

Statistical Methods for Research

Longhai Li

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1 Introduction to Statistical Methods for Research

Welcome

This book contains lecture notes for **STAT 845: Statistical Methods for Research** at the **University of Saskatchewan**.

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2 R for Data Analysis

2.1 Basic R Objects and Operations

```
## create a vector
x <- 1:10
x <- seq(30,3, by = -2)
a <- c(66.32, 69.87, 70.12, 90.37, 50.08, 61.20, 65.00, 57.65)
d <- a[1]
a[1] <- 85.34

mean(a)
```

```
[1] 68.70375
```

```
ma <- mean(a)
## read a vector of numbers from a file
x <- scan("numbers.txt")
x2 <- scan("number2.txt")

## one can also read number without saving to a file
y <- scan(text = "7 8 9 10 11 12 13 13 14 17 17 45")
```

```
## create a matrix
A <- matrix(0, 4, 2)

A <- matrix(1:8, 4, 2)

A
```

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

2 R for Data Analysis

```
D <- matrix (a, 4, 2, byrow=T)

D <- matrix(1:8, 2, 4)
D
```

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

```
## create another matrix with all entry 0
B <- matrix (1:5000, 100, 50)

## assign a number to B
B[2,4] <- 45
B[1,]
```

```
[1]    1   101   201   301   401   501   601   701   801   901   1001  1101  1201  1301  1401
[16] 1501  1601  1701  1801  1901  2001  2101  2201  2301  2401  2501  2601  2701  2801  2901
[31] 3001  3101  3201  3301  3401  3501  3601  3701  3801  3901  4001  4101  4201  4301  4401
[46] 4501  4601  4701  4801  4901
```

```
B[,1]
```

```
[1]    1    2    3    4    5    6    7    8    9    10   11   12   13   14   15   16   17   18
[19]   19   20   21   22   23   24   25   26   27   28   29   30   31   32   33   34   35   36
[37]   37   38   39   40   41   42   43   44   45   46   47   48   49   50   51   52   53   54
[55]   55   56   57   58   59   60   61   62   63   64   65   66   67   68   69   70   71   72
[73]   73   74   75   76   77   78   79   80   81   82   83   84   85   86   87   88   89   90
[91]   91   92   93   94   95   96   97   98   99  100
```

```
B[1,] <- 1:50
```

```
## create a list
E <- list (newa = a, newA = A)
## list the names of components
names (E)
```

```
[1] "newa" "newA"
```

```
## to look at the component of E
E$newA
```

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

```
E$newa <- 10:17
```

```
## create a dataframe
scores <- c(30, 45, 50)
names <- c("Peter", "John", "Alice")
stat245_scores <- data.frame(names, scores)
stat245_scores
```

```
  names scores
1 Peter     30
2 John      45
3 Alice     50
```

```
stat245_scores$names
```

```
[1] "Peter" "John"  "Alice"
```

```
stat245_scores$scores [1] <- 40
stat245_scores
```

```
  names scores
1 Peter     40
2 John      45
3 Alice     50
```

```
stat245_scores$perc <- stat245_scores$scores/50 * 100
stat245_scores
```

```
  names scores perc
1 Peter     40    80
2 John      45    90
3 Alice     50   100
```

2 R for Data Analysis

```
stat245_scores$adj <- stat245_scores$perc + 10  
stat245_scores
```

```
names scores perc adj  
1 Peter      40    80   90  
2 John       45    90  100  
3 Alice      50   100  110
```

```
#####
```

2.2 Import a dataset into R environment and Simple Operation

```
#####  
  
## import myagpop.csv into an R data frame called 'myagpop'  
agpop <- read.csv("agpop.csv")  
  
## Now, we can use the data:  
  
## preview agpop  
head (agpop)
```

	county	state	acres92	acres87	acres82	farms92	farms87	farms82
1	ALEUTIAN ISLANDS AREA	AK	683533	726596	764514	26	27	28
2	ANCHORAGE AREA	AK	47146	59297	256709	217	245	223
3	FAIRBANKS AREA	AK	141338	154913	204568	168	175	170
4	JUNEAU AREA	AK	210	214	127	8	8	12
5	KENAI PENINSULA AREA	AK	50810	85712	98035	93	119	137
6	AUTAUGA COUNTY	AL	107259	116050	145044	322	388	453

	largef92	largef87	largef82	smallf92	smallf87	smallf82	region
1	14	16	20	6	4	1	W
2	9	10	11	41	52	38	W
3	25	28	21	12	18	25	W
4	0	0	0	5	4	8	W
5	9	18	17	12	18	19	W
6	25	32	32	8	19	17	S

```
## look at the variable name  
colnames (agpop)
```

2.2 Import a dataset into R environment and Simple Operation

```
[1] "county"    "state"     "acres92"   "acres87"   "acres82"   "farms92"  
[7] "farms87"   "farms82"   "largef92"   "largef87"   "largef82"   "smallf92"  
[13] "smallf87"  "smallf82"  "region"
```

```
## find number of cols  
ncol (agpop)
```

```
[1] 15
```

```
## find number of rows  
nrow (agpop)
```

```
[1] 3078
```

```
## access a certain row  
agpop [2, ]
```

```
county state acres92 acres87 acres82 farms92 farms87 farms82 largef92  
2 ANCHORAGE AREA AK 47146 59297 256709 217 245 223 9  
largef87 largef82 smallf92 smallf87 smallf82 region  
2 10 11 41 52 38 W
```

```
## access a certain column  
agpop [1:20, "acres92"] ## equivalent to
```

```
[1] 683533 47146 141338 210 50810 107259 167832 177189 48022 137426  
[11] 144799 96427 73841 109555 121504 99466 67950 61426 68478 47200
```

```
agpop$acres92[1:20]
```

```
[1] 683533 47146 141338 210 50810 107259 167832 177189 48022 137426  
[11] 144799 96427 73841 109555 121504 99466 67950 61426 68478 47200
```

```
agpop$largef92[1:20]
```

```
[1] 14 9 25 0 9 25 24 40 6 9 29 18 4 22 24 8 9 13 4 5
```

```
## find mean of acres92  
mean (agpop $acres92)
```

```
[1] 306677
```

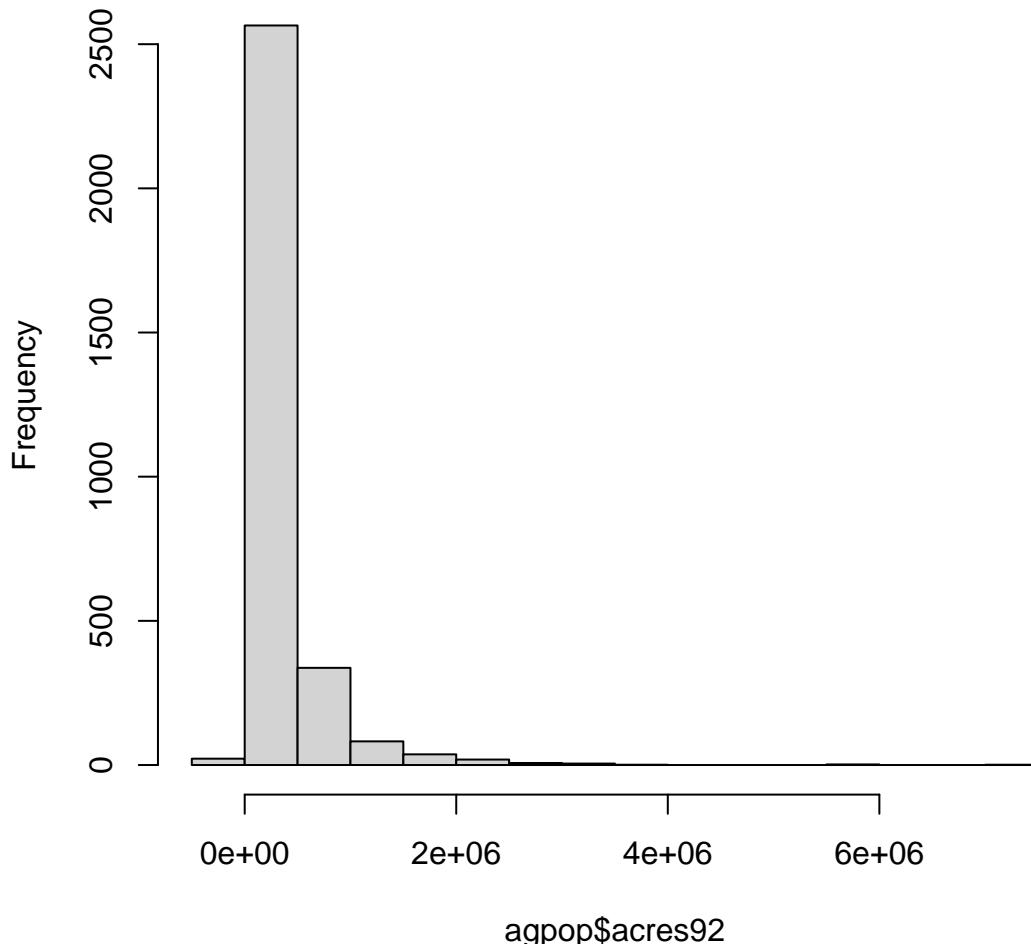
2 R for Data Analysis

```
## find sd of acres92  
sd (agpop $acres92)
```

```
[1] 424686.7
```

```
agpop_AK <- agpop [agpop$state == "AK", ]  
agpop_AK <- subset (agpop, state == "AK")  
agpop_W <- subset (agpop, region == "W")  
agpop_largefarm <- subset (agpop, largef92 > 10)  
  
hist (agpop$acres92)
```

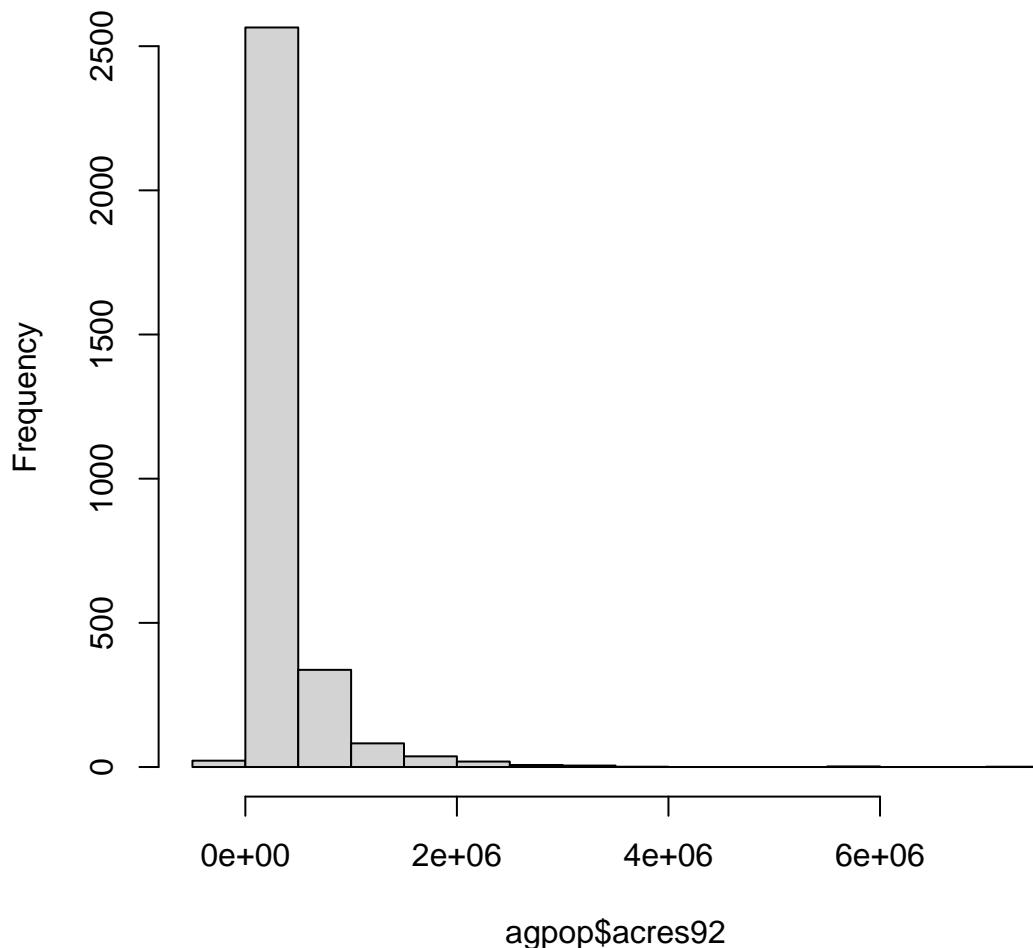
Histogram of agpop\$acres92



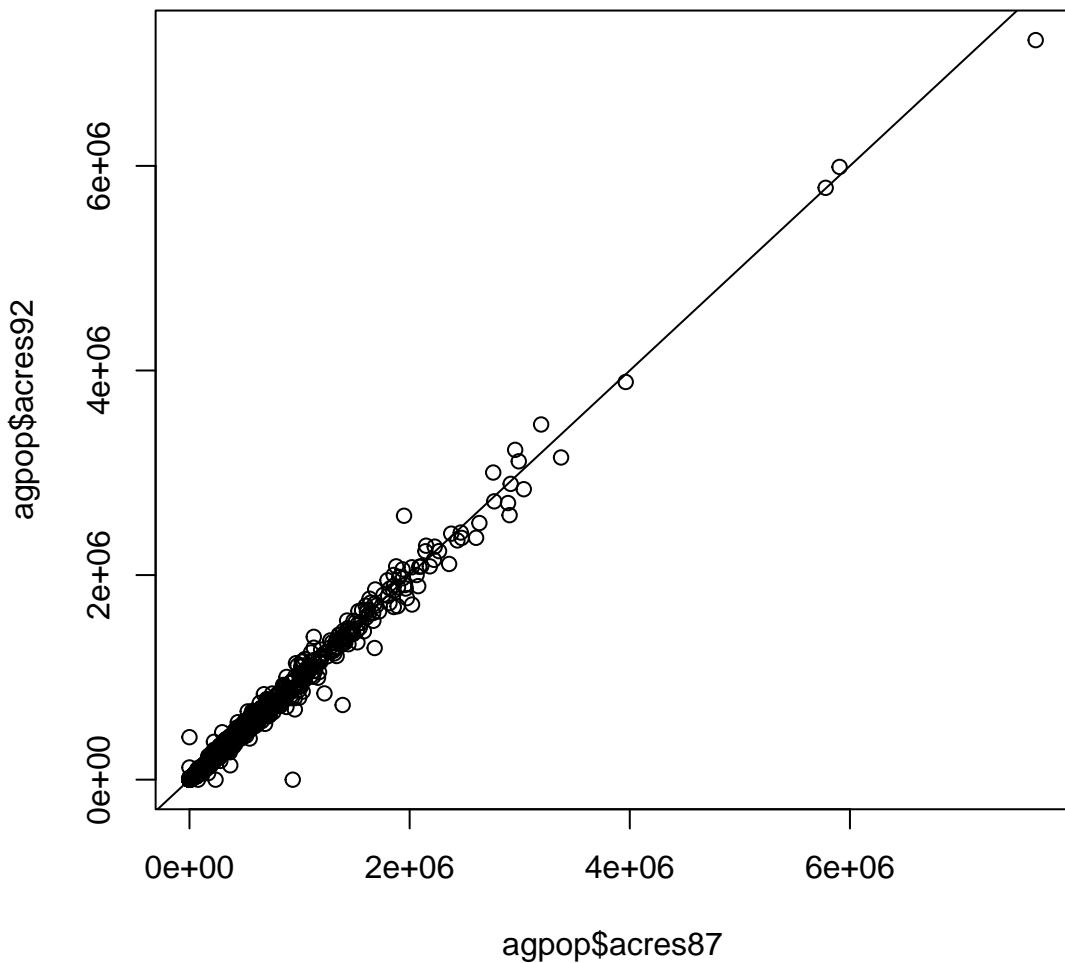
Produce Plots

```
#pdf ("hist_acres92.pdf") ## use this command and dev.off to save the output to a file  
hist (agpop$acres92)
```

Histogram of agpop\$acres92



```
#dev.off()  
  
#jpeg ("agpop_acres_87v92.jpg")  
  
plot (agpop$acres87, agpop$acres92)  
abline (a = 0, b = 1)
```



```
#dev.off()## this is used to close the jpeg file
```

2.3 Create your own function

```
### data is a matrix or data.frame
means_col <- function (data)
{
  n <- ncol (data)
  cmeans <- rep (NA, n)
  for (j in 1:n)
  {
    cmeans[j] <- mean (data[,j])
  }
  cmeans
```

2 R for Data Analysis

```
}  
  
### apply function  
means_col (agpop[, 3:13])  
  
[1] 306676.97141 313016.37817 320193.69298      625.50357    678.28428  
[6]    728.06238     56.17674     54.86160      52.62248    54.09227  
[11]   59.53769
```

```
### R built-in function  
colMeans (agpop[, 3:13])
```

acres92	acres87	acres82	farms92	farms87	farms82
306676.97141	313016.37817	320193.69298	625.50357	678.28428	728.06238
largef92	largef87	largef82	smallf92	smallf87	
56.17674	54.86160	52.62248	54.09227	59.53769	

