 3465

# weights:  36 (22 variable)
initial  value 1507.296060
iter  10 value 1134.575036
iter  20 value 1037.413231
iter  30 value 1007.705242
iter  30 value 1007.705235
iter  30 value 1007.705235
final  value 1007.705235
converged

Error in match.arg(type): 'arg' should be one of "class", "probs"
```

A `traceback()` (not shown) reveals that the problem is that the default method of `cv()` calls the `"multinom"` method for `predict()` with the argument `type="response"`, when the correct argument should be `type="class"`. We therefore must write a `"multinom"` method for `cv()`, but that proves to be very simple:

```
R> cv.multinom <- function (model, data, criterion=BayesRuleMulti, k, reps,
+                           seed, ...){
+   NextMethod(type="class", criterion=criterion)
+ }
```

That is, we simply call the default `cv()` method with the `type` argument properly set. In addition to supplying the correct `type` argument, our method sets the default `criterion` for the `cv.multinom()` method to `BayesRuleMulti`.

Then:

```
R> m.beps <- update(m.beps, trace=FALSE)
R> cv(m.beps, seed=3465)

R RNG seed set to 3465

10-Fold Cross Validation
cross-validation criterion = 0.3245902
bias-adjusted cross-validation criterion = 0.3236756
95% CI for bias-adjusted CV criterion = (0.300168, 0.3471831)
full-sample criterion = 0.3186885
```

Prior to invoking `cv()`, we called `update()` with `trace=FALSE` to suppress the iteration history reported by default by `multinom()`—it would be tedious to see the iteration history for each fold. The cross-validated polytomous Bayes-rule criterion confirms that the fitted model does substantially better than the marginal Bayes-rule prediction that everyone votes for Labour.

Mixed-effects models

Adding a `cv()` method for a mixed-model class is somewhat more complicated. We provide the `cvMixed()` function to facilitate this process, and to see how that works, consider the `"lme"` method from the **cv** package:

```
R> cv:::cv.lme
```

```
function(model, data = insight::get_data(model), criterion = mse,
                    k, reps = 1, seed, ncores = 1, clusterVariables, ...){
  cvMixed(
    model,
    package="nlme",
    data=data,
    criterion=criterion,
    k=k,
    reps=reps,
    seed=seed,
    ncores=ncores,
    clusterVariables=clusterVariables,
    predict.clusters.args=list(object=model,
                               newdata=data,
                               level=0),
    predict.cases.args=list(object=model,
                            newdata=data,
                            level=1),
    ...)
}
<bytecode: 0x148948190>
<environment: namespace:cv>
```

Notice that `cv.lme()` sets up a call to `cvMixed()`, which does the computational work.

Most of the arguments of `cvMixed()` are familiar:

- `model` is the mixed-model object, here of class `"lme"`.
- `package` is the name of the package in which the mixed-modeling function used to fit the model, here `lme()`, resides—i.e., `"nlme"`; `cvMixed()` uses this argument to retrieve the package namespace.
- `data` is the data set to which the model is fit, by default extracted by the `get_data()` function in the **insight** package.

- `criterion` is the CV criterion, defaulting to the `mse()` function.
- `k` is the number of CV folds, defaulting to `"loo"` for CV by clusters and `10` for CV by cases.
- `reps` is the number of times the CV process is repeated, defaulting to `1`.
- `seed` is the seed for R's random-number generator, defaulting to a randomly selected (and saved) value.
- `ncores` is the number of cores to use for parallel computation; if `1`, the default, then the computation isn't parallelized.
- `clusterVariables` is a character vector of the names of variables defining clusters; if missing, then CV is based on cases rather than clusters.

The remaining two arguments are unfamiliar:

- `predict.clusters.args` is a named list of arguments to be passed to the `predict()` function to obtain predictions for the full data set from a model fit to a subset of the data for cluster-based CV. The first two arguments should be `object` and `newdata`. It is typically necessary to tell `cvMixed()` how to base predictions only on fixed effects; in the case of `"lme"` models, this is done by setting `level = 0`.
- Similarly, `predict.cases.args` is a named list of arguments to be passed to `predict()` for case-based CV. Setting `level = 1` includes random effects in the predictions.

Finally, any additional arguments, absorbed by `...`, are passed to `update()` when the model is refit with each fold omitted. `cvMixed()` returns an object of class `"cv"`.

Now imagine that we want to support a new class of mixed-effects models. To be concrete, we illustrate with the `glmmPQL()` function in the **MASS** package (Venables and Ripley 2002), which fits generalized-linear mixed-effects models by penalized quasi-likelihood.[16] Not coincidentally, the arguments of `glmmPQL()` are similar to those of `lme()` (with an additional `family` argument), because the former iteratively invokes the latter; so `cv.glmmPQL()` should resemble `cv.lme()`.

As it turns out, neither the default method for `GetResponse()` nor `insight::get_data()` work for `"glmmPQL"` objects. These objects include a `"data"` element, however, and so we can simply extract this element as the default for the `data` argument of our `cv.glmmPQL()` method.

To get the response variable is more complicated: We refit the fixed part of the model as a GLM with only the regression constant on the right-hand side, and extract the response from that; because all we need is the response variable, we limit the number of GLM iterations to 1 and suppress warning messages about non-convergence:

[16]This example is somewhat artificial in that `glmmPQL()` has largely been superseded by computationally superior functions, such the `glmer()` function in the **lme4** package. There is, however, one situation in which `glmmPQL()` might prove useful: to specify serial dependency in case-level errors within clusters for longitudinal data, which is not currently supported by `glmer()`.

```
R> GetResponse.glmmPQL <- function(model, ...){
+   f <- formula(model)
+   f[[3]] <- 1 # regression constant only on RHS
+   model <- suppressWarnings(glm(f, data=model$data, family=model$family,
+                                 control=list(maxit=1)))
+   cv::GetResponse(model)
+ }
```

Writing the `cv()` method is then straightforward:

```
R> cv.glmmPQL <- function(model, data = model$data, criterion = mse,
+                         k, reps = 1, seed, ncores = 1, clusterVariables, ...){
+   cvMixed(
+     model,
+     package="MASS",
+     data=data,
+     criterion=criterion,
+     k=k,
+     reps=reps,
+     seed=seed,
+     ncores=ncores,
+     clusterVariables=clusterVariables,
+     predict.clusters.args=list(object=model,
+                                newdata=data,
+                                level=0,
+                                type="response"),
+     predict.cases.args=list(object=model,
+                             newdata=data,
+                             level=1,
+                             type="response"),
+     verbose=FALSE,
+     ...)
+ }
```

We set the argument `verbose=FALSE` to suppress `glmmPQL()`'s iteration counter when `cvMixed()` calls `update()`.

Let's apply our newly minted method to a logistic regression with a random intercept in an example that appears in `?glmmPQL`:

```
R> library("MASS")
R> m.pql <- glmmPQL(y ~ trt + I(week > 2), random = ~ 1 | ID,
+              family = binomial, data = bacteria)

iteration 1

iteration 2
```

```
iteration 3

iteration 4

iteration 5

iteration 6

R> summary(m.pql)

Linear mixed-effects model fit by maximum likelihood
  Data: bacteria
  AIC BIC logLik
   NA  NA     NA

Random effects:
 Formula: ~1 | ID
        (Intercept)  Residual
StdDev:    1.410637 0.7800511

Variance function:
 Structure: fixed weights
 Formula: ~invwt
Fixed effects:  y ~ trt + I(week > 2)
                    Value Std.Error  DF   t-value p-value
(Intercept)      3.412014 0.5185033 169  6.580506  0.0000
trtdrug         -1.247355 0.6440635  47 -1.936696  0.0588
trtdrug+        -0.754327 0.6453978  47 -1.168779  0.2484
I(week > 2)TRUE -1.607257 0.3583379 169 -4.485311  0.0000
 Correlation:
                (Intr) trtdrg trtdr+
trtdrug         -0.598
trtdrug+        -0.571  0.460
I(week > 2)TRUE -0.537  0.047 -0.001

Standardized Within-Group Residuals:
       Min         Q1        Med         Q3        Max
-5.1985361  0.1572336  0.3513075  0.4949482  1.7448845

Number of Observations: 220
Number of Groups: 50
```

We compare this result to that obtained from `glmer()` in the **lme4** package:

```
R> library("lme4")
R> m.glmer <- glmer(y ~ trt + I(week > 2) + (1 | ID),
+                 family = binomial, data = bacteria)
R> summary(m.glmer)
```

```
Generalized linear mixed model fit by maximum likelihood (Laplace
  Approximation) [glmerMod]
 Family: binomial  ( logit )
Formula: y ~ trt + I(week > 2) + (1 | ID)
   Data: bacteria

     AIC      BIC   logLik deviance df.resid
   202.3    219.2    -96.1    192.3      215

Scaled residuals:
    Min      1Q  Median      3Q     Max
-4.5615  0.1359  0.3022  0.4217  1.1276

Random effects:
 Groups Name        Variance Std.Dev.
 ID     (Intercept) 1.543    1.242
Number of obs: 220, groups:  ID, 50

Fixed effects:
                Estimate Std. Error z value Pr(>|z|)
(Intercept)       3.5479     0.6958   5.099 3.41e-07
trtdrug          -1.3667     0.6770  -2.019 0.043517
trtdrug+         -0.7826     0.6831  -1.146 0.251925
I(week > 2)TRUE  -1.5985     0.4759  -3.359 0.000783

Correlation of Fixed Effects:
            (Intr) trtdrg trtdr+
trtdrug     -0.593
trtdrug+    -0.537  0.487
I(wk>2)TRUE -0.656  0.126  0.064

R>   # comparison of fixed effects:
R> car::compareCoefs(m.pql, m.glmer)

Warning in car::compareCoefs(m.pql, m.glmer): models to be compared are of
different classes

Calls:
1: glmmPQL(fixed = y ~ trt + I(week > 2), random = ~1 | ID, family =
  binomial, data = bacteria)
2: glmer(formula = y ~ trt + I(week > 2) + (1 | ID), data = bacteria,
  family = binomial)

                Model 1 Model 2
(Intercept)       3.412   3.548
SE                0.514   0.696
```

```
trtdrug          -1.247  -1.367
SE                0.638   0.677

trtdrug+         -0.754  -0.783
SE                0.640   0.683

I(week > 2)TRUE  -1.607  -1.598
SE                0.355   0.476
```

The two sets of estimates are similar, but not identical

Finally, we try out our `cv.glmmPQL()` method, cross-validating both by clusters and by cases,

```
R> cv(m.pql, clusterVariables="ID", criterion=BayesRule)

n-Fold Cross Validation based on 50 {ID} clusters
cross-validation criterion = 0.1954545
bias-adjusted cross-validation criterion = 0.1954545
full-sample criterion = 0.1954545

R> cv(m.pql, data=bacteria, criterion=BayesRule, seed=1490)