2.4 Include Images Saved in An External File

Using the following R code to include your images saved in an external file.

```
knitr::include_graphics("handwriting.png")
```

$$\begin{aligned} Q_1 : \\ a+b &= c \\ Q_2 : \\ c &= 1+2 \end{aligned}$$

You can hide the above R code by setting “echo=FALSE” for the r chunk. For example, I will include the image once again as follows:

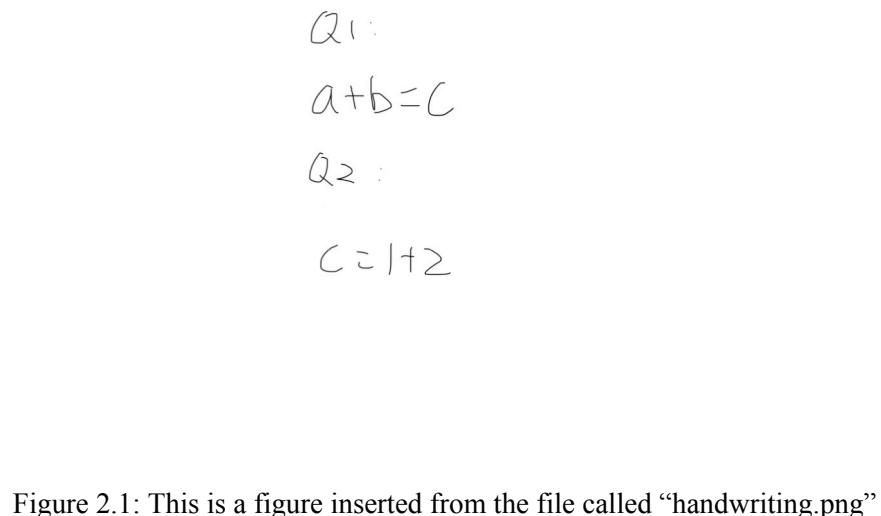


Figure 2.1: This is a figure inserted from the file called “handwriting.png”

3 Simple Linear Regression

A Simulation Illustration with R

```
require("knitr")
knitr::opts_chunk$set(
  comment = "#",
  fig.width = 6,
  fig.height = 6,
  cache = TRUE
)
set.seed(47)

options(sim_rebuild=FALSE)
```

3.1 Overview of Simple Linear Regression

To make the simple linear regression model concrete, let's first visualize a simulated dataset that follows

$$Y_i = \beta_0 + \beta_1 X_i + \varepsilon_i, \quad \varepsilon_i \sim \mathcal{N}(0, \sigma^2).$$

Here, β_0 is the intercept, β_1 is the slope, and ε_i represents random noise.

```
set.seed(2025)
n <- 40
beta0 <- 2; beta1 <- 1.5; sigma <- 2
x <- runif(n, 0, 10)
y <- beta0 + beta1 * x + rnorm(n, 0, sigma)
dat <- data.frame(x, y)

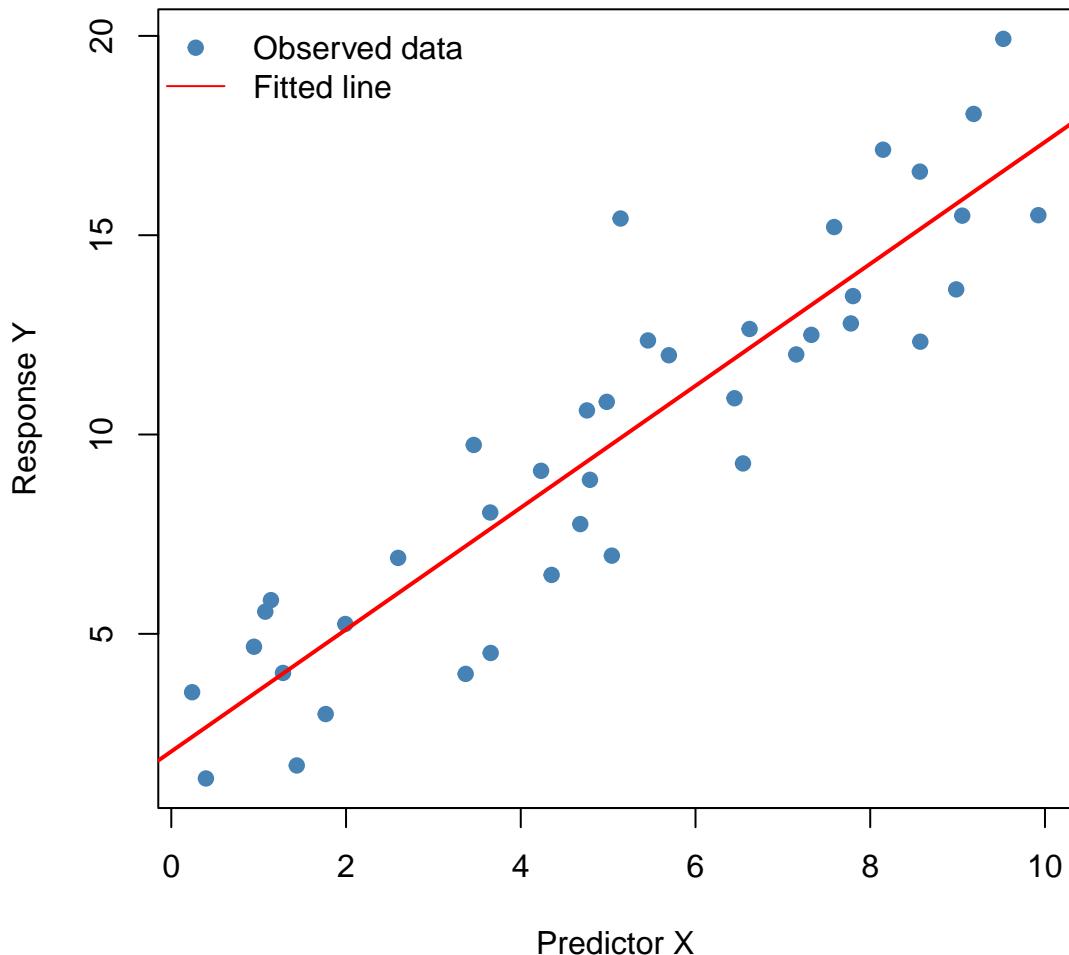
fit <- lm(y ~ x, data = dat)

plot(x, y, pch = 19, col = "steelblue",
      xlab = "Predictor X", ylab = "Response Y",
      main = "Simulated Data with Fitted Linear Regression Line")
```

3 Simple Linear Regression

```
abline(fit, col = "red", lwd = 2)
legend("topleft", legend = c("Observed data", "Fitted line"),
       pch = c(19, NA), lty = c(NA, 1), col = c("steelblue", "red"), bty = "n")
```

Simulated Data with Fitted Linear Regression Line



The scatterplot shows data points scattered around a line — the red line is the fitted regression model.

3.1.1 Least Squares Estimation

Goal: Find $\hat{\beta}_0$ and $\hat{\beta}_1$ that minimize

$$\text{SSE} = \sum_{i=1}^n (y_i - \hat{\beta}_0 - \hat{\beta}_1 x_i)^2.$$

Solutions:

$$\hat{\beta}_1 = \frac{\sum_i (x_i - \bar{x})(y_i - \bar{y})}{\sum_i (x_i - \bar{x})^2} = \frac{S_{xy}}{S_{xx}}, \quad \hat{\beta}_0 = \bar{y} - \hat{\beta}_1 \bar{x}.$$

Here

$$S_{xy} = \sum_i (x_i - \bar{x})(y_i - \bar{y}), \quad S_{xx} = \sum_i (x_i - \bar{x})^2.$$

Shortcut (computational) formulas:

$$S_{xy} = \sum_i x_i y_i - n \bar{x} \bar{y}, \quad S_{xx} = \sum_i x_i^2 - n \bar{x}^2.$$

Interpretation:

- $\hat{\beta}_1$ measures the estimated change in Y for each unit increase in X .
 - $\hat{\beta}_0$ represents the fitted value of Y when $X = 0$.
-

3.1.2 Residual and Sum of Squares Definitions

Let $\hat{y}_i = \hat{\beta}_0 + \hat{\beta}_1 x_i$ and $e_i = y_i - \hat{y}_i$.

Symbol	Definition	Computing Formula (in terms of S_{xx} , S_{xy} , etc.)
SST	Total Sum of Squares	$\sum_i (y_i - \bar{y})^2 = S_{yy} = \sum_i y_i^2 - n \bar{y}^2$
SSR	Regression Sum of Squares	$\sum_i (\hat{y}_i - \bar{y})^2 = \hat{\beta}_1^2 S_{xx} = \frac{S_{xy}^2}{S_{xx}}$
SSE	Error (Residual) Sum of Squares	$\sum_i (y_i - \hat{y}_i)^2 = S_{yy} - \frac{S_{xy}^2}{S_{xx}}$

Identity:

$$\text{SST} = \text{SSR} + \text{SSE}.$$

Here,

$$S_{xx} = \sum_i (x_i - \bar{x})^2 = \sum_i x_i^2 - n \bar{x}^2, \quad S_{yy} = \sum_i (y_i - \bar{y})^2 = \sum_i y_i^2 - n \bar{y}^2, \quad S_{xy} = \sum_i (x_i - \bar{x})(y_i - \bar{y}) = \sum_i x_i y_i - n \bar{x} \bar{y}.$$

3 Simple Linear Regression

3.1.3 Coefficient of Determination (R^2)

Measures the proportion of total variation in Y explained by X :

$$R^2 = \frac{\text{SSR}}{\text{SST}} = 1 - \frac{\text{SSE}}{\text{SST}}.$$

Interpretation:

- $R^2 = 1$ means perfect linear fit;
 - $R^2 = 0$ means the model explains none of the variation.
-

3.1.4 F-test for Overall Significance

Tests whether X is linearly related to Y .

Hypotheses:

$$H_0 : \beta_1 = 0 \quad \text{vs.} \quad H_A : \beta_1 \neq 0.$$

Test Statistic:

$$F = \frac{\text{MSR}}{\text{MSE}} = \frac{\text{SSR}/1}{\text{SSE}/(n-2)} \sim F_{1,n-2} \quad (H_0).$$

p-value approach for observe F^{obs} :

Given the observed statistic F^{obs} with $(1, n-2)$ df,

$$p\text{-value} = \Pr(F_{1,n-2} \geq F^{\text{obs}}) = \text{pf}(F^{\text{obs}}, 1, n-2, \text{lower.tail} = \text{FALSE}).$$

```
## -- Inputs (provide these from your analysis context) -----
## n    <- ...   # sample size
## SSR <- ...   # regression sum of squares
## SSE <- ...   # error sum of squares
n    <- 20
SSR <- 5
SSE <- 40

df1  <- 1
df2  <- n - 2
Fobs <- (SSR/df1) / (SSE/df2)           # observed F
pval <- pf(Fobs, df1 = df1, df2 = df2, lower.tail = FALSE)
pval
```

```
[1] 0.1509505
```

```
## -- Plot F density and shade the p-value tail (with proper annotations) -----
xmax <- max(qf(0.995, df1, df2), Fobs * 1.2) # extra space for labels
peak <- max(df(seq(0, xmax, length.out = 500), df1, df2))

## Density curve
curve(df(x, df1, df2), from = 0, to = xmax,
      xlab = "F", ylab = "Density",
      main = sprintf("F(%d, %d) density | observed F = %.3f", df1, df2, Fobs))

## Shade right tail (p-value region)
xs <- seq(Fobs, xmax, length.out = 300)
ys <- df(xs, df1, df2)
polygon(c(Fobs, xs, xmax), c(0, ys, 0),
        col = rgb(0, 0, 0, 0.18), border = NA)

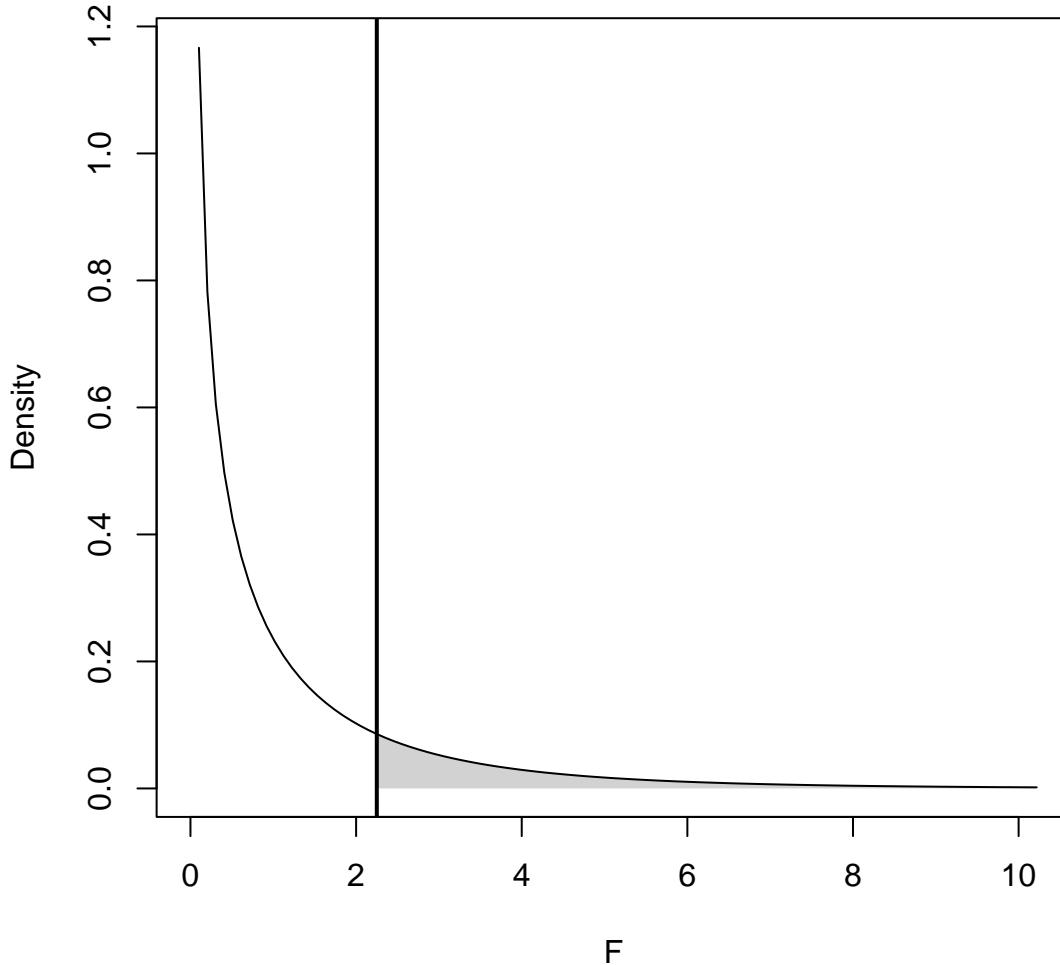
## Vertical line at Fobs (optional visual aid)
abline(v = Fobs, lwd = 2)

## ----- Annotation for F^obs pointing to the x-axis value (Fobs, 0) -----
x_txt_F <- Fobs + 0.06 * xmax
y_txt_F <- 0.45 * peak
arrows(x0 = x_txt_F, y0 = y_txt_F, x1 = Fobs, y1 = 0,
       length = 0.08, lwd = 1.5)
text(x_txt_F, y_txt_F,
     labels = bquote(F^{obs} == .(format(Fobs, digits = 3))),
     pos = 4)

## ----- Annotation for p-value pointing into the shaded tail -----
x_tip_p <- (Fobs + xmax) / 1.7
y_tip_p <- df(x_tip_p, df1, df2)
x_txt_p <- Fobs + 0.08 * xmax
y_txt_p <- 0.80 * peak
arrows(x0 = x_txt_p, y0 = y_txt_p, x1 = x_tip_p, y1 = y_tip_p,
       length = 0.08, lwd = 1.5)
text(x_txt_p, y_txt_p,
     labels = bquote(p == .(format(pval, digits = 4, scientific = TRUE))),
     pos = 4)
```

3 Simple Linear Regression

F(1, 18) density | observed F = 2.250



3.1.5 t-test for the Slope β_1

Equivalent to the F -test in simple regression since $t^2 = F$.

Formula:

$$t = \frac{\hat{\beta}_1}{\text{SE}(\hat{\beta}_1)}, \quad \text{SE}(\hat{\beta}_1) = \sqrt{\frac{\hat{\sigma}^2}{\sum_i (x_i - \bar{x})^2}}, \quad \hat{\sigma}^2 = \frac{\text{SSE}}{n - 2}.$$

Distribution:

$$t \sim t_{n-2} \quad (H_0 : \beta_1 = 0).$$

3.2 Example 1: Vehicle Insurance Premium (warm-up)

3.1.6 Prediction for a New Case x_0

Predicted mean response:

$$\hat{y}(x_0) = \hat{\beta}_0 + \hat{\beta}_1 x_0.$$

95% Confidence interval for mean response:

$$\hat{y}(x_0) \pm t_{1-\alpha/2, n-2} \hat{\sigma}, \sqrt{\frac{1}{n} + \frac{(x_0 - \bar{x})^2}{\sum_i (x_i - \bar{x})^2}}.$$

95% Prediction interval for a new observation:

$$\hat{y}(x_0) \pm t_{1-\alpha/2, n-2} \hat{\sigma}, \sqrt{1 + \frac{1}{n} + \frac{(x_0 - \bar{x})^2}{\sum_i (x_i - \bar{x})^2}}.$$

Summary Cheat Sheet

Concept	Key Formula
Model	$Y_i = \beta_0 + \beta_1 X_i + \varepsilon_i$
LS Estimates	$\hat{\beta}_1 = S_{xy}/S_{xx}$, $\hat{\beta}_0 = \bar{y} - \hat{\beta}_1 \bar{x}$
Decomposition	$SST = SSR + SSE$
R^2	$R^2 = 1 - SSE/SST$
F -test	$F = (SSR/1)/(SSE/(n-2))$
t -test	$t = \hat{\beta}_1 / SE(\hat{\beta}_1)$
Prediction	$\hat{y}(x_0) = \hat{\beta}_0 + \hat{\beta}_1 x_0$

3.2 Example 1: Vehicle Insurance Premium (warm-up)

We examine premiums y vs. driving amount x . The scatterplot hints at a **downward trend**.

3.2.1 Input data

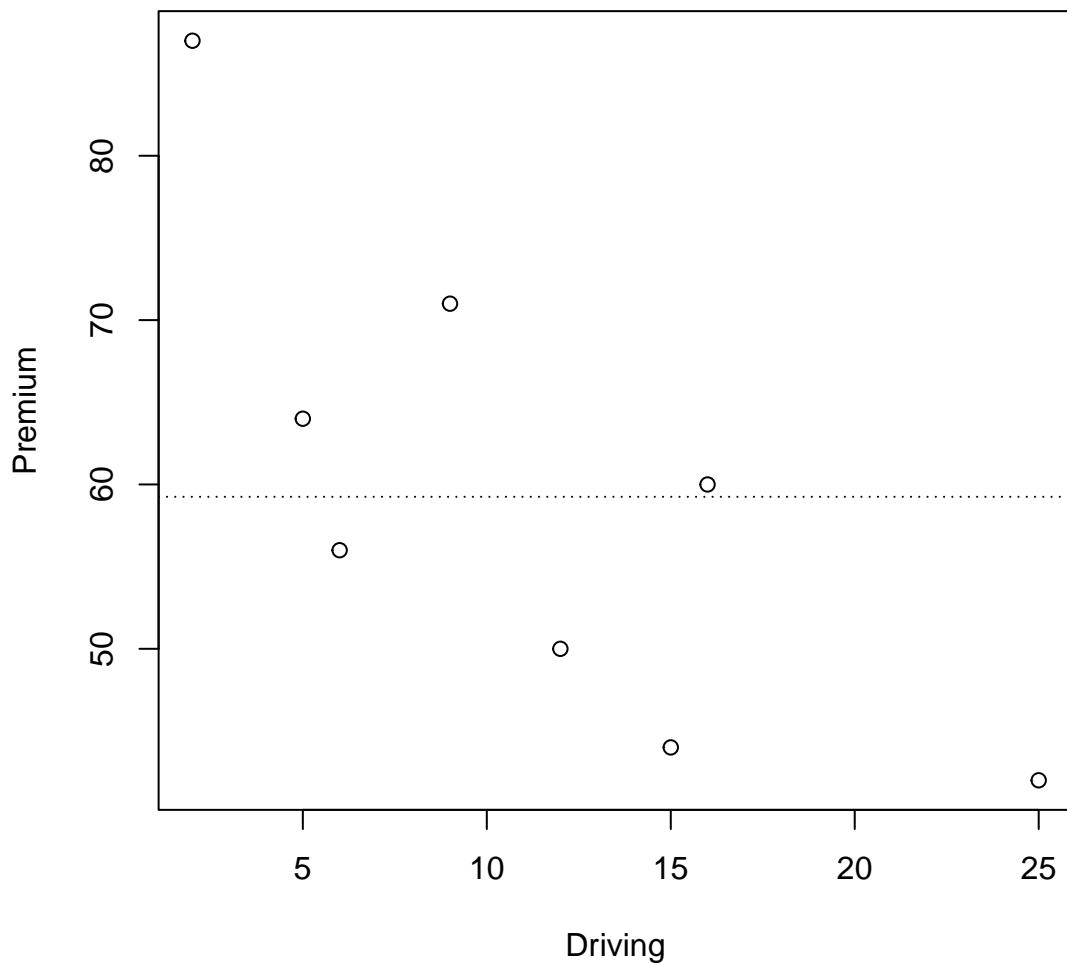
```
issu <- data.frame(
  driving = c(5, 2, 12, 9, 15, 6, 25, 16),
  premium = c(64, 87, 50, 71, 44, 56, 42, 60)
)
```

3 Simple Linear Regression

```
y <- issu$premium
x <- issu$driving
xbar <- mean(x); ybar <- mean(y); n <- length(y)

plot(x, y, xlab = "Driving", ylab = "Premium",
      main = "Vehicle Insurance: Premium vs. Driving")
abline(h = ybar, lty = 3)
```

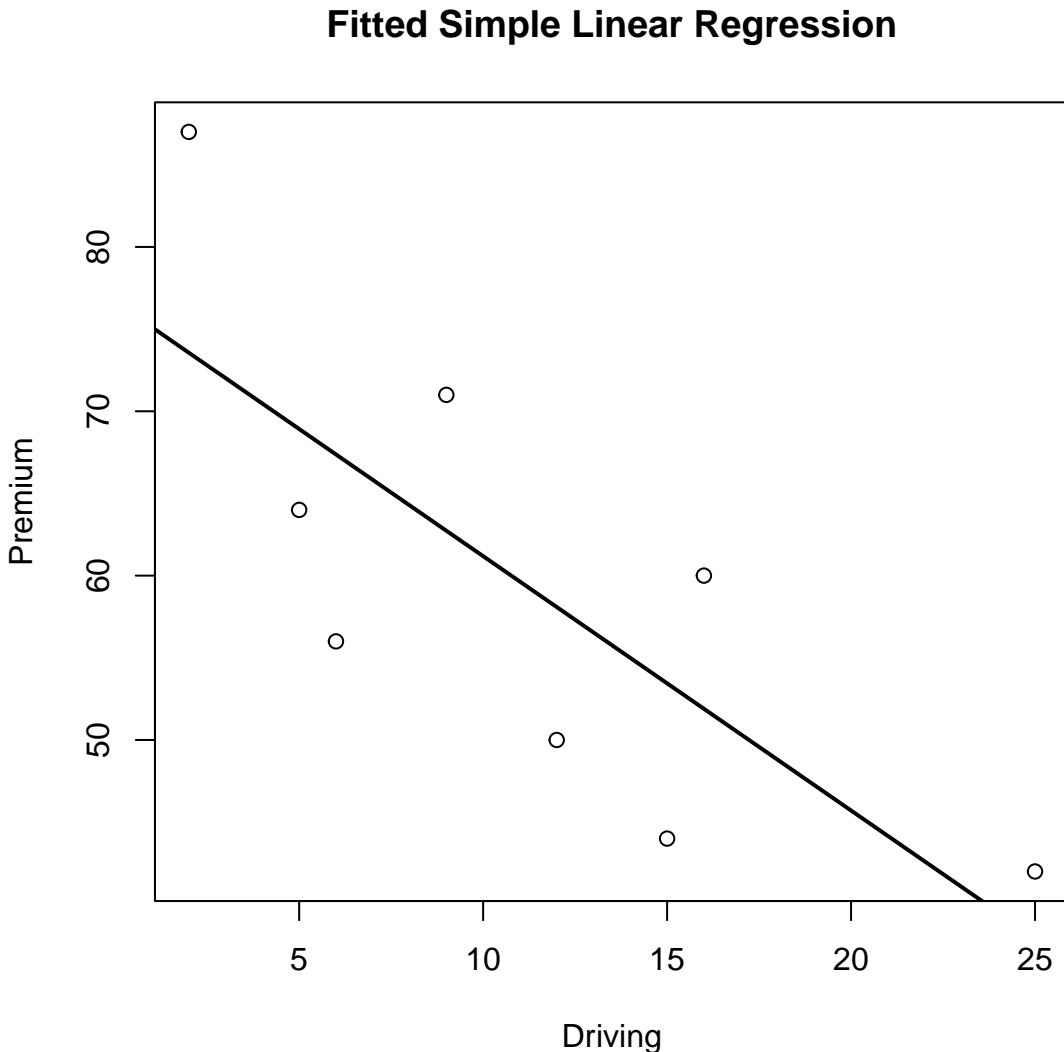
Vehicle Insurance: Premium vs. Driving



Narrative. The horizontal line at \bar{y} represents the intercept-only model. Any fitted line that tilts away from this must earn its keep by reducing residual variation enough to offset the loss of one degree of freedom.

3.2.2 Estimating regression coefficients

```
fit.issu <- lm(y ~ x)
plot(x, y, xlab = "Driving", ylab = "Premium",
     main = "Fitted Simple Linear Regression")
abline(fit.issu, lwd = 2)
```



The slope estimate $\hat{\beta}_1$ captures the **marginal change in premium per unit of driving** (units of y per unit of x). Inference on β_1 tells us whether the pattern rises above noise.

3.2.3 Residuals and fitted values (geometry picture)

Let $\hat{y}_i = \hat{\beta}_0 + \hat{\beta}_1 x_i$ and $\tilde{y}_i = \bar{y}$. Residuals are $e_i = y_i - \hat{y}_i$ (model) and $y_i - \bar{y}$ (null). Visualizing all three clarifies the ANOVA identity.

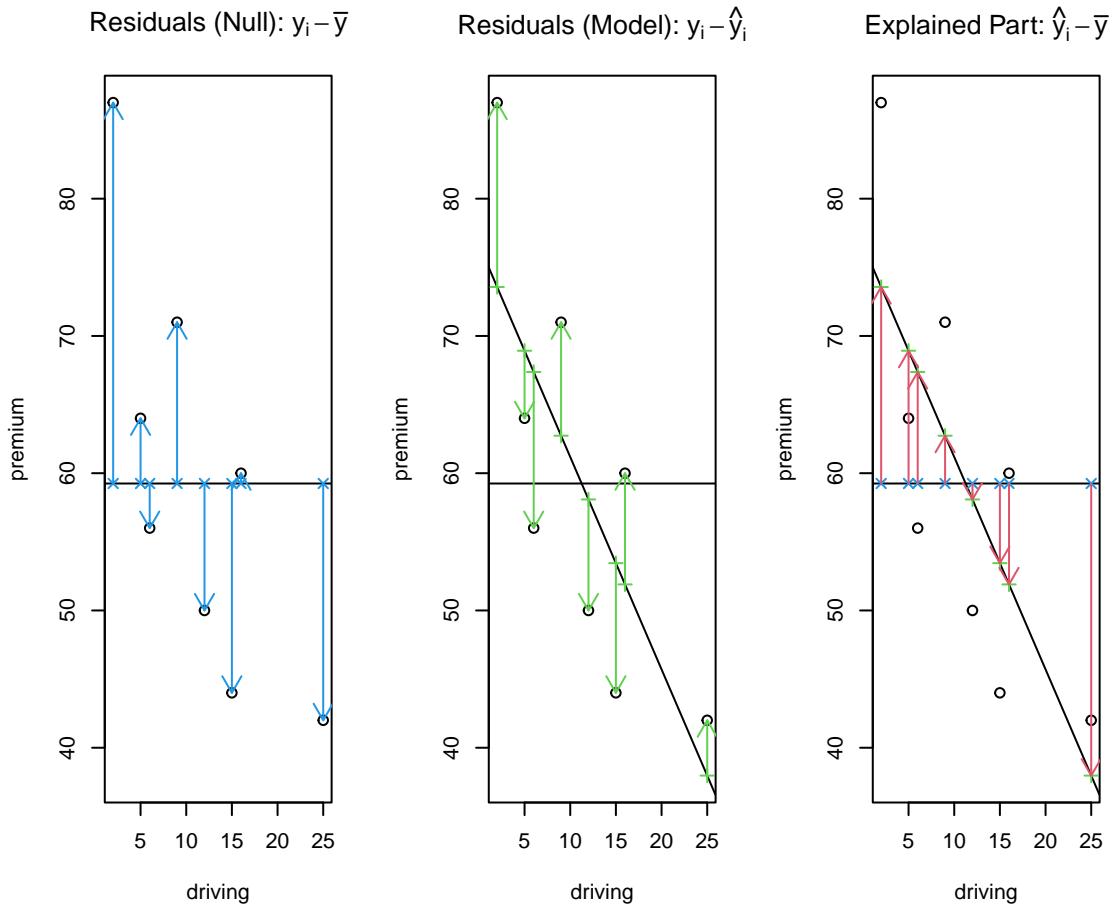
3 Simple Linear Regression

```
beta0 <- coef(fit.issu)[1]
beta1 <- coef(fit.issu)[2]
fitted1 <- beta0 + beta1 * x
fitted0 <- rep(ybar, n)
residual1 <- y - fitted1
residual0 <- y - fitted0

data.frame(y, fitted0, residual0, fitted1, residual1,
           diff.fitted = fitted1 - fitted0)
```

	y	fitted0	residual0	fitted1	residual1	diff.fitted
1	64	59.25	4.75	68.92243	-4.922425	9.672425
2	87	59.25	27.75	73.56519	13.434811	14.315189
3	50	59.25	-9.25	58.08931	-8.089309	-1.160691
4	71	59.25	11.75	62.73207	8.267927	3.482073
5	44	59.25	-15.25	53.44654	-9.446545	-5.803455
6	56	59.25	-3.25	67.37484	-11.374837	8.124837
7	42	59.25	-17.25	37.97066	4.029335	-21.279335
8	60	59.25	0.75	51.89896	8.101043	-7.351043

3.2 Example 1: Vehicle Insurance Premium (warm-up)



3.2.4 SST, SSR, SSE and their meanings

- $SST = \sum(y_i - \bar{y})^2$ quantifies **total** variability around the mean.
- $SSR = \sum(\hat{y}_i - \bar{y})^2$ is the part **explained by x** .
- $SSE = \sum(y_i - \hat{y}_i)^2$ is the **leftover** (unexplained) variability.

```
SST <- sum((y - fitted0)^2); SST
```

```
[1] 1557.5
```

```
SSE <- sum((y - fitted1)^2); SSE
```

```
[1] 639.0065
```

```
SSR <- SST - SSE; SSR
```

3 Simple Linear Regression

```
[1] 918.4935
```

Direct check: $\text{SSR} = \sum(\hat{y}_i - \bar{y})^2$.

```
sum((fitted1 - fitted0)^2)
```

```
[1] 918.4935
```

3.2.5 Visual ANOVA on an RSS plot

We place the **residual sum of squares** against model dimension to show the trade-off between fit and df.

```
## Recompute cleanly
SST <- sum((y - mean(y))^2)
SSE <- sum(resid(fit.issu)^2)
SSR <- SST - SSE
df_SSR <- 1
df_SSE <- n - 2

par(mar = c(6, 4, 4, 2) + 0.1)
plot(c(1, 2, n), c(SST, SSE, 0), type = "b", pch = 19,
      xlab = "Number of Parameters in Model",
      ylab = "Residual Sum of Squares (RSS)",
      main = "ANOVA Geometry on RSS vs. Model Size",
      xlim = c(0, 14), ylim = c(-400, SST * 1.1), xaxt = "n")
axis(1, at = c(1, 2, n), labels = c("1 (Intercept)", "2 (+Slope)", paste(n, "(Saturated)")))
abline(h = seq(0, 2000, by = 100), lty = 3, col = "grey")

par(xpd = TRUE)
arrows(9, 0, 9, SSE, col = "blue", code = 3, angle = 90, length = 0.1, lwd = 2)
text(9, SSE/2, "SSE", col = "blue", pos = 4, font = 2, cex = 1.2)

arrows(9, SSE, 9, SST, col = "red", code = 3, angle = 90, length = 0.1, lwd = 2)
text(9, (SST + SSE)/2, "SSR", col = "red", pos = 4, font = 2, cex = 1.2)

arrows(2, -200, n, -200, col = "blue", code = 3, angle = 90, length = 0.1, lwd = 2)
text((2 + n)/2, -250, paste("df_SSE =", df_SSE), col = "blue", font = 2)

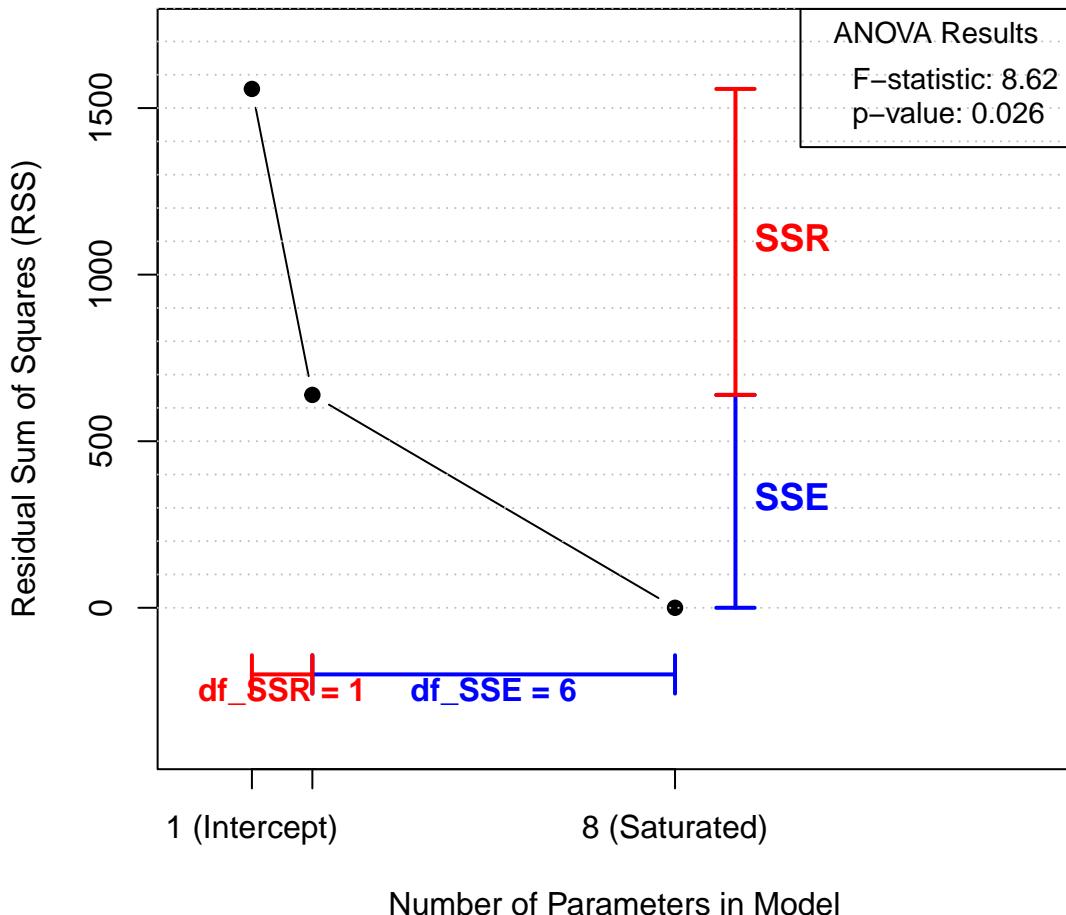
arrows(1, -200, 2, -200, col = "red", code = 3, angle = 90, length = 0.1, lwd = 2)
text(1.5, -250, paste("df_SSR =", df_SSR), col = "red", font = 2)
par(xpd = FALSE)

f_value <- (SSR/df_SSR) / (SSE/df_SSE)
```