R RNG seed set to 1490

10-Fold Cross Validation
cross-validation criterion = 0.2090909
bias-adjusted cross-validation criterion = 0.2072727
full-sample criterion = 0.1454545
```

and again compare to `glmer()`:

```
R> cv(m.glmer, clusterVariables="ID", criterion=BayesRule)

n-Fold Cross Validation based on 50 {ID} clusters
cross-validation criterion = 0.1954545
bias-adjusted cross-validation criterion = 0.1954545
full-sample criterion = 0.1954545

R> cv(m.glmer, data=bacteria, criterion=BayesRule, seed=1490)

R RNG seed set to 1490

10-Fold Cross Validation
cross-validation criterion = 0.1954545
bias-adjusted cross-validation criterion = 0.1936364
full-sample criterion = 0.15
```

7.3. Adding a model-selection procedure

The `selectStepAIC()` function supplied by the **cv** package, which is based on the `stepAIC()` function from the **nnet** package (Venables and Ripley 2002) for stepwise model selection, is suitable for the `procedure` argument of `cvSelect()`. The use of `selectStepAIC()` is illustrated in the principal vignette for the package.

We'll employ `selectStepAIC()` as a "template" for writing a CV model-selection procedure. To see the code for this function, type `cv::selectStepAIC` at the R command prompt, or examine the sources for the **cv** package at https://github.com/gmonette/cv (the code for `selectStepAIC()` is in https://github.com/gmonette/cv/blob/main/R/cvSelect.R).

Another approach to model selection is all-subsets regression. The `regsubsets()` function in the **leaps** package (Lumley and Miller 2020) implements an efficient algorithm for selecting the best-fitting linear least-squares regressions for subsets of predictors of all sizes, from 1 through the maximum number of candidate predictors.[17] To illustrate the use of `regsubsets()`, we employ the `swiss` data frame supplied by the **leaps** package:

```
R> library("leaps")
R> head(swiss)
```

```
             Fertility Agriculture Examination Education Catholic
Courtelary        80.2        17.0          15        12     9.96
Delemont          83.1        45.1           6         9    84.84
Franches-Mnt      92.5        39.7           5         5    93.40
Moutier           85.8        36.5          12         7    33.77
Neuveville        76.9        43.5          17        15     5.16
Porrentruy        76.1        35.3           9         7    90.57
             Infant.Mortality
Courtelary               22.2
Delemont                 22.2
Franches-Mnt             20.2
Moutier                  20.3
Neuveville               20.6
Porrentruy               26.6
```

```
R> nrow(swiss)
```

```
[1] 47
```

The data set includes the following variables, for each of 47 French-speaking Swiss provinces circa 1888:

- `Fertility`: A standardized fertility measure.

[17] The `regsubsets()` function computes several measures of model predictive performance, including the R^2 and R^2 adjusted for degrees of freedom, the residual sums of squares, Mallows's C_p, and the BIC. Several of these are suitable for comparing models with differing numbers of coefficients—we use the BIC below—but all necessarily agree when comparing models with the *same* number of coefficients.

- `Agriculture`: The percentage of the male population engaged in agriculture.
- `Examination`: The percentage of draftees into the Swiss army receiving the highest grade on an examination.
- `Education`: The percentage of draftees with more than a primary-school education.
- `Catholic`: The percentage of the population who were Catholic.
- `Infant.Mortality`: The infant-mortality rate, expressed as the percentage of live births surviving less than a year.

Following Lumley and Miller (2020), we treat `Fertility` as the response and the other variables as predictors in a linear least-squares regression:

```
R> m.swiss <- lm(Fertility ~ ., data=swiss)
R> summary(m.swiss)


Call:
lm(formula = Fertility ~ ., data = swiss)

Residuals:
     Min       1Q   Median       3Q      Max
-15.2743  -5.2617   0.5032   4.1198  15.3213

Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
(Intercept)      66.91518   10.70604   6.250 1.91e-07
Agriculture      -0.17211    0.07030  -2.448  0.01873
Examination      -0.25801    0.25388  -1.016  0.31546
Education        -0.87094    0.18303  -4.758 2.43e-05
Catholic          0.10412    0.03526   2.953  0.00519
Infant.Mortality  1.07705    0.38172   2.822  0.00734

Residual standard error: 7.165 on 41 degrees of freedom
Multiple R-squared:  0.7067,    Adjusted R-squared:  0.671
F-statistic: 19.76 on 5 and 41 DF,  p-value: 5.594e-10


R> cv(m.swiss, seed=8433)


R RNG seed set to 8433


10-Fold Cross Validation
method: Woodbury
criterion: mse
cross-validation criterion = 59.68315
bias-adjusted cross-validation criterion = 58.84614
full-sample criterion = 44.78815
```

Thus, the RMSE for the model fit to the complete data is considerably smaller than the CV estimate of the RMSE. Can we do better by selecting a subset of the predictors, taking account of the additional uncertainty induced by model selection?

First, let's apply best-subset selection to the complete data set:

```
R> swiss.sub <- regsubsets(Fertility ~ ., data=swiss)
R> summary(swiss.sub)

Subset selection object
Call: regsubsets.formula(Fertility ~ ., data = swiss)
5 Variables  (and intercept)
                 Forced in Forced out
Agriculture          FALSE      FALSE
Examination          FALSE      FALSE
Education            FALSE      FALSE
Catholic             FALSE      FALSE
Infant.Mortality     FALSE      FALSE
1 subsets of each size up to 5
Selection Algorithm: exhaustive
         Agriculture Examination Education Catholic Infant.Mortality
1  ( 1 ) " "         " "         "*"       " "      " "
2  ( 1 ) " "         " "         "*"       "*"      " "
3  ( 1 ) " "         " "         "*"       "*"      "*"
4  ( 1 ) "*"         " "         "*"       "*"      "*"
5  ( 1 ) "*"         "*"         "*"       "*"      "*"