3.2 Example 1: Vehicle Insurance Premium (warm-up)

```
p_value <- pf(f_value, df1 = df_SSR, df2 = df_SSE, lower.tail = FALSE)
legend("topright",
       legend = c(sprintf("F-statistic: %.2f", f_value),
                  sprintf("p-value: %.3f", p_value)),
       title = "ANOVA Results", bty = "o", cex = 0.9)
```

ANOVA Geometry on RSS vs. Model Size



3.2.6 R^2 , F and a compact ANOVA table

```
R2 <- SSR / SST; R2
```

```
[1] 0.5897229
```

3 Simple Linear Regression

```
f <- (SSR/1) / (SSE/(n-2)); f
```

```
[1] 8.624264
```

```
pvf <- pf(f, df1 = 1, df2 = n-2, lower.tail = FALSE); pvf
```

```
[1] 0.0260588
```

```
Ftable <- data.frame(  
  Source = c("Regression", "Error"),  
  df      = c(1, n - 2),  
  SS      = c(SSR, SSE),  
  MS      = c(SSR/1, SSE/(n-2)),  
  F       = c(f, NA),  
  pvalue = c(pvf, NA),  
  R2part = c(SSR, SSE) / SST  
)  
Ftable
```

	Source	df	SS	MS	F	pvalue	R2part
1	Regression	1	918.4935	918.4935	8.624264	0.0260588	0.5897229
2	Error	6	639.0065	106.5011		NA	0.4102771

A call to `anova()` reproduces the same test:

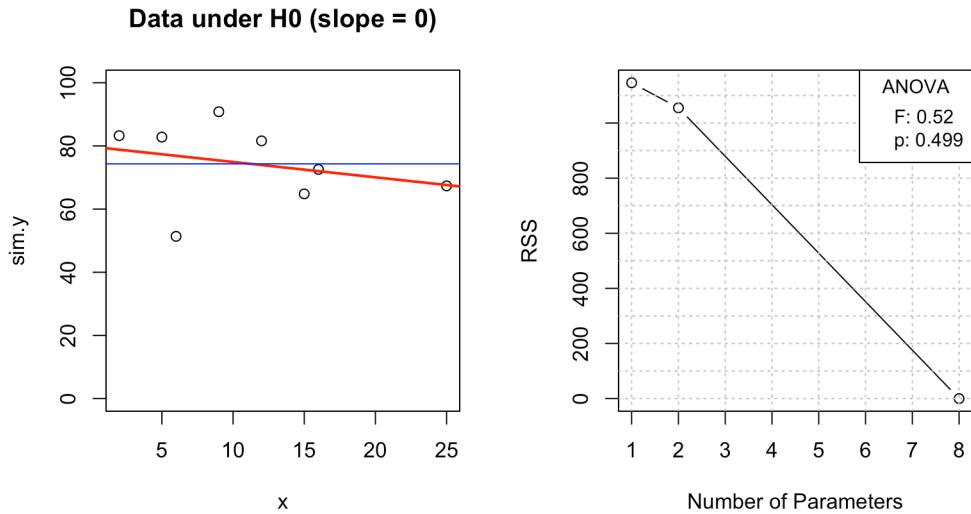
```
anova(fit.issu)
```

Analysis of Variance Table

```
Response: y  
          Df Sum Sq Mean Sq F value    Pr(>F)  
x           1  918.49   918.49  8.6243 0.02606 *  
Residuals   6  639.01   106.50  
---  
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

3.2.7 Sampling distributions via animation

Under $H_0 : \beta_1 = 0$, F follows $F_{1,n-2}$. Under H_A , the distribution shifts right (noncentral F).

Figure 3.1: Simulation under H_0 : animated GIF (HTML) and static PNG (PDF).

3.2.7.1 Null world (H_0 true)

3.2.7.2 Alternative world (H_1 true)

3.3 Example 2: Oxygen Purity Data

We model oxygen purity y as a function of hydrocarbon level x and report both **mean response** and **prediction uncertainty**.

3.3.1 Data

```
x <- c(0.99, 1.02, 1.15, 1.29, 1.46, 1.36, 0.87, 1.23, 1.55, 1.40, 1.19,
      1.15, 0.98, 1.01, 1.11, 1.20, 1.26, 1.32, 1.43, 0.95)
y <- c(90.01, 89.05, 91.43, 93.74, 96.73, 94.45, 87.59, 91.77, 99.42, 93.65,
      93.54, 92.52, 90.56, 89.54, 89.85, 90.39, 93.25, 93.41, 94.98, 87.33)
n <- length(x); n
```

[1] 20

3 Simple Linear Regression

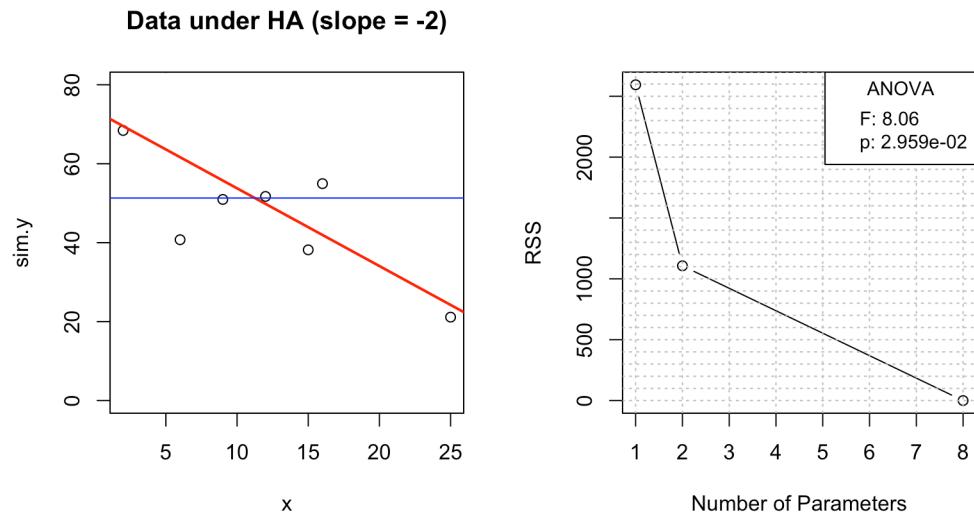


Figure 3.2: Simulation under HA (slope = -2): animated GIF for HTML, static PNG for PDF.

```
purity.data <- data.frame(x = x, y = y)
head(purity.data)
```

```
x      y
1 0.99 90.01
2 1.02 89.05
3 1.15 91.43
4 1.29 93.74
5 1.46 96.73
6 1.36 94.45
```

3.3.2 Fit and quick summary

```
fit <- lm(y ~ x, data = purity.data)
summary(fit)
```

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

Residuals:

Min	1Q	Median	3Q	Max
-----	----	--------	----	-----

```

-1.83029 -0.73334  0.04497  0.69969  1.96809

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 74.283     1.593   46.62 < 2e-16 ***
x           14.947     1.317   11.35 1.23e-09 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.087 on 18 degrees of freedom
Multiple R-squared:  0.8774,    Adjusted R-squared:  0.8706
F-statistic: 128.9 on 1 and 18 DF,  p-value: 1.227e-09

```

Interpretation. The slope's sign gives the direction of association; its t test (or F with 1 df) assesses evidence for a trend. Look at $\hat{\sigma}$ for noise scale and R^2 for variance explained.

3.3.3 Scatter with fitted line

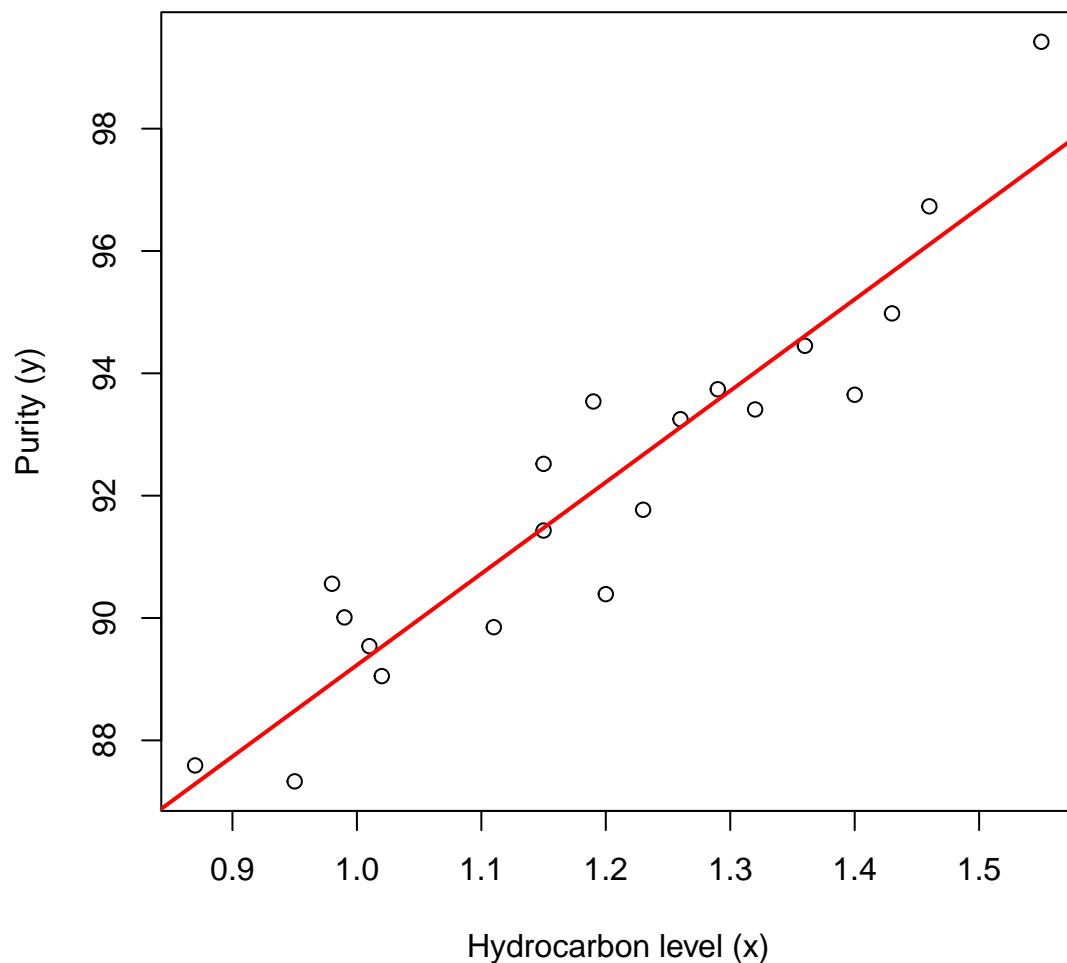
```

plot(purity.data$x, purity.data$y,
      xlab = "Hydrocarbon level (x)", ylab = "Purity (y)",
      main = "Oxygen Purity vs Hydrocarbon Level")
abline(fit, col = "red", lwd = 2)

```

3 Simple Linear Regression

Oxygen Purity vs Hydrocarbon Level



3.3.4 Coefficient CIs and ANOVA

```
confint(fit, level = 0.95)
```

```
2.5 %    97.5 %
(Intercept) 70.93555 77.63108
x           12.18107 17.71389
```

```
anova(fit)
```

Analysis of Variance Table

```
Response: y
          Df Sum Sq Mean Sq F value    Pr(>F)
x           1 152.13 152.127  128.86 1.227e-09 ***
Residuals 18  21.25   1.181
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

3.3.5 Mean-response and prediction bands

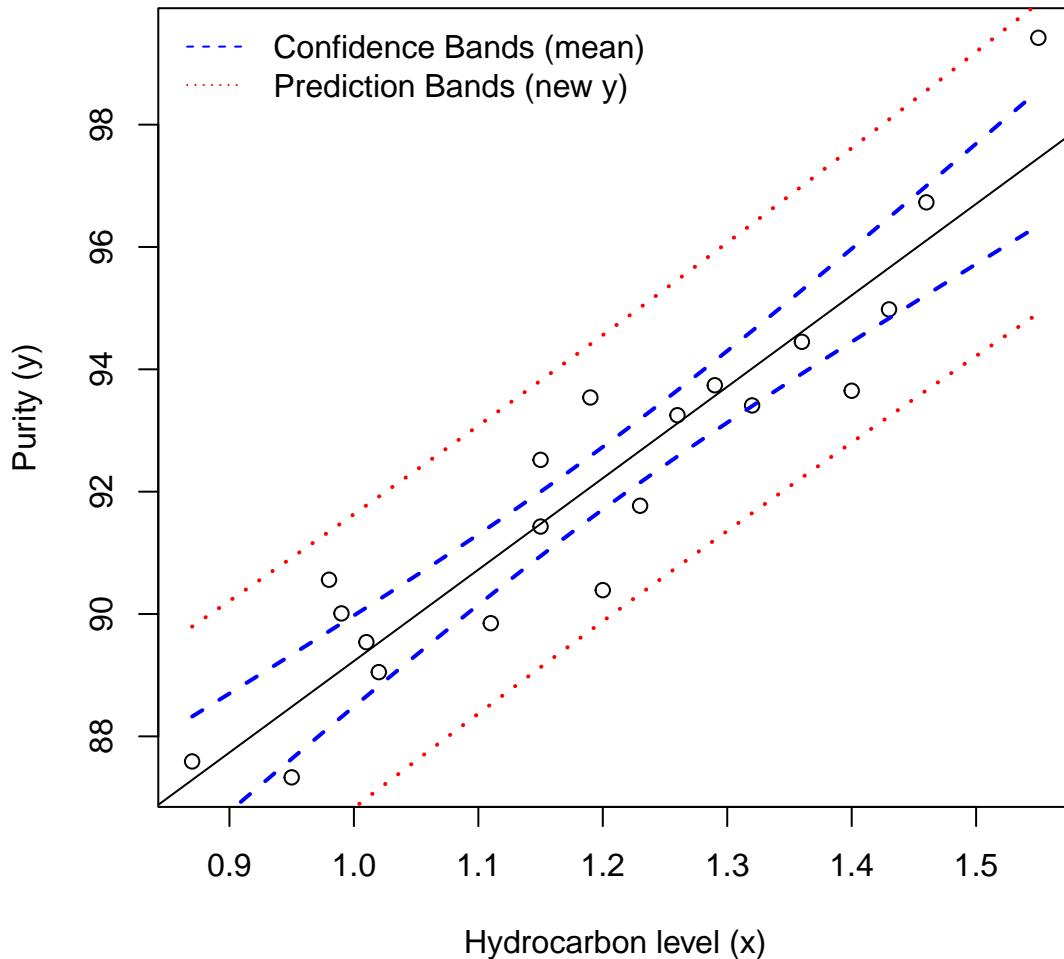
The **mean-response CI** narrows near \bar{x} and widens at the extremes; the **prediction band** is wider by the irreducible noise term.

```
x0 <- seq(min(purity.data$x), max(purity.data$x), length = 50)
newdata <- data.frame(x = x0)

est.mean <- predict(fit, newdata = newdata, interval = "confidence", level = 0.95)
pred.new <- predict(fit, newdata = newdata, interval = "prediction", level = 0.95)
```

```
plot(purity.data$x, purity.data$y,
      xlab = "Hydrocarbon level (x)", ylab = "Purity (y)",
      main = "Regression Line with Confidence and Prediction Bands")
abline(fit)
matlines(x0, est.mean[, 2:3], col = "blue", lty = 2, lwd = 2)
matlines(x0, pred.new[, 2:3], col = "red", lty = 3, lwd = 2)
legend("topleft", c("Confidence Bands (mean)", "Prediction Bands (new y)"),
       col = c("blue", "red"), lty = 2:3, bty = "n")
```

Regression Line with Confidence and Prediction Bands



3.3.6 Residual diagnostics (assumptions check)

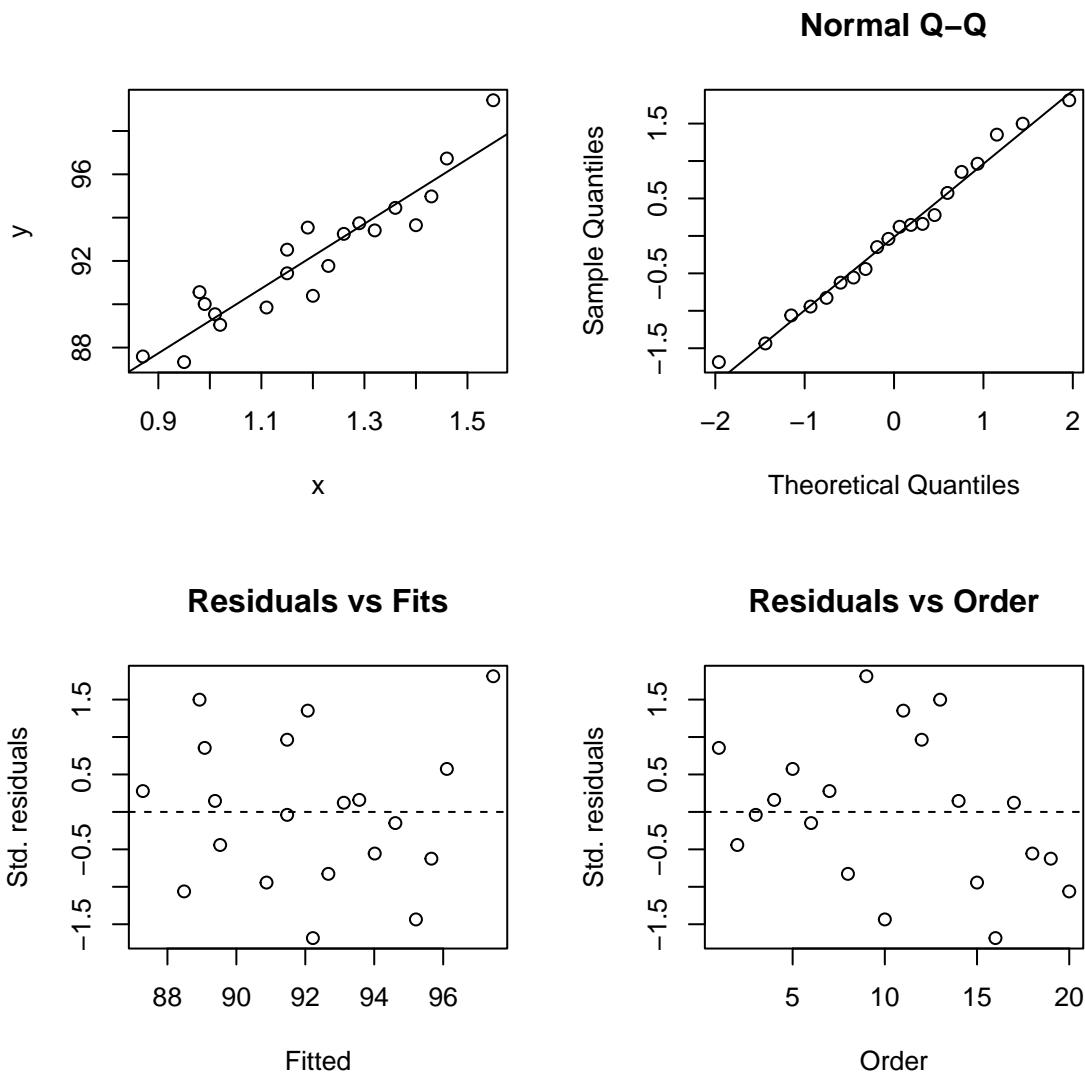
We look for **no pattern** in residuals vs. fits and **approximate straightness** in the Q–Q plot.

```

pred <- fitted.values(fit)
e <- resid(fit)
d <- e / summary(fit)$sigma

par(mfrow = c(2,2))
plot(purity.data$x, purity.data$y, xlab = "x", ylab = "y"); abline(fit)
qqnorm(d, main = "Normal Q-Q"); qqline(d)
plot(pred, d, xlab = "Fitted", ylab = "Std. residuals", main = "Residuals vs Fits"); abline(h=0)
plot(1:n, d, xlab = "Order", ylab = "Std. residuals", main = "Residuals vs Order"); abline(h=0)

```



```
par(mfrow = c(1,1))
```

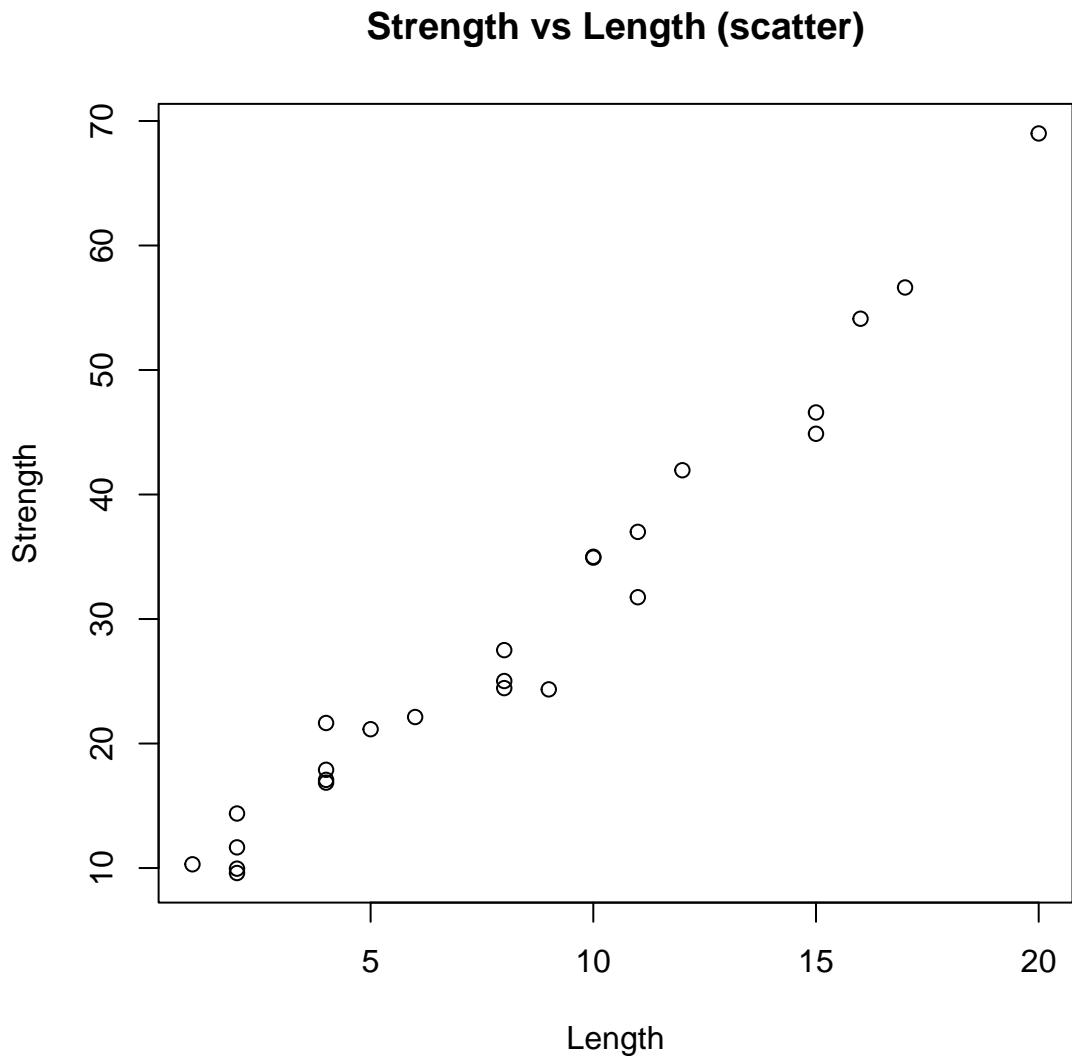
3.4 Correlation analysis (for comparison, not causation)

Correlation summarizes linear association without fitting a line or making model assumptions.

3.4.1 Data and scatter

3 Simple Linear Regression

```
strength <- c(9.95,24.45,31.75,35.00,25.02,16.86,14.38,9.60,24.35,
             27.50,17.08,37.00,41.95,11.66,21.65,17.89,69.00,10.30,
             34.93,46.59,44.88,54.12,56.63,22.13,21.15)
length <- c(2,8,11,10,8,4,2,2,9,8,4,11,12,2,4,4,20,1,10,
          15,15,16,17,6,5)
plot(length, strength, xlab = "Length", ylab = "Strength",
     main = "Strength vs Length (scatter)")
```



3.4.2 Pearson correlation and test

```
cor(strength, length)
```

```
[1] 0.9818118
```

```
cor.test(strength, length)
```

```
Pearson's product-moment correlation

data: strength and length
t = 24.801, df = 23, p-value < 2.2e-16
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
0.9585414 0.9920735
sample estimates:
cor
0.9818118
```

Note. A large $|r|$ and small p indicate linear association; regression further quantifies the slope and supports prediction, with diagnostics to check assumptions.

3.5 What to report (checklist)

- Estimated line $\hat{y} = \hat{\beta}_0 + \hat{\beta}_1 x$ with units.
- t/F test for slope, p -value and CI for β_1 .
- R^2 and $\hat{\sigma}$ (RMSE) for fit quality.
- Mean-response and prediction intervals at substantively relevant x_0 .
- Residual diagnostics and any remedies (transformations, robust methods) if needed.

4 Multiple Linear Regression

4.1 An Example: Wire Bond Strength Dataset

4.1.1 Loading Data and Visualization

Note: You must change the file paths in the `read.csv()` functions below to match the location of the files on your computer (for example `C:\\\\Users\\\\<YourUsername>\\\\Documents` on Windows).

```
## Read data. Change the path as necessary.  
## Example: bond.data <- read.csv("wire-bond.csv")  
bond.data <- read.csv("wire-bond.csv")  
  
## This will now be automatically rendered as a paged table  
bond.data
```

	strength	length	height
1	9.95	2	50
2	24.45	8	110
3	31.75	11	120
4	35.00	10	550
5	25.02	8	295
6	16.86	4	200
7	14.38	2	375
8	9.60	2	52
9	24.35	9	100
10	27.50	8	300
11	17.08	4	412
12	37.00	11	400
13	41.95	12	500
14	11.66	2	360
15	21.65	4	205
16	17.89	4	400
17	69.00	20	600
18	10.30	1	585
19	34.93	10	540
20	46.59	15	250
21	44.88	15	290

4 Multiple Linear Regression

```

22      54.12      16     510
23      56.63      17     590
24     22.13       6    100
25     21.15       5    400

```

2D Visualization

```

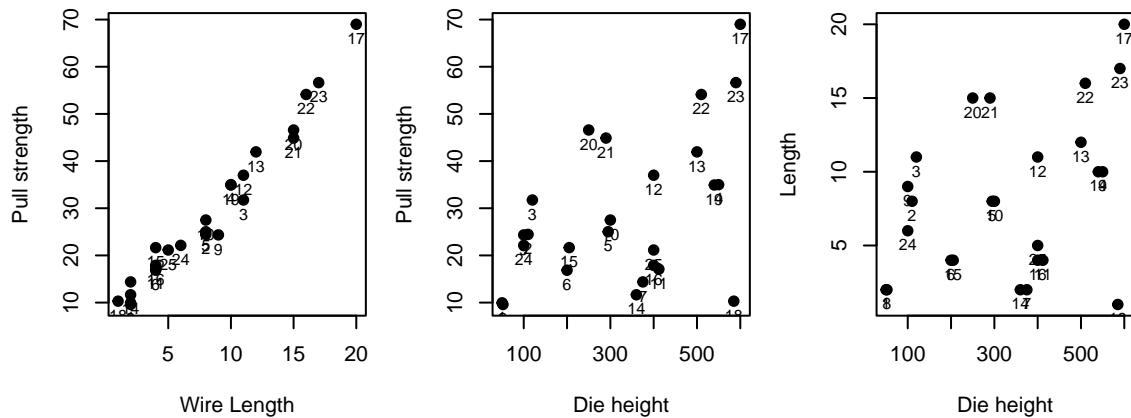
par(mfrow = c(1, 3), mar = c(5, 4, 2, 1))

## 1) length vs strength
i1 <- which(!is.na(bond.data$length) & !is.na(bond.data$strength))
plot(bond.data$length[i1], bond.data$strength[i1],
     xlab = "Wire Length", ylab = "Pull strength", pch = 19)
text(bond.data$length[i1], bond.data$strength[i1],
     labels = i1, pos = 1, offset = 0.4, cex = 0.75)

## 2) height vs strength
i2 <- which(!is.na(bond.data$height) & !is.na(bond.data$strength))
plot(bond.data$height[i2], bond.data$strength[i2],
     xlab = "Die height", ylab = "Pull strength", pch = 19)
text(bond.data$height[i2], bond.data$strength[i2],
     labels = i2, pos = 1, offset = 0.4, cex = 0.75)

## 3) height vs length
i3 <- which(!is.na(bond.data$height) & !is.na(bond.data$length))
plot(bond.data$height[i3], bond.data$length[i3],
     xlab = "Die height", ylab = "Length", pch = 19)
text(bond.data$height[i3], bond.data$length[i3],
     labels = i3, pos = 1, offset = 0.4, cex = 0.75)

```



3D Visualize

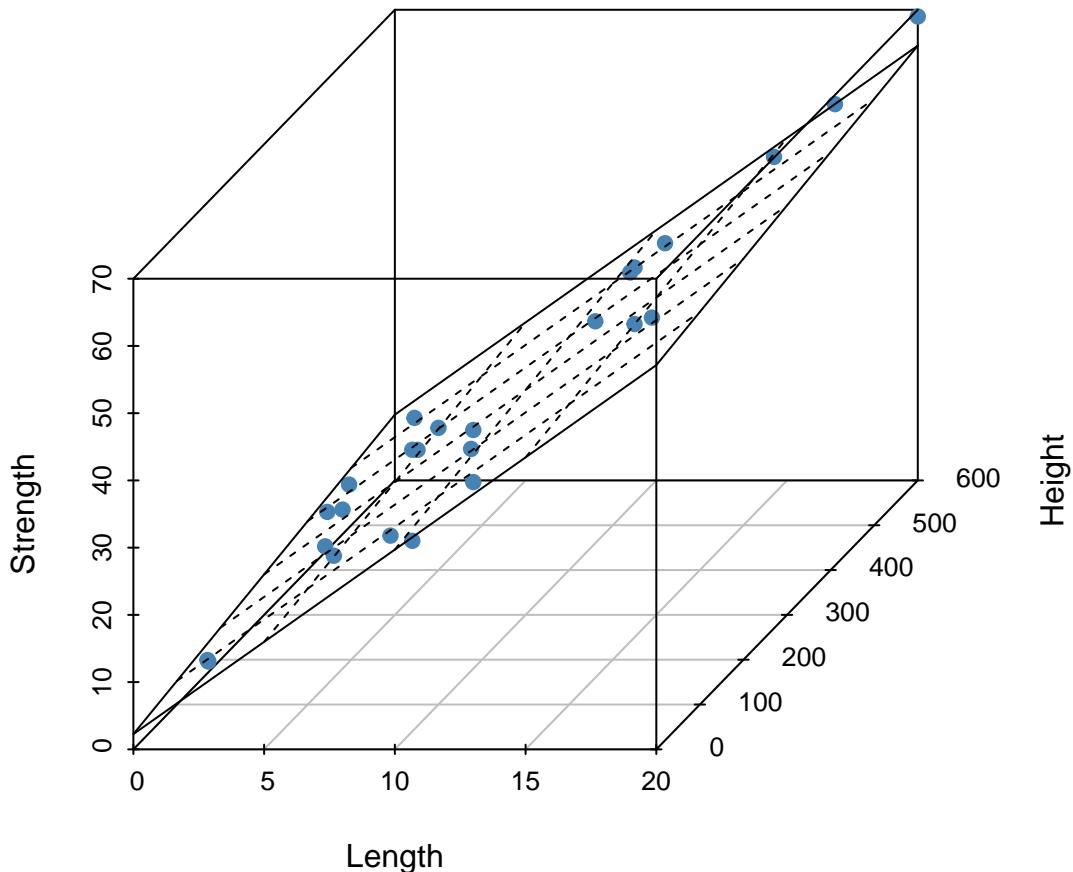
4.1 An Example: Wire Bond Strength Dataset

```
library(scatterplot3d)

par(mfrow = c(1,1))
s3d <- with(bond.data, scatterplot3d(
  x = length,
  y = height,
  z = strength,
  pch = 19,
  color = "steelblue",
  main = "3D Scatterplot: Strength vs. Length and Height",
  xlab = "Length",
  ylab = "Height",
  zlab = "Strength",
  angle = 60
))

fit <- lm(strength ~ length + height, data = bond.data)
s3d$plane3d(fit, lty.box = "solid")
```

3D Scatterplot: Strength vs. Length and Height



4.1.2 Model Fitting and Summary

We fit a multiple linear regression model with strength as the response variable and length and height as predictors.

```
fit <- lm(strength ~ length + height, data = bond.data)
summary(fit)
```

```
Call:
lm(formula = strength ~ length + height, data = bond.data)

Residuals:
    Min      1Q  Median      3Q     Max 
-3.865 -1.542 -0.362  1.196  5.841
```

```

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 2.263791   1.060066   2.136 0.044099 *
length       2.744270   0.093524  29.343 < 2e-16 ***
height      0.012528   0.002798   4.477 0.000188 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.288 on 22 degrees of freedom
Multiple R-squared:  0.9811,    Adjusted R-squared:  0.9794
F-statistic: 572.2 on 2 and 22 DF,  p-value: < 2.2e-16

```

The summary provides the ANOVA F-test for overall significance, R^2 , adjusted R^2 , and t-tests for individual coefficients.