R> (bics <- summary(swiss.sub)$bic)

[1] -19.60287 -28.61139 -35.65643 -37.23388 -34.55301

R> which.min(bics)

[1] 4

R> car::subsets(swiss.sub, legend="topright")
```

The graph, produced by the `subsets()` function in the **car** package, shows that the model with the smallest BIC is the best model with 4 predictors, including `Agriculture`, `Education`, `Catholic`, and `Infant.Mortality`, but not `Examination`:

```
R> m.best <- update(m.swiss, . ~ . - Examination)
R> summary(m.best)


Call:
lm(formula = Fertility ~ Agriculture + Education + Catholic +
```

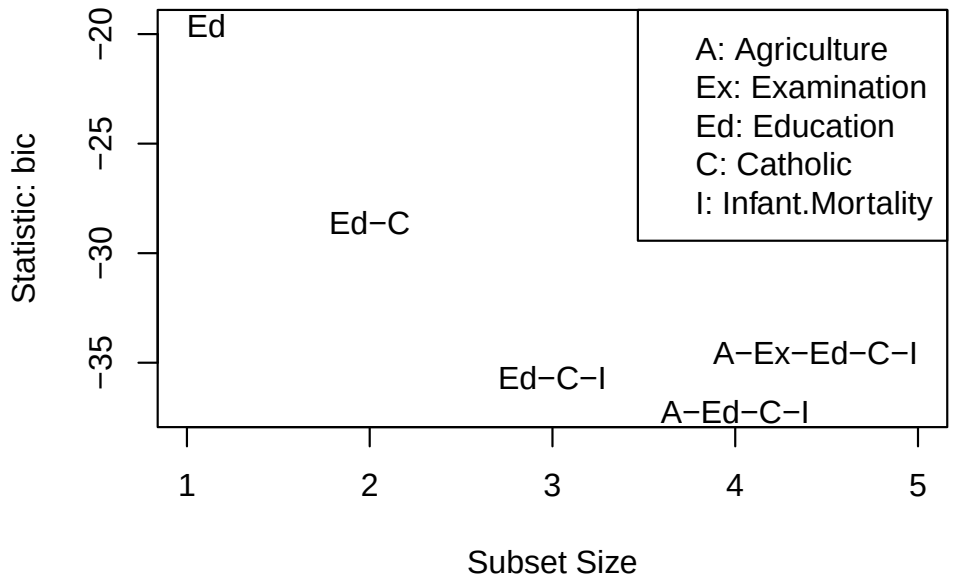


Figure 23: Selecting the best model of each size.

```
    Infant.Mortality, data = swiss)

Residuals:
     Min       1Q   Median       3Q      Max
-14.6765  -6.0522   0.7514   3.1664  16.1422

Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
(Intercept)      62.10131    9.60489   6.466 8.49e-08
Agriculture      -0.15462    0.06819  -2.267  0.02857
Education        -0.98026    0.14814  -6.617 5.14e-08
Catholic          0.12467    0.02889   4.315 9.50e-05
Infant.Mortality  1.07844    0.38187   2.824  0.00722

Residual standard error: 7.168 on 42 degrees of freedom
Multiple R-squared:  0.6993,    Adjusted R-squared:  0.6707
F-statistic: 24.42 on 4 and 42 DF,  p-value: 1.717e-10

R> cv(m.best, seed=8433) # use same folds as before

R RNG seed set to 8433

10-Fold Cross Validation
method: Woodbury
criterion: mse
cross-validation criterion = 58.46664
bias-adjusted cross-validation criterion = 57.7779
full-sample criterion = 45.91637
```

The RMSE for the selected model is (of course) slightly higher than for the full model fit previously, but the cross-validated RMSE is a bit lower; as we explain in the main vignette, however, it isn't kosher to select and cross-validate a model on the same data.

Here's a function named `selectSubsets()`, meant to be used with `cvSelect()`, suitable for cross-validating the model-selection process:

```
R> selectSubsets <- function(data=insight::get_data(model),
+                            model,
+                            indices,
+                            criterion=mse,
+                            save.coef=TRUE, ...){
+
+   if (inherits(model, "lm", which=TRUE) != 1)
+     stop("selectSubsets is appropriate only for 'lm' models")
+
+   y <- GetResponse(model)
+   formula <- formula(model)
+   X <- model.matrix(model)
+
+   if (missing(indices)) {
+     # select the best model from the full data by BIC
+     sel <- leaps::regsubsets(formula, data=data, ...)
+     bics <- summary(sel)$bic
+     best <- coef(sel, 1:length(bics))[[which.min(bics)]]
+     x.names <- names(best)
+     # fit the best model; intercept is already in X, hence - 1:
+     m.best <- lm(y ~ X[, x.names] - 1)
+     fit.all <- predict(m.best, newdata=data)
+     return(criterion(y, fit.all)) # return the CV criterion
+   }
+
+   # select the best model omitting the i-th fold (given by indices)
+   sel.i <- leaps::regsubsets(formula, data[-indices, ], ...)
+   bics.i <- summary(sel.i)$bic
+   best.i <- coef(sel.i, 1:length(bics.i))[[which.min(bics.i)]]
+   x.names.i <- names(best.i)
+   m.best.i <- lm(y[-indices] ~ X[-indices, x.names.i] - 1)
+               # predict() doesn't work here:
+   fit.all.i <- as.vector(X[, x.names.i] %*% coef(m.best.i))
+   fit.i <- fit.all.i[indices]
+   # return the fitted values for i-th fold, CV criterion for all cases,
+   #   and the regression coefficients
+   list(fit.i=fit.i, # fitted values for i-th fold
+        crit.all.i=criterion(y, fit.all.i), # CV crit for all cases
+        coefficients = if (save.coef){ # regression coefficients
+          coefs <- coef(m.best.i)
+
```