4.1.3 Confidence Intervals and Model Components

```

## Confidence intervals
confint(fit)

             2.5 %     97.5 %
(Intercept) 0.065348613 4.46223426
length       2.550313061 2.93822623
height      0.006724246 0.01833138

```

```

## Fitted values and residuals
pred <- fitted.values(fit)
e <- resid(fit)
data.frame(y = bond.data$strength, y.hat = pred, e = e)

```

	y	y.hat	e
1	9.95	8.378721	1.57127871
2	24.45	25.596008	-1.14600783
3	31.75	33.954095	-2.20409488
4	35.00	36.596784	-1.59678413
5	25.02	27.913653	-2.89365294
6	16.86	15.746432	1.11356772
7	14.38	12.450260	1.92974001
8	9.60	8.403777	1.19622309
9	24.35	28.214999	-3.86499936
10	27.50	27.976292	-0.47629200

4 Multiple Linear Regression

```
11 17.08 18.402328 -1.32232830
12 37.00 37.461882 -0.46188206
13 41.95 41.458933  0.49106715
14 11.66 12.262343 -0.60234282
15 21.65 15.809071  5.84092866
16 17.89 18.251995 -0.36199456
17 69.00 64.665871  4.33412887
18 10.30 12.336831 -2.03683074
19 34.93 36.471506 -1.54150602
20 46.59 46.559789  0.03021107
21 44.88 47.060901 -2.18090138
22 54.12 52.561290  1.55871047
23 56.63 56.307784  0.32221591
24 22.13 19.982190  2.14780957
25 21.15 20.996264  0.15373580
```

```
## Covariance matrix and standard errors
cov.mat <- vcov(fit)
cov.mat
```

```
(Intercept)      length      height
(Intercept) 1.123740429 -3.921612e-02 -1.781991e-03
length       -0.039216122  8.746709e-03 -9.903775e-05
height        -0.001781991 -9.903775e-05  7.831149e-06
```

```
data.frame(std.error = sqrt(diag(cov.mat)))
```

```
std.error
(Intercept) 1.060066238
length      0.093523844
height      0.002798419
```

4.2 RSS-based Inference: F-test, and adjusted R^2

The General Linear Model

The general linear model is:

$$y = X\beta + \epsilon$$

- y : $n \times 1$ vector of responses
- X : $n \times p$ design matrix (first column often ones)
- β : $p \times 1$ parameter vector, where $p = k + 1$
- ϵ : $n \times 1$ error vector

4.2.1 RSS-Based Quantities

4.2.1.1 RSS-Based Quantities

Source	Sum of Squares	R^2	df	Mean Squares	F	SS_{adj}	$\hat{\sigma}^2$	R_{adj}^2
$x^\top \beta$	$\text{SSR} = \sum_{i=1}^n (\hat{y}_i - \bar{y})^2$	$\frac{\text{SSR}}{\text{SST}}$	k	$\text{MSR} = \frac{\text{SSR}}{k}$	MSR	SSR_{adj}	$\hat{\sigma}_{x^\top \beta}^2 = \frac{\text{SSR}_{\text{adj}}}{n-1}$	$\frac{\text{SSR}_{\text{adj}}}{\text{SST}} = 1 - \frac{\text{MSE}}{\text{MST}}$
ϵ	$\text{SSE} = \sum_{i=1}^n (y_i - \hat{y}_i)^2$	—	$n-p$	$\text{MSE} = \frac{\text{SSE}}{n-p}$	—	SSE	$\hat{\sigma}_\epsilon^2 = \text{MSE}$	—
y	$\text{SST} = \sum_{i=1}^n (y_i - \bar{y})^2$	—	$n-1$	$\text{MST} = \frac{\text{SST}}{n-1}$	—	SST	$\hat{\sigma}_y^2 = \text{MST}$	—

Interpretation of the $\hat{\sigma}^2$ Column

The $\hat{\sigma}^2$ column highlights how each sum of squares corresponds to an estimated variance. This view makes the adjusted coefficient of determination clear:

$$R_{\text{adj}}^2 = 1 - \frac{\hat{\sigma}_\epsilon^2}{\hat{\sigma}_y^2} = \frac{\hat{\sigma}_{x^\top \beta}^2}{\hat{\sigma}_y^2}.$$

Hence, the adjusted R^2 simply expresses the **proportion of total estimated variance** attributable to the fitted model $X\beta$ rather than the residual noise ϵ .

4.2.2 Remarks

4.2.2.1 Fundamental Identities

$$\begin{aligned} \text{SST} &= \text{SSR} + \text{SSE}, \\ \text{MST} &= \text{MSE} + \frac{\text{SSR}_{\text{adj}}}{n-1}. \end{aligned}$$

where

$$\text{SSR}_{\text{adj}} = (n - 1)MST - (n - p + k)\text{MSE} = \text{SST} - \text{SSE} - k \text{MSE} = \text{SSR} - k \text{MSE}.$$

4.2.2.2 Difference of $\hat{\sigma}^2$ and Mean Squares

The quantity $\hat{\sigma}^2$ represents the **estimated variance** associated with each component of the model. MSE and MST are the estimated variances of the ϵ and y itself. However, the MSR, although called **Mean Square for Regression (MSR)** is *NOT* an estimate of the variance or sample variance of $x^\top \beta$. The name of “mean” here is used to indicate a different thing. Its name “Mean Square” reflects that it is also an estimate estimate of noise variance σ^2 under $H_0: \beta = 0$:

$$E[\text{MSR} | H_0] = \sigma^2, \quad E[\text{MSR} | H_1] > \sigma^2.$$

Hence the F-statistic

$$F = \frac{\text{MSR}}{\text{MSE}}$$

is approximately equal to 1 subject to the variability as characterized with F-distribution with degree freedoms of k and $n - p$. This test is to test whether any regression coefficients are not equal to 0.

4.2.2.3 $\hat{\sigma}_{x^\top \beta}^2 = \frac{\text{SSR}_{\text{adj}}}{n-1}$

$\hat{\sigma}_{x^\top \beta}^2$ is an unbiased estimator of the variance of linear signal when x is regarded as a random variable. This can be seen from the following equations:

$$E[\text{SSR}] = k \sigma^2 + \beta^\top X^\top (I - J/n) X \beta, \quad E[\text{MSE}] = \sigma^2.$$

Hence,

$$\begin{aligned} E[\text{SSR}_{\text{adj}}] &= E[\text{SSR}] - k E[\text{MSE}] \\ &= \beta^\top X^\top (I - J/n) X \beta \\ &= \sum_{i=1}^n (\mu_i - \bar{\mu})^2, \end{aligned}$$

where

$$\begin{aligned} \mu_i &= x_i^\top \beta \\ \bar{\mu} &= \frac{1}{n} \sum_{i=1}^n \mu_i \end{aligned}$$

4.2 RSS-based Inference: F-test, and adjusted R^2

For fixed X , $\text{SSR}_{\text{adj}}/(n - 1)$ equals the **sample variance** of the true means $\{\mu_i\}$ over the observed design points. If the rows of X are independently sampled with covariance matrix Σ_X (the random- X model), then

$$\mathbb{E}_X \left[\frac{\text{SSR}_{\text{adj}}}{n - 1} \right] = \beta^\top \Sigma_X \beta = \text{Var}(x^\top \beta),$$

4.2.2.4 Connection to Rao-Blackwell Formula

The decomposition of $\hat{\sigma}^2$ is consistent with the **Rao-Blackwell formula** for total variance:

$$\text{Var}(y) = \text{Var}(E[y | x]) + E(\text{Var}[y | x]).$$

Here,

- $\text{Var}(E[y | x])$ corresponds to the **explained variation** due to the regression component $x^\top \beta$, and
- $E(\text{Var}[y | x])$ corresponds to the **residual variation** due to ϵ .

4.2.3 A Simulation Study to Understand the Distributions of RSS

Data Generating Model

For $n = 30$ and $p_{max} = 20$, simulate with either $H_0 : \beta = \mathbf{0}$ or H_1 where only $\beta_1 \neq 0$; $\epsilon_i \sim N(0, 1)$.

Sequence of Fitted Models

Model Name	# of Predictors (k)	# of Parameters (p)	R Formula
Model 0	0	1	$y \sim 1$
Model 1	2	3	$y \sim x_1 + x_2$
...
Final Model	20	21	$y \sim x_1 + \dots + x_20$

4 Multiple Linear Regression

4.2.3.1 When H_0 is true

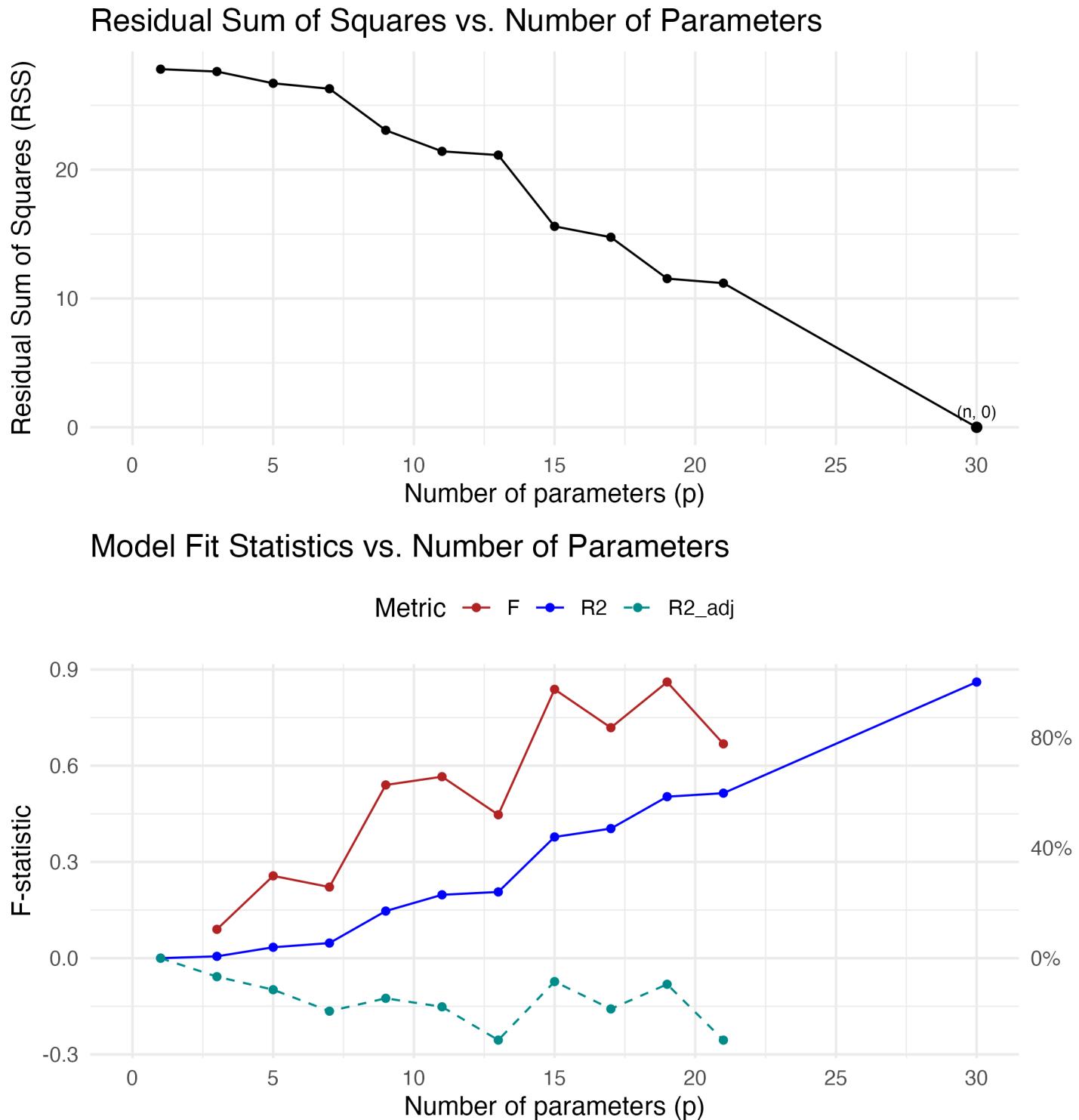
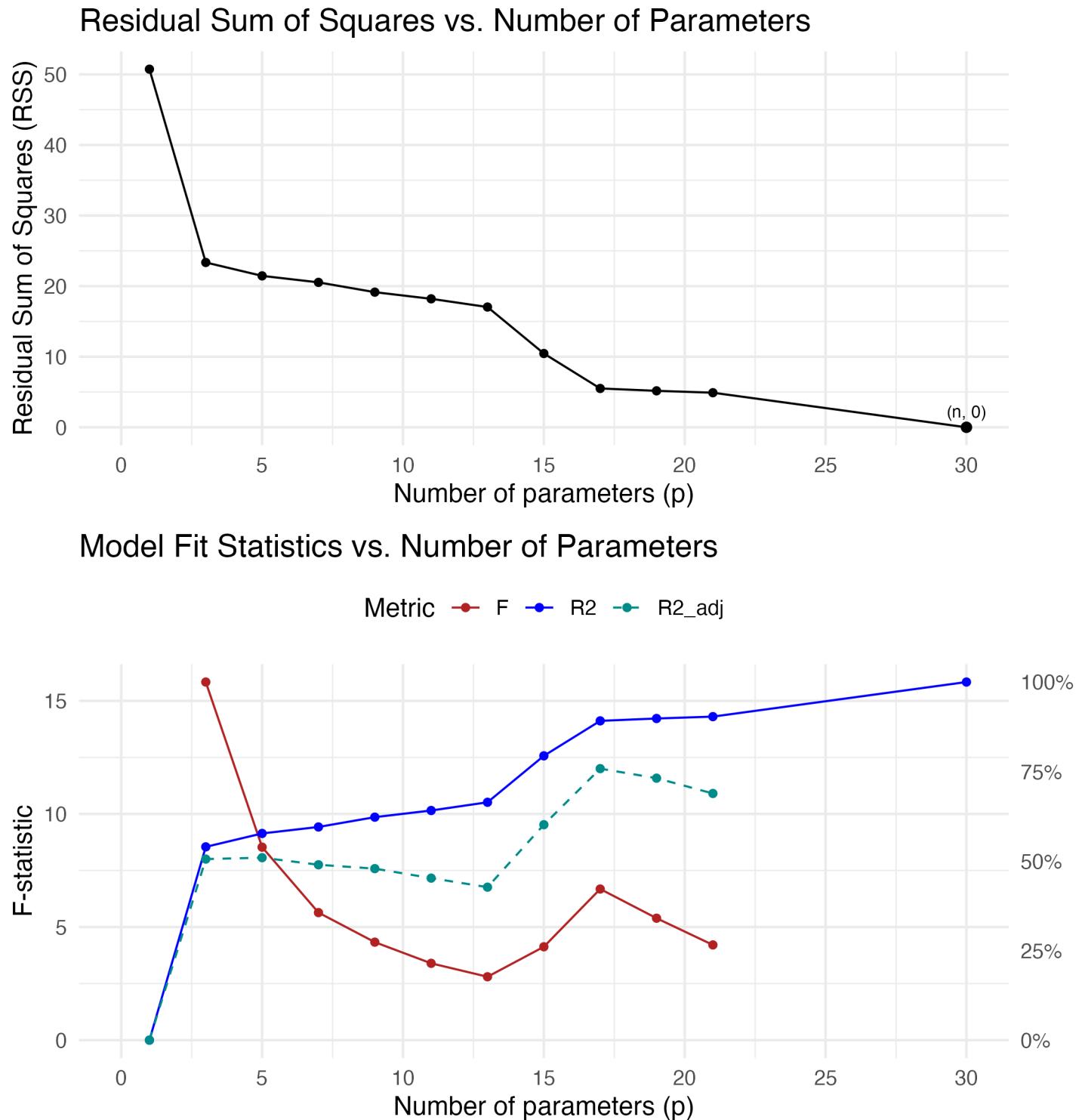


Figure 4.1: When H_0 is true: MP4 animation (HTML) or a representative static frame (PDF).

4 Multiple Linear Regression

4.2.3.2 When H_1 is true

Figure 4.2: When H_1 is true: MP4 animation (HTML) or a representative static frame (PDF).

4 Multiple Linear Regression

4.2.4 Example: Modelling Children Weight with Height and Age

```
## Data: Weight, height and age of children
wgt <- c(64, 71, 53, 67, 55, 58, 77, 57, 56, 51, 76, 68)
hgt <- c(57, 59, 49, 62, 51, 50, 55, 48, 42, 42, 61, 57)
age <- c(8, 10, 6, 11, 8, 7, 10, 9, 10, 6, 12, 9)
child.data <- data.frame(wgt, hgt, age)
```

4.2.4.1 Problem 1: Height then Age

```
fit_hgt_age <- lm(wgt ~ hgt + age, data = child.data)
summary(fit_hgt_age)
```

Call:

```
lm(formula = wgt ~ hgt + age, data = child.data)
```

Residuals:

Min	1Q	Median	3Q	Max
-6.8708	-1.7004	0.3454	1.4642	10.2336

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	6.5530	10.9448	0.599	0.5641
hgt	0.7220	0.2608	2.768	0.0218 *
age	2.0501	0.9372	2.187	0.0565 .

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 4.66 on 9 degrees of freedom

Multiple R-squared: 0.78, Adjusted R-squared: 0.7311

F-statistic: 15.95 on 2 and 9 DF, p-value: 0.001099

```
fit_hgt <- lm(wgt ~ hgt, data = child.data)
summary(fit_hgt)
```

Call:

```
lm(formula = wgt ~ hgt, data = child.data)
```

Residuals:

Min	1Q	Median	3Q	Max
-5.8736	-3.8973	-0.4402	2.2624	11.8375

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	6.1898	12.8487	0.482	0.64035
hgt	1.0722	0.2417	4.436	0.00126 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 5.471 on 10 degrees of freedom
 Multiple R-squared: 0.663, Adjusted R-squared: 0.6293
 F-statistic: 19.67 on 1 and 10 DF, p-value: 0.001263

```
anova(fit_hgt, fit_hgt_age)
```

Analysis of Variance Table

Model 1: wgt ~ hgt
 Model 2: wgt ~ hgt + age

Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
1	299.33				
2	195.43	1	103.9	4.7849	0.05649 .

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```
anova(fit_hgt_age)
```

Analysis of Variance Table

Response: wgt

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
hgt	1	588.92	588.92	27.1216	0.0005582 ***
age	1	103.90	103.90	4.7849	0.0564853 .
Residuals	9	195.43	21.71		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

4.2.4.2 Problem 2: Age then Height

4 Multiple Linear Regression

```
fit_age <- lm(wgt ~ age, data = child.data)
summary(fit_age)
```

Call:
lm(formula = wgt ~ age, data = child.data)

Residuals:

Min	1Q	Median	3Q	Max
-11.000	-3.911	1.143	4.071	10.000

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	30.5714	8.6137	3.549	0.00528 **
age	3.6429	0.9551	3.814	0.00341 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 6.015 on 10 degrees of freedom
Multiple R-squared: 0.5926, Adjusted R-squared: 0.5519
F-statistic: 14.55 on 1 and 10 DF, p-value: 0.003407

```
fit_age_hgt <- lm(wgt ~ age + hgt, data = child.data)
summary(fit_age_hgt)
```

Call:
lm(formula = wgt ~ age + hgt, data = child.data)

Residuals:

Min	1Q	Median	3Q	Max
-6.8708	-1.7004	0.3454	1.4642	10.2336

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	6.5530	10.9448	0.599	0.5641
age	2.0501	0.9372	2.187	0.0565 .
hgt	0.7220	0.2608	2.768	0.0218 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 4.66 on 9 degrees of freedom
Multiple R-squared: 0.78, Adjusted R-squared: 0.7311

```
F-statistic: 15.95 on 2 and 9 DF, p-value: 0.001099
```

```
anova(fit_age, fit_age_hgt)
```

Analysis of Variance Table

```
Model 1: wgt ~ age
Model 2: wgt ~ age + hgt
Res.Df   RSS Df Sum of Sq    F  Pr(>F)
1      10 361.86
2       9 195.43  1     166.43 7.6646 0.02181 *
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova(fit_age_hgt)
```

Analysis of Variance Table

```
Response: wgt
Df Sum Sq Mean Sq F value    Pr(>F)
age      1 526.39 526.39 24.2419 0.0008205 ***
hgt      1 166.43 166.43 7.6646 0.0218070 *
Residuals 9 195.43 21.71
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

4.2.5 Example: Wire bond strength

```
fit_len_hgt <- lm(strength ~ length + height, data = bond.data)
fit_hgt_len <- lm(strength ~ height+length, data = bond.data)
anova(fit_len_hgt)
```

Analysis of Variance Table

```
Response: strength
Df Sum Sq Mean Sq F value    Pr(>F)
length      1 5885.9 5885.9 1124.293 < 2.2e-16 ***
height      1 104.9 104.9  20.041 0.0001883 ***
Residuals 22 115.2      5.2
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

4 Multiple Linear Regression

```
anova(fit_hgt_len)
```

Analysis of Variance Table

Response: strength

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
height	1	1483.2	1483.2	283.32	4.731e-14 ***
length	1	4507.5	4507.5	861.01	< 2.2e-16 ***
Residuals	22	115.2	5.2		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```
summary(fit_hgt_len)
```

Call:

```
lm(formula = strength ~ height + length, data = bond.data)
```

Residuals:

Min	1Q	Median	3Q	Max
-3.865	-1.542	-0.362	1.196	5.841

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	2.263791	1.060066	2.136	0.044099 *
height	0.012528	0.002798	4.477	0.000188 ***
length	2.744270	0.093524	29.343	< 2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.288 on 22 degrees of freedom

Multiple R-squared: 0.9811, Adjusted R-squared: 0.9794

F-statistic: 572.2 on 2 and 22 DF, p-value: < 2.2e-16

```
summary(fit_len_hgt)
```

Call:

```
lm(formula = strength ~ length + height, data = bond.data)
```

Residuals:

Min	1Q	Median	3Q	Max
-----	----	--------	----	-----

4.3 Predictions for Mean Response and a Future Observation

```
-3.865 -1.542 -0.362  1.196  5.841

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 2.263791   1.060066   2.136 0.044099 *
length       2.744270   0.093524  29.343 < 2e-16 ***
height      0.012528   0.002798   4.477 0.000188 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.288 on 22 degrees of freedom
Multiple R-squared:  0.9811,    Adjusted R-squared:  0.9794
F-statistic: 572.2 on 2 and 22 DF,  p-value: < 2.2e-16
```

4.2.6 Relationship between t-test and partial F-test

- A t-test for a single coefficient is a special case of the partial F-test; the relationship is $F = t^2$ for 1 df in the numerator.
- The p-value from t-test (output of `summary(lm())`) is the same as anova test for: $H_0 : \beta_j = 0$ vs H_1 : all covariates have non-zero effects.

4.3 Predictions for Mean Response and a Future Observation

4.3.1 Confidence Interval for Mean Response

```
predict(fit, newdata = data.frame(length = 8, height = 275),
        interval = "confidence", level = 0.95)
```

```
fit      lwr      upr
1 27.6631 26.66324 28.66296
```

4.3.2 Prediction Interval for a New Observation

```
predict(fit, newdata = data.frame(length = 8, height = 275),
        interval = "prediction", level = 0.95)
```

```
fit      lwr      upr
1 27.6631 22.81378 32.51241
```

4.4 Model Diagnostics

4.4.1 Residual Calculations

```
residuals_df <- data.frame(
  hat_values = hatvalues(fit),
  ordinary_resid = resid(fit),
  standardized_resid = resid(fit) / sigma(fit),
  studentized_internal = rstandard(fit),
  studentized_external = rstudent(fit)
)
residuals_df
```

	hat_values	ordinary_resid	standardized_resid	studentized_internal
1	0.15728923	1.57127871	0.68673363	0.74808172
2	0.11164598	-1.14600783	-0.50086730	-0.53140990
3	0.14191905	-2.20409488	-0.96330846	-1.03992315
4	0.10188923	-1.59678413	-0.69788088	-0.73640435
5	0.04178381	-2.89365294	-1.26468257	-1.29196212
6	0.07486842	1.11356772	0.48668921	0.50599936
7	0.11806106	1.92974001	0.84340057	0.89807919
8	0.15608149	1.19622309	0.52281407	0.56911105
9	0.12797685	-3.86499936	-1.68921340	-1.80892479
10	0.04131672	-0.47629200	-0.20816532	-0.21260369
11	0.09253979	-1.32232830	-0.57792886	-0.60668127
12	0.05256700	-0.46188206	-0.20186740	-0.20739197
13	0.08202675	0.49106715	0.21462286	0.22400668
14	0.11291577	-0.60234282	-0.26325633	-0.27950939
15	0.07373697	5.84092866	2.55280118	2.65246601
16	0.08794942	-0.36199456	-0.15821117	-0.16566382
17	0.25934228	4.33412887	1.89424832	2.20104100
18	0.29287870	-2.03683074	-0.89020500	-1.05862725
19	0.09617553	-1.54150602	-0.67372136	-0.70866056
20	0.14726101	0.03021107	0.01320387	0.01429859
21	0.12963943	-2.18090138	-0.95317165	-1.02169558
22	0.13580052	1.55871047	0.68124063	0.73281364
23	0.18237610	0.32221591	0.14082575	0.15574183
24	0.10908869	2.14780957	0.93870874	0.99452024
25	0.07287021	0.15373580	0.06719084	0.06978142
		studentized_external		
1		0.74035927		
2		-0.52255660		
3		-1.04194550		

```

4      -0.72850799
5      -1.31305171
6       0.49726770
7       0.89397096
8       0.56016499
9      -1.91552083
10     -0.20792931
11     -0.59775404
12     -0.20282206
13      0.21910643
14     -0.27356920
15      3.14216850
16     -0.16195600
17      2.43521394
18     -1.06168251
19     -0.70040768
20      0.01396991
21     -1.02276424
22      0.72486668
23      0.15224503
24      0.99426154
25      0.06818458

```

4.4.2 Residual Plots

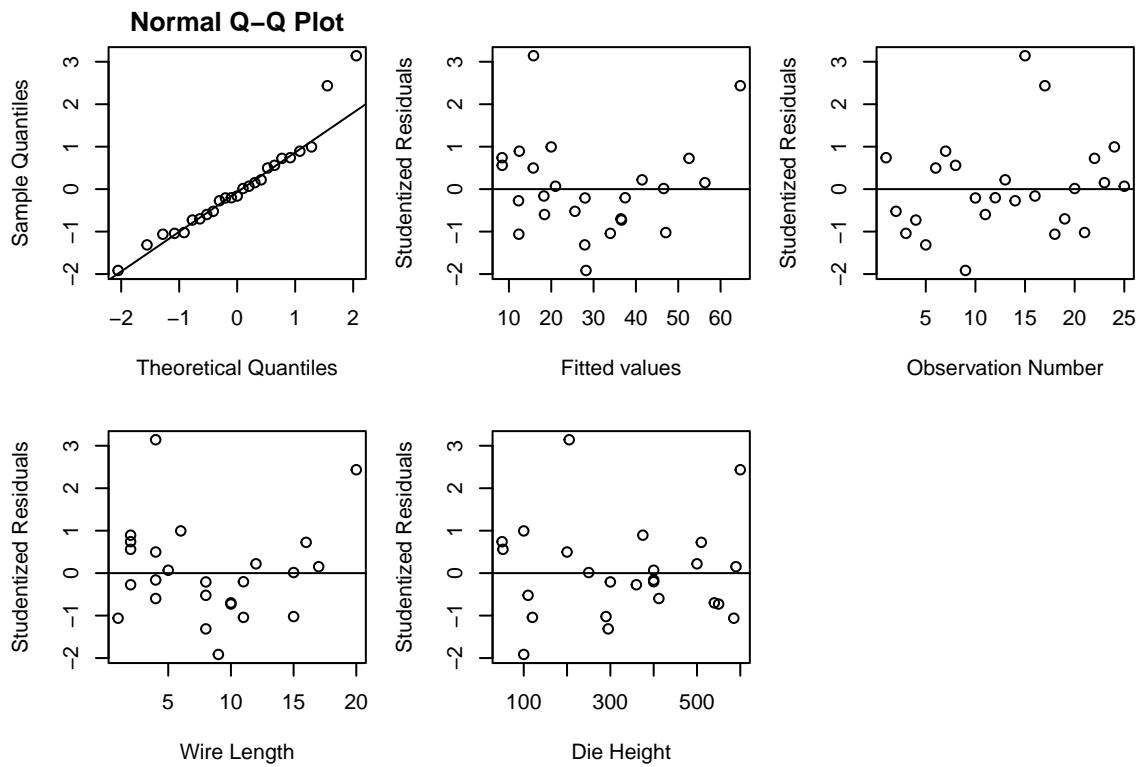
```

n <- nrow(bond.data)
r <- rstudent(fit)
y.hat <- fitted.values(fit)

par(mfrow = c(2, 3), mar = c(4, 4, 2, 1))
qqnorm(r, main = "Normal Q-Q Plot"); qqline(r)
plot(y.hat, r, xlab = "Fitted values", ylab = "Studentized Residuals"); abline(h = 0)
plot(1:n, r, xlab = "Observation Number", ylab = "Studentized Residuals"); abline(h = 0)
plot(bond.data$length, r, xlab = "Wire Length", ylab = "Studentized Residuals"); abline(h = 0)
plot(bond.data$height, r, xlab = "Die Height", ylab = "Studentized Residuals"); abline(h = 0)

```

4 Multiple Linear Regression



4.5 Influential Observations

```
influence_df <- data.frame(dffits = dffits(fit),
                             cook.D = cooks.distance(fit),
                             dfbetas(fit))
influence_df
```

	dffits	cook.D	X.Intercept.	length	height
1	0.319854702	3.481748e-02	0.3179493921	-0.100534181	-0.200085326
2	-0.185251548	1.183028e-02	-0.1403477437	-0.051464370	0.148315370
3	-0.423741713	5.962023e-02	-0.2219151046	-0.237135616	0.339340552
4	-0.245376811	2.050736e-02	0.0787635526	0.022343842	-0.184260891
5	-0.274191565	2.426179e-02	-0.1572410603	-0.009662357	0.055328303
6	0.141461363	6.906752e-03	0.1301249135	-0.058073567	-0.049408295
7	0.327082639	3.598953e-02	0.1479853099	-0.261848970	0.142220906
8	0.240902557	1.996750e-02	0.2394962591	-0.076575387	-0.149787102
9	-0.733818383	1.600749e-01	-0.5011686139	-0.283749099	0.605559181
10	-0.043165927	6.493384e-04	-0.0241138520	-0.001038287	0.007460760
11	-0.190885522	1.251125e-02	-0.0602003847	0.132053762	-0.102733745
12	-0.047774650	7.954763e-04	0.0017554145	-0.016926531	-0.008495572

```

13 0.065496465 1.494604e-03 -0.0224255162 0.017340091 0.033756253
14 -0.097602753 3.314830e-03 -0.0483552961 0.077880727 -0.038066705
15 0.886553487 1.866936e-01 0.8097463528 -0.374290156 -0.292048214
16 -0.050292599 8.821617e-04 -0.0177647675 0.034746758 -0.025275682
17 1.441003392 5.654455e-01 -0.8513738015 1.008880052 0.413618783
18 -0.683268805 1.547244e-01 -0.0218935465 0.521608456 -0.532432956
19 -0.228476293 1.781295e-02 0.0700729860 0.018004228 -0.167581999
20 0.005805362 1.176892e-05 0.0005613509 0.004752581 -0.003094588
21 -0.394724862 5.182743e-02 -0.0084618169 -0.324109965 0.170622396
22 0.287343813 2.812893e-02 -0.1326208213 0.183002776 0.076391058
23 0.071903545 1.803448e-03 -0.0412553376 0.040164093 0.030365108
24 0.347915085 4.036930e-02 0.3084561584 0.016541769 -0.262089402
25 0.019115733 1.275757e-04 0.0062730782 -0.011614674 0.009459029