```
+          # fix coefficient names
+          names(coefs) <- sub("X\\[-indices, x.names.i\\]", "",
+                              names(coefs))
+
+          coefs
+        }  else {
+          NULL
+        }
+   )
+ }
```

A slightly tricky point is that because of scoping issues, `predict()` doesn't work with the model fit omitting the ith fold, and so the fitted values for all cases are computed directly as $\widehat{\mathbf{y}}_{-i} = \mathbf{X}\mathbf{b}_{-i}$, where $\mathbf{X}$ is the model-matrix for all of the cases, and $\mathbf{b}_{-i}$ is the vector of least-squares coefficients for the selected model with the ith fold omitted.

Additionally, the command `lm(y[-indices] ~ X[-indices, x.names.i] - 1)`, which is the selected model with the ith fold deleted, produces awkward coefficient names like `"X[-indices, x.names.i]Infant.Mortality"`. Purely for aesthetic reasons, the command `sub("X\\[-indices, x.names.i\\]", "", names(coefs))` fixes these awkward names, removing the extraneous text, `"X[-indices, x.names.i]"`.

Applying `selectSubsets()` to the full data produces the full-data cross-validated RMSE (which we obtained previously): %%`{r test-selectSubsets} %%selectSubsets(model=m.swiss) %%` Similarly, applying the function to an imaginary "fold" of 5 cases returns the RMSE for the cases in the fold, based on the model selected and fit to the cases omitting the fold; the RMSE for all of the cases, based on the same model; and the coefficients of the selected model, which includes 4 or the 5 predictors (and the intercept): %%`{r test-selectSubsets-fold} %%selectSubsets(model=m.swiss, indices=seq(5, 45, by=10)) %%`

Then, using `selectSubsets()` in cross-validation, we get:

```
R> (cv.swiss <- cvSelect(selectSubsets, model=m.swiss,
+                        data=swiss, seed=8433)) # use same folds

R RNG seed set to 8433

10-Fold Cross Validation
cross-validation criterion = 65.83495
bias-adjusted cross-validation criterion = 63.64431
full-sample criterion = 45.91637
```

Cross-validation shows that model selection exacts a penalty in RMSE. Examining the models selected for the 10 folds reveals that there is some uncertainty in identifying the predictors in the "best" model, with `Agriculture` sometimes appearing and sometimes not:

```
R> compareFolds(cv.swiss)
```

```
        (Intercept) Catholic Education Infant.Mortality Agriculture
Fold 1      59.0852   0.1397   -1.0203           1.2985       -0.17
Fold 2      67.0335   0.1367   -1.0499           0.9413       -0.20
Fold 3      55.0453   0.1221   -0.8757           1.3541       -0.15
Fold 4      62.5543   0.1236   -0.9719           1.0679       -0.16
Fold 5      50.4643   0.1057   -0.7863           1.2144
Fold 6      68.0289   0.1195   -1.0073           0.8294       -0.17
Fold 7      66.5219   0.1357   -1.0827           0.9523       -0.19
Fold 8      46.3507   0.0776   -0.7637           1.4463
Fold 9      62.2632   0.1230   -1.0067           1.1000       -0.17
Fold 10     52.5112   0.1005   -0.7232           1.0809
```

8. Computational notes

8.1. Efficient computations for linear and generalized linear models

The most straightforward way to implement cross-validation in R for statistical modeling functions that are written in the canonical manner is to use `update()` to refit the model with each fold removed. This is the approach taken in the default method for `cv()`, and it is appropriate if the cases are independently sampled. Refitting the model in this manner for each fold is generally feasible when the number of folds in modest, but can be prohibitively costly for leave-one-out cross-validation when the number of cases is large.

The `"lm"` and `"glm"` methods for `cv()` take advantage of computational efficiencies by avoiding refitting the model with each fold removed. Consider, in particular, the weighted linear model $\mathbf{y}_{n\times 1} = \mathbf{X}_{n\times p}\boldsymbol{\beta}_{p\times 1} + \boldsymbol{\varepsilon}_{n\times 1}$, where $\boldsymbol{\varepsilon} \sim \mathbf{N}_n\left(\mathbf{0}, \sigma^2\mathbf{W}^{-1}_{n\times n}\right)$. Here, $\mathbf{y}$ is the response vector, $\mathbf{X}$ the model matrix, and $\boldsymbol{\varepsilon}$ the error vector, each for n cases, and $\boldsymbol{\beta}$ is the vector of p population regression coefficients. The errors are assumed to be multivariately normally distributed with 0 means and covariance matrix $\sigma^2\mathbf{W}^{-1}$, where $\mathbf{W} = \text{diag}(w_i)$ is a diagonal matrix of inverse-variance weights. For the linear model with constant error variance, the weight matrix is taken to be $\mathbf{W} = \mathbf{I}_n$, the order-$n$ identity matrix.

The weighted-least-squares (WLS) estimator of $\boldsymbol{\beta}$ is (see, e.g., Fox 2016, Sec. 12.2.2) [18]

$$\mathbf{b}_{\text{WLS}} = \left(\mathbf{X}^T\mathbf{W}\mathbf{X}\right)^{-1}\mathbf{X}^T\mathbf{W}\mathbf{y}$$

Fitted values are then $\widehat{\mathbf{y}} = \mathbf{X}\mathbf{b}_{\text{WLS}}$.

The LOO fitted value for the ith case can be efficiently computed by $\widehat{y}_{-i} = y_i - e_i/(1-h_i)$ where $h_i = \mathbf{x}_i^T\left(\mathbf{X}^T\mathbf{W}\mathbf{X}\right)^{-1}\mathbf{x}_i$ (the so-called "hatvalue"). Here, $\mathbf{x}_i^T$ is the ith row of $\mathbf{X}$, and $\mathbf{x}_i$ is the ith row written as a column vector. This approach can break down when one or more hatvalues are equal to 1, in which case the formula for $\widehat{y}_{-i}$ requires division by 0.

[18] This is a definitional formula, which assumes that the model matrix $\mathbf{X}$ is of full column rank, and which can be subject to numerical instability when $\mathbf{X}$ is ill-conditioned. `lm()` uses the singular-value decomposition of the model matrix to obtain computationally more stable results.

To compute cross-validated fitted values when the folds contain more than one case, we make use of the Woodbury matrix identify ("Woodbury matrix identity" 2023),

$$(\mathbf{A}_{m\times m} + \mathbf{U}_{m\times k}\mathbf{C}_{k\times k}\mathbf{V}_{k\times m})^{-1} = \mathbf{A}^{-1} - \mathbf{A}^{-1}\mathbf{U}\left(\mathbf{C}^{-1} + \mathbf{V}\mathbf{A}^{-1}\mathbf{U}\right)^{-1}\mathbf{V}\mathbf{A}^{-1}$$

where $\mathbf{A}$ is a nonsingular order-n matrix. We apply this result by letting

$$\begin{aligned}\mathbf{A} &= \mathbf{X}^T\mathbf{W}\mathbf{X}\\ \mathbf{U} &= \mathbf{X}_\mathbf{j}^T\\ \mathbf{V} &= -\mathbf{X}_\mathbf{j}\\ \mathbf{C} &= \mathbf{W}_\mathbf{j}\end{aligned}$$

where the subscript $\mathbf{j} = (i_{j1}, \ldots, i_{jm})^T$ represents the vector of indices for the cases in the jth fold, $j = 1, \ldots, k$. The negative sign in $\mathbf{V} = -\mathbf{X}_\mathbf{j}$ reflects the *removal*, rather than addition, of the cases in $\mathbf{j}$.

Applying the Woodbury identity isn't quite as fast as using the hatvalues, but it is generally much faster than refitting the model. A disadvantage of the Woodbury identity, however, is that it entails explicit matrix inversion and thus may be numerically unstable. The inverse of $\mathbf{A} = \mathbf{X}^T\mathbf{W}\mathbf{X}$ is available directly in the `"lm"` object, but the second term on the right-hand side of the Woodbury identity requires a matrix inversion with each fold deleted. (In contrast, the inverse of each $\mathbf{C} = \mathbf{W}_\mathbf{j}$ is straightforward because $\mathbf{W}$ is diagonal.)

The Woodbury identity also requires that the model matrix be of full rank. We impose that restriction in our code by removing redundant regressors from the model matrix for all of the cases, but that doesn't preclude rank deficiency from surfacing when a fold is removed. Rank deficiency of $\mathbf{X}$ doesn't disqualify cross-validation because all we need are fitted values under the estimated model.

`glm()` computes the maximum-likelihood estimates for a generalized linear model by iterated weighted least squares (see, e.g., Fox and Weisberg 2019, Sec. 6.12). The last iteration is therefore just a WLS fit of the "working response" on the model matrix using "working weights." Both the working weights and the working response at convergence are available from the information in the object returned by `glm()`.

We then treat re-estimation of the model with a case or cases deleted as a WLS problem, using the hatvalues or the Woodbury matrix identity. The resulting fitted values for the deleted fold aren't exact—that is, except for the Gaussian family, the result isn't identical to what we would obtain by literally refitting the model—but in our (limited) experience, the approximation is very good, especially for LOO CV, which is when we would be most tempted to use it. Nevertheless, because these results are approximate, the default for the `"glm"` `cv()` method is to perform the exact computation, which entails refitting the model with each fold omitted.

8.2. Computation of the bias-corrected CV criterion and confidence intervals

Let $\text{CV}(\mathbf{y}, \widehat{\mathbf{y}})$ represent a cross-validation cost criterion, such as mean-squared error, computed for all of the n values of the response $\mathbf{y}$ based on fitted values $\widehat{\mathbf{y}}$ from the model fit to

all of the data. We require that $\mathrm{CV}(\mathbf{y}, \widehat{\mathbf{y}})$ is the mean of casewise components, that is, $\mathrm{CV}(\mathbf{y}, \widehat{\mathbf{y}}) = \frac{1}{n}\sum_{i=1}^{n} \mathrm{cv}(y_i, \widehat{y}_i)$.[19] For example, $\mathrm{MSE}(\mathbf{y}, \widehat{\mathbf{y}}) = \frac{1}{n}\sum_{i=1}^{n}(y_i - \widehat{y}_i)^2$.

We divide the n cases into k folds of approximately $n_j \approx n/k$ cases each, where $n = \sum n_j$. As above, let $\mathbf{j}$ denote the indices of the cases in the jth fold.

Now define $\mathrm{CV}_j = \mathrm{CV}(\mathbf{y}, \widehat{\mathbf{y}}^{(j)})$. The superscript (j) on $\widehat{\mathbf{y}}^{(j)}$ represents fitted values computed for all of the cases from the model with fold j omitted. Let $\widehat{\mathbf{y}}^{(-i)}$ represent the vector of fitted values for all n cases where the fitted value for the ith case is computed from the model fit with the fold including the ith case omitted (i.e., fold j for which $i \in \mathbf{j}$).

Then the cross-validation criterion is just $\mathrm{CV} = \mathrm{CV}(\mathbf{y}, \widehat{\mathbf{y}}^{(-i)})$. Following Davison and Hinkley (1997, pp. 293–295), the bias-adjusted cross-validation criterion is

$$\mathrm{CV}_{\mathrm{adj}} = \mathrm{CV} + \mathrm{CV}(\mathbf{y}, \widehat{\mathbf{y}}) - \frac{1}{n}\sum_{j=1}^{k} n_j \mathrm{CV}_j$$

We compute the standard error of CV as

$$\mathrm{SE}(\mathrm{CV}) = \frac{1}{\sqrt{n}}\sqrt{\frac{\sum_{i=1}^{n}\left[\mathrm{cv}(y_i, \widehat{y}_i^{(-i)}) - \mathrm{CV}\right]^2}{n-1}}$$

that is, as the standard deviation of the casewise components of CV divided by the square-root of the number of cases.

We then use SE(CV) to construct a $100 \times (1-\alpha)\%$ confidence interval around the *adjusted* CV estimate of error:

$$\left[\mathrm{CV}_{\mathrm{adj}} - z_{1-\alpha/2}\mathrm{SE}(\mathrm{CV}), \mathrm{CV}_{\mathrm{adj}} + z_{1-\alpha/2}\mathrm{SE}(\mathrm{CV})\right]$$

where $z_{1-\alpha/2}$ is the $1-\alpha/2$ quantile of the standard-normal distribution (e.g, $z \approx 1.96$ for a 95% confidence interval, for which $1-\alpha/2 = .975$).

Bates *et al.* (2023) show that the coverage of this confidence interval is poor for small samples, and they suggest a much more computationally intensive procedure, called *nested cross-validation*, to compute better estimates of error and confidence intervals with better coverage for small samples. We may implement Bates et al.'s approach in a later release of the **cv** package. At present we use the confidence interval above for sufficiently large n, which, based on Bates et al.'s results, we take by default to be $n \geq 400$.

9. Why the complement of AUC isn't a casewise CV criterion

Consider calculating AUC for folds in which a validation set contains n_v observations. To calculate AUC in the validation set, we need the vector of prediction criteria, $\widehat{\mathbf{y}}_{v_{(n_v \times 1)}} = (\widehat{y}_1, ..., \widehat{y}_{n_v})^T$, and the vector of observed responses in the validation set, $\mathbf{y}_{v_{(n_v \times 1)}} = (y_1, \ldots, y_{n_v})^T$ with $y_i \in \{0, 1\},\ i = 1, \ldots, n_v$.

To construct the ROC curve, only the ordering of the values in $\widehat{\mathbf{y}}_v$ is relevant. Thus, assuming that there are no ties, and reordering observations if necessary, we can set $\widehat{\mathbf{y}}_v = (1, 2, \ldots, n_v)^T$.

[19] Arlot and Celisse (2010) term the casewise loss, $\mathrm{cv}(y_i, \widehat{y}_i)$, the "contrast function."

If the AUC can be expressed as the casewise mean or sum of a function $\text{cv}(\widehat{y}_i, y_i)$, where $\text{cv} : \{1, 2, ..., n_v\} \times \{0, 1\} \to [0, 1]$, then

$$\sum_{i=1}^{n_v} \text{cv}(\widehat{y}_i, y_i) = \text{AUC}(\widehat{\mathbf{y}}_v, \mathbf{y}_v) \tag{1}$$

must hold for all 2^{n_v} possible values of $\mathbf{y}_v = (y_1, ..., y_{n_v})^T$. If all ys have the same value, either 1 or 0, then the definition of AUC is ambiguous. AUC could be considered undefined, or it could be set to 0 if all ys are 0 and to 1 if all ys are 1. If AUC is considered to be undefined in these cases, we have $2^{n_v} - 2$ admissible values for $\mathbf{y}_v$.

Thus, equation (1) produces either 2^{n_v} or $2^{n_v} - 2$ constraints. Although there are only $2n_v$ possible values for the $\text{cv}(\cdot)$ function, equation (1) could, nevertheless, have consistent solutions. We therefore need to determine whether there is a value of n_v for which (1) has no consistent solution for all admissible values of $\mathbf{y}_v$. In that eventuality, we will have shown that AUC cannot, in general, be expressed through a casewise sum.

If $n_v = 3$, we show below that (1) has no consistent solution if we include all possibilities for $\mathbf{y}_v$, but does if we exclude cases where all ys have the same value. If $n_v = 4$, we show that there are no consistent solutions in either case.

The following R function computes AUC from $\widehat{\mathbf{y}}_v$ and $\mathbf{y}_v$, accommodating the cases where $\mathbf{y}_v$ is all 0s or all 1s:

```
R> AUC <- function(y, yhat = seq_along(y)) {
+   s <- sum(y)
+   if (s == 0) return(0)
+   if (s == length(y)) return(1)
+   Metrics::auc(y, yhat)
+ }
```

We then define a function to generate all possible $\mathbf{y}_v$s of length n_v as rows of the matrix $\mathbf{Y}_{(2^{n_v} \times n_v)}$:

```
R> Ymat <- function(n_v, exclude_identical = FALSE) {
+   stopifnot(n_v > 0 && round(n_v) == n_v)    # n_v must be a positive integer
+   ret <- sapply(0:(2^n_v - 1),
+                 function(x) as.integer(intToBits(x)) )[1:n_v, ]
+   ret <- if (is.matrix(ret)) t(ret) else matrix(ret)
+   colnames(ret) <- paste0("y", 1:ncol(ret))
+   if (exclude_identical) ret[-c(1, nrow(ret)), ] else ret
+ }
```

For $n_v = 3$,

```
R> Ymat(3)

     y1 y2 y3
[1,]  0  0  0
```

```
[2,]  1  0  0
[3,]  0  1  0
[4,]  1  1  0
[5,]  0  0  1
[6,]  1  0  1
[7,]  0  1  1
[8,]  1  1  1
```

If we exclude $\mathbf{y}_v$s with identical values, then

```
R> Ymat(3, exclude_identical = TRUE)
```

```
     y1 y2 y3
[1,]  1  0  0
[2,]  0  1  0
[3,]  1  1  0
[4,]  0  0  1
[5,]  1  0  1
[6,]  0  1  1
```

Here is $\mathbf{Y}$ with corresponding values of AUC:

```
R> cbind(Ymat(3), AUC = apply(Ymat(3), 1, AUC))
```

```
     y1 y2 y3 AUC
[1,]  0  0  0 0.0
[2,]  1  0  0 0.0
[3,]  0  1  0 0.5
[4,]  1  1  0 0.0
[5,]  0  0  1 1.0
[6,]  1  0  1 0.5
[7,]  0  1  1 1.0
[8,]  1  1  1 1.0
```

The values of $\text{cv}(\widehat{y}_i, y_i)$ that express AUC as a sum of casewise values are solutions of equation (1), which can be written as solutions of the following system of 2^{n_v} linear simultaneous equations in $2n_v$ unknowns:

$$(\mathbf{U} - \mathbf{Y})\mathbf{c}_0 + \mathbf{Y}\mathbf{c}_1 = [\mathbf{U} - \mathbf{Y}, \mathbf{Y}] \begin{bmatrix} \mathbf{c}_0 \\ \mathbf{c}_1 \end{bmatrix} = \text{AUC}(\widehat{\mathbf{Y}}, \mathbf{Y}) \tag{2}$$

where $\mathbf{U}_{(2^{n_v} \times n_v)}$ is a matrix of 1s conformable with $\mathbf{Y}$; $\mathbf{c}_0 = [\text{cv}(1,0), c(2,0), ..., \text{cv}(n_v, 0)]^T$; $\mathbf{c}_1 = [\text{cv}(1,1), c(2,1), ..., \text{cv}(n_v, 1)]^T$; $[\mathbf{U} - \mathbf{Y}, \mathbf{Y}]_{(2^{n_v} \times 2n_v)}$ and $\begin{bmatrix} \mathbf{c}_0 \\ \mathbf{c}_1 \end{bmatrix}_{(2n_v \times 1)}$ are partitioned matrices; and $\widehat{\mathbf{Y}}_{(2^{n_v} \times n_v)}$ is a matrix each of whose rows consists of the integers 1 to n_v.

We can test whether equation (2) has a solution for any given n_v by trying to solve it as a least-squares problem, considering whether the residuals of the associated linear model are all 0, using the "design matrix" $[\mathbf{U} - \mathbf{Y}, \mathbf{Y}]$ to predict the "outcome" $\text{AUC}(\widehat{\mathbf{Y}}, \mathbf{Y})_{(2^{n_v} \times 1)}$:

```
R> resids <- function(n_v, exclude_identical = FALSE,
+                     tol = sqrt(.Machine$double.eps)) {
+   Y <- Ymat(n_v, exclude_identical = exclude_identical)
+   AUC <- apply(Y, 1, AUC)
+   X <- cbind(1-Y, Y)
+   opts <- options(warn = -1)
+   on.exit(options(opts))
+   fit <- lsfit(X, AUC, intercept = FALSE)
+   ret <- max(abs(residuals(fit)))
+   if(ret < tol){
+     ret <- 0
+     solution <- coef(fit)
+     names(solution) <- paste0("c(", c(1:n_v, 1:n_v), ",",
+                               rep(0:1, each = n_v), ")")
+     attr(ret, "solution") <- zapsmall(solution)
+   }
+   ret
+ }
```

The case $n_v = 3$, excluding identical ys, has a solution:

```
R> resids(3, exclude_identical = TRUE)

[1] 0
attr(,"solution")
c(1,0) c(2,0) c(3,0) c(1,1) c(2,1) c(3,1)
   1.0    0.0   -0.5    0.5    0.0    0.0
```

But, if identical ys are included, the equation is not consistent:

```
R> resids(3, exclude_identical = FALSE)

[1] 0.125
```

For $n_v = 4$, there are no solutions in either case:

```
R> resids(4, exclude_identical = TRUE)

[1] 0.08333333

R> resids(4, exclude_identical = FALSE)

[1] 0.25
```

Consequently, the widely employed AUC measure of fit for binary regression cannot in general be used for a casewise cross-validation criterion.

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