```

4.5.1 Plotting with the olsrr Package

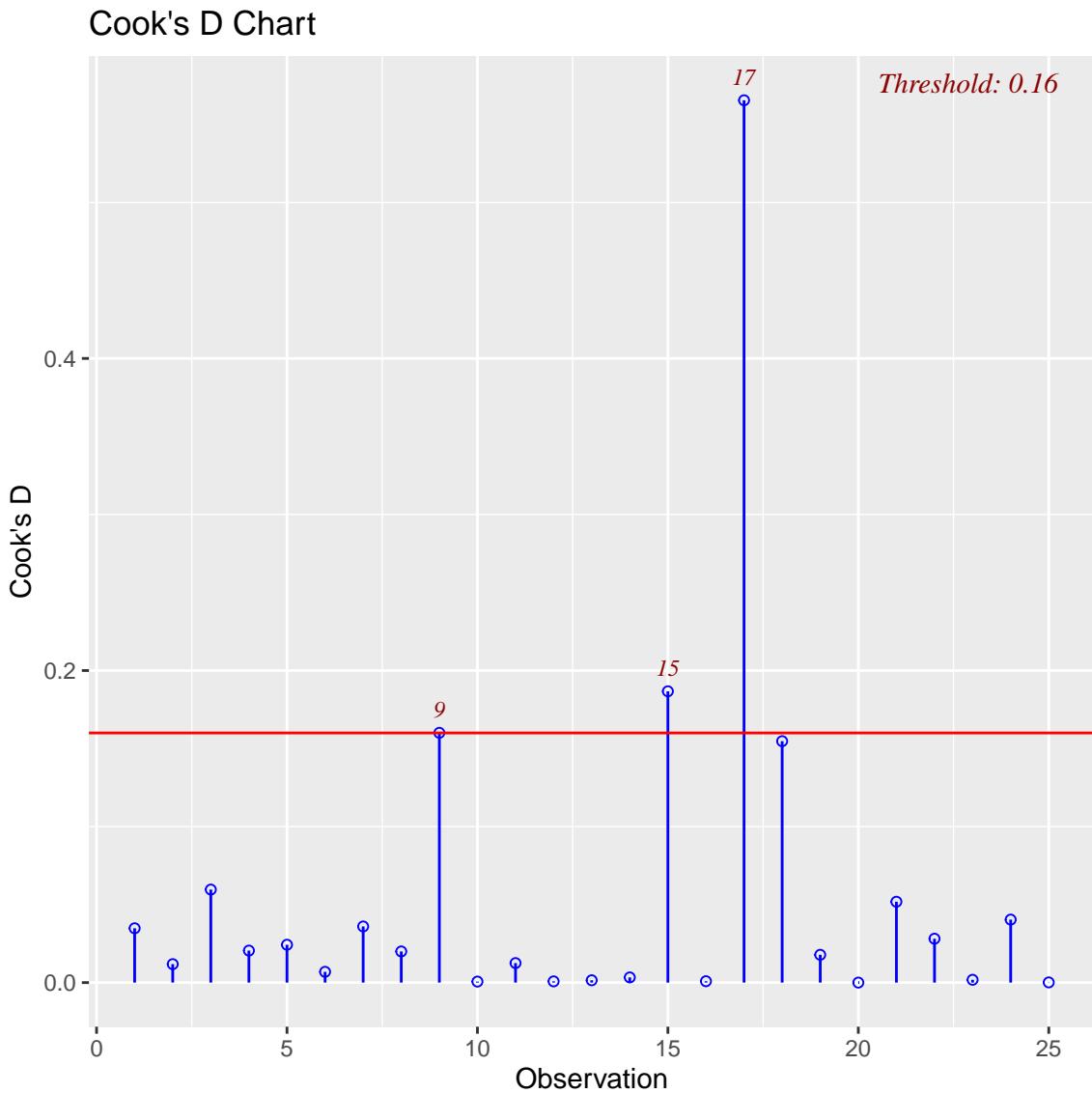
```

## install.packages("olsrr") # Run once if needed
library(olsrr)

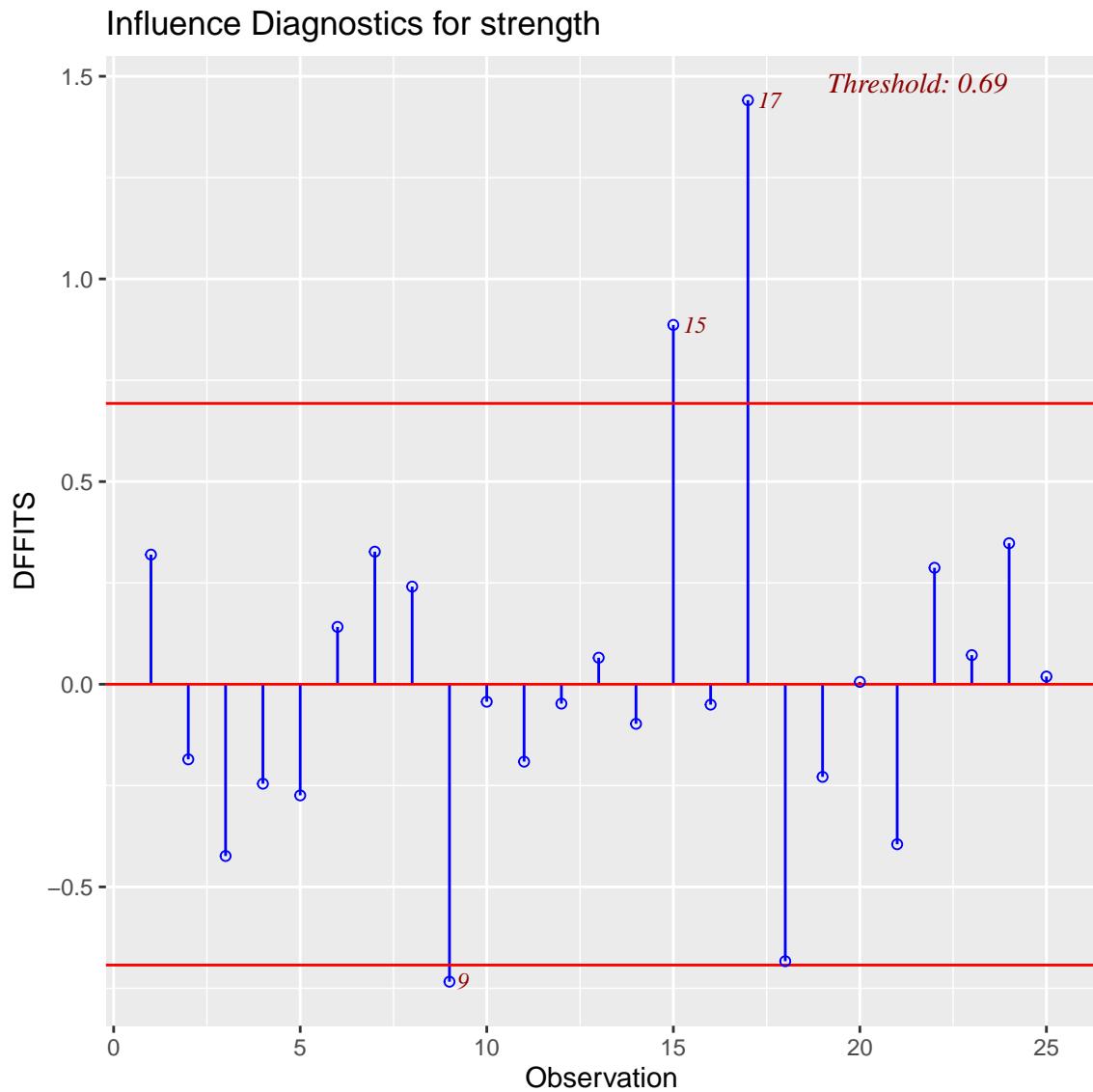
ols_plot_cooksd_chart(fit)

```

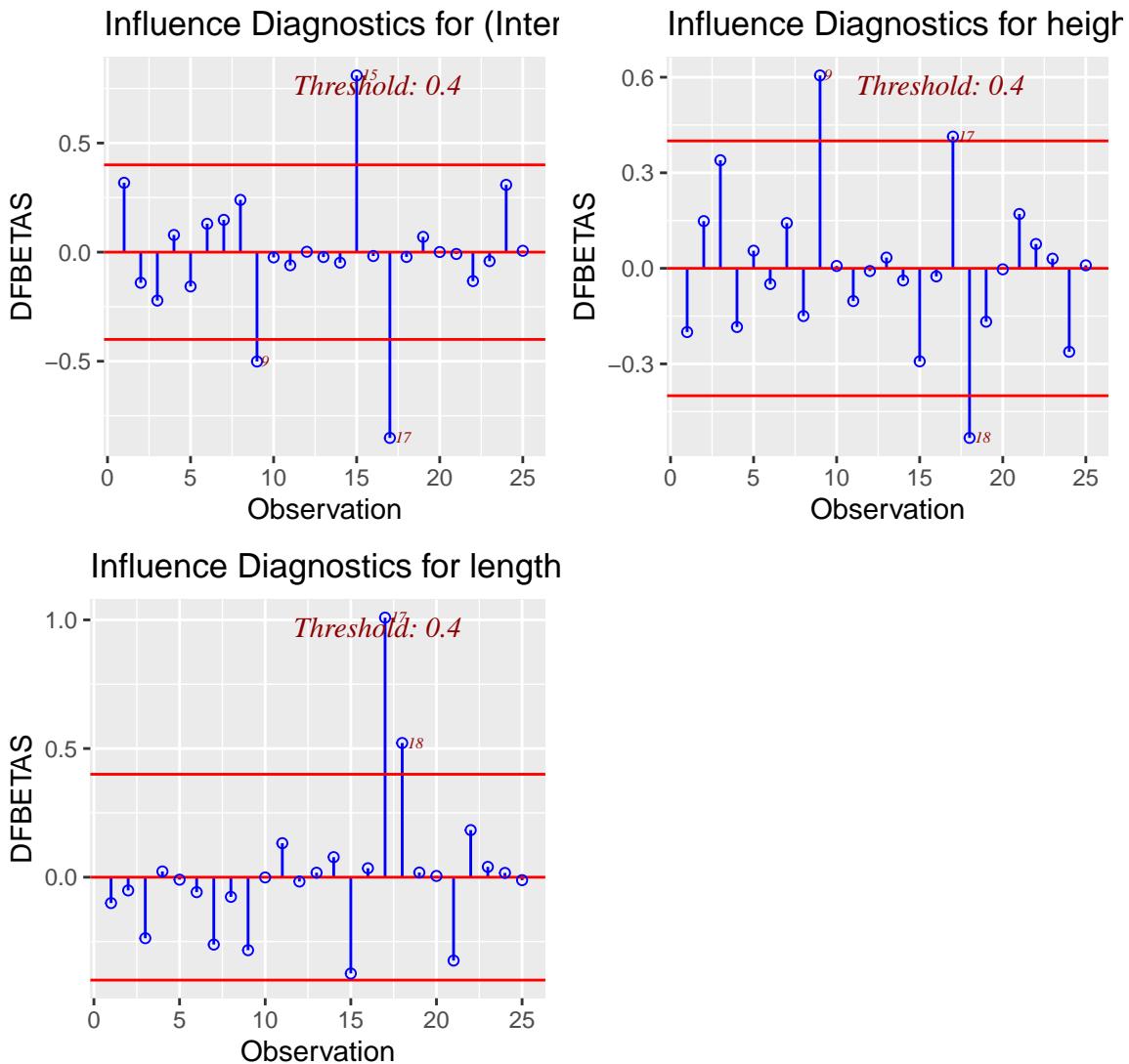
4 Multiple Linear Regression



```
ols_plot_dffits(fit)
```



```
ols_plot_dfbetas(fit)
```



4.6 Polynomial Regression

```
y <- c(1.81, 1.70, 1.65, 1.55, 1.48, 1.40, 1.30, 1.26, 1.24, 1.21, 1.20, 1.18)
x <- c(20, 25, 30, 35, 40, 50, 60, 65, 70, 75, 80, 90)
fit_poly <- lm(y ~ x + I(x^2))
summary(fit_poly)
```

Call:
`lm(formula = y ~ x + I(x^2))`

```

Residuals:
    Min      1Q   Median      3Q     Max
-0.0174763 -0.0065087  0.0001297  0.0071482  0.0151887

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 2.198e+00 2.255e-02 97.48 6.38e-15 ***
x           -2.252e-02 9.424e-04 -23.90 1.88e-09 ***
I(x^2)       1.251e-04 8.658e-06 14.45 1.56e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.01219 on 9 degrees of freedom
Multiple R-squared:  0.9975,    Adjusted R-squared:  0.9969
F-statistic: 1767 on 2 and 9 DF,  p-value: 2.096e-12

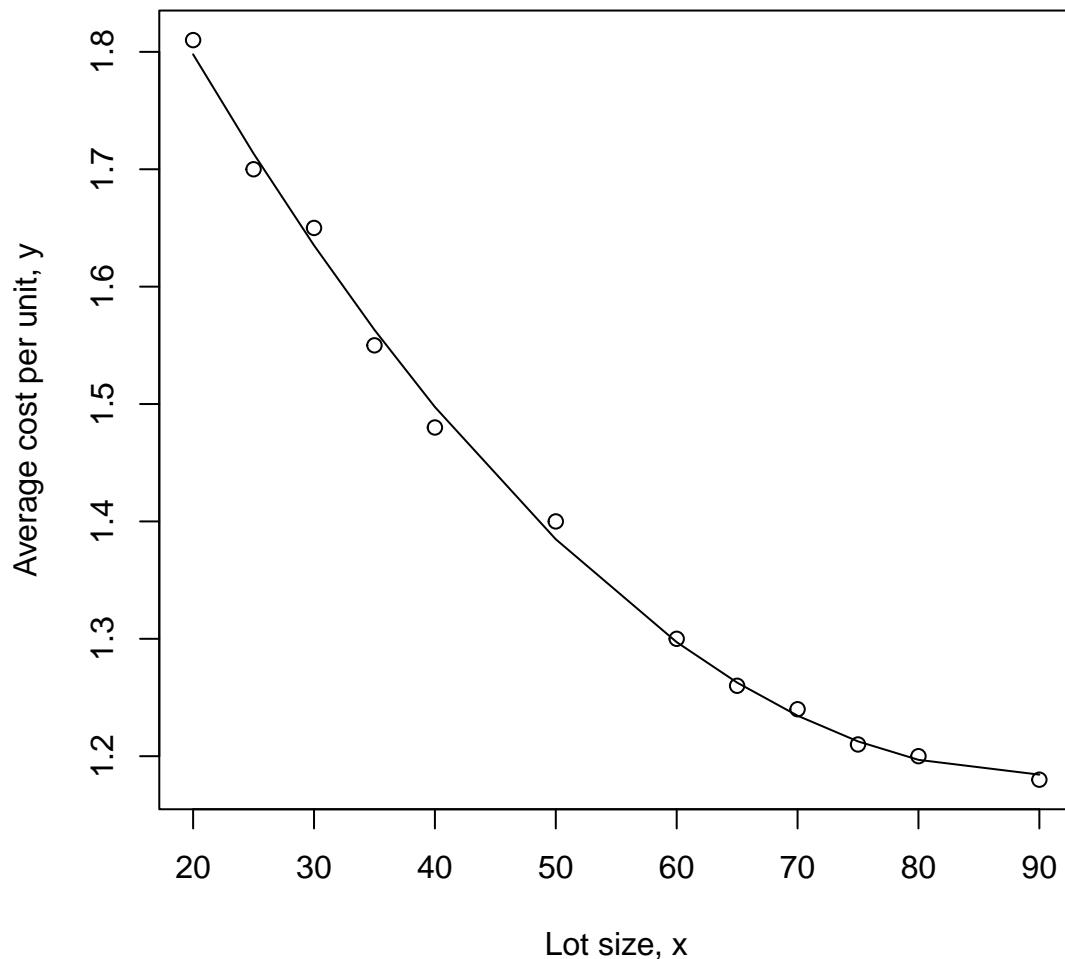
```

```

plot(x, y, xlab = "Lot size, x", ylab = "Average cost per unit, y")
lines(x, predict(fit_poly, newdata = data.frame(x = x)), type = "l")

```

4 Multiple Linear Regression



```
fit1 <- lm(y ~ x)
anova(fit1, fit_poly)
```

Analysis of Variance Table

```
Model 1: y ~ x
Model 2: y ~ x + I(x^2)
  Res.Df   RSS Df Sum of Sq    F    Pr(>F)
1     10 0.032340
2      9 0.001337  1  0.031002 208.67 1.564e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

4.7 Handling Categorical Variables with Dummy Variables

Investigate the common observation that males tend to have higher blood pressure than females of similar age.

4.7 Handling Categorical Variables with Dummy Variables

```
## Note: Update this path to your local file location  
sbpdata <- read.csv("sbpdata.csv")  
sbpdata
```

	sex	sbp	age
1	0	144	39
2	0	138	45
3	0	145	47
4	0	162	65
5	0	142	46
6	0	170	67
7	0	124	42
8	0	158	67
9	0	154	56
10	0	162	64
11	0	150	56
12	0	140	59
13	0	110	34
14	0	128	42
15	0	130	48
16	0	135	45
17	0	114	17
18	0	116	20
19	0	124	19
20	0	136	36
21	0	142	50
22	0	120	39
23	0	120	21
24	0	160	44
25	0	158	53
26	0	144	63
27	0	130	29
28	0	125	25
29	0	175	69
30	1	158	41
31	1	185	60
32	1	152	41
33	1	159	47
34	1	176	66
35	1	156	47
36	1	184	68
37	1	138	43
38	1	172	68
39	1	168	57

4 Multiple Linear Regression

```
40 1 176 65
41 1 164 57
42 1 154 61
43 1 124 36
44 1 142 44
45 1 144 50
46 1 149 47
47 1 128 19
48 1 130 22
49 1 138 21
50 1 150 38
51 1 156 52
52 1 134 41
53 1 134 18
54 1 174 51
55 1 174 55
56 1 158 65
57 1 144 33
58 1 139 23
59 1 180 70
60 1 165 56
61 1 172 62
62 1 160 51
63 1 157 48
64 1 170 59
65 1 153 40
66 1 148 35
67 1 140 33
68 1 132 26
69 1 169 61
```

4.7.1 Four Models Involving “sex”

4.7.1.1 Coincidence Model (Age Only)

```
## Ensure sex is a factor (labels will appear in the legend)
sbpdata$sex <- as.factor(sbpdata$sex)

## Fit (you already have this)
fit.age <- lm(sbp ~ age, data = sbpdata)

## Generate predictions over the observed age range
new_age <- seq(min(sbpdata$age, na.rm = TRUE),
```

```
max(sbpdata$age, na.rm = TRUE),
length.out = 200)
pred <- predict(fit.age, newdata = data.frame(age = new_age))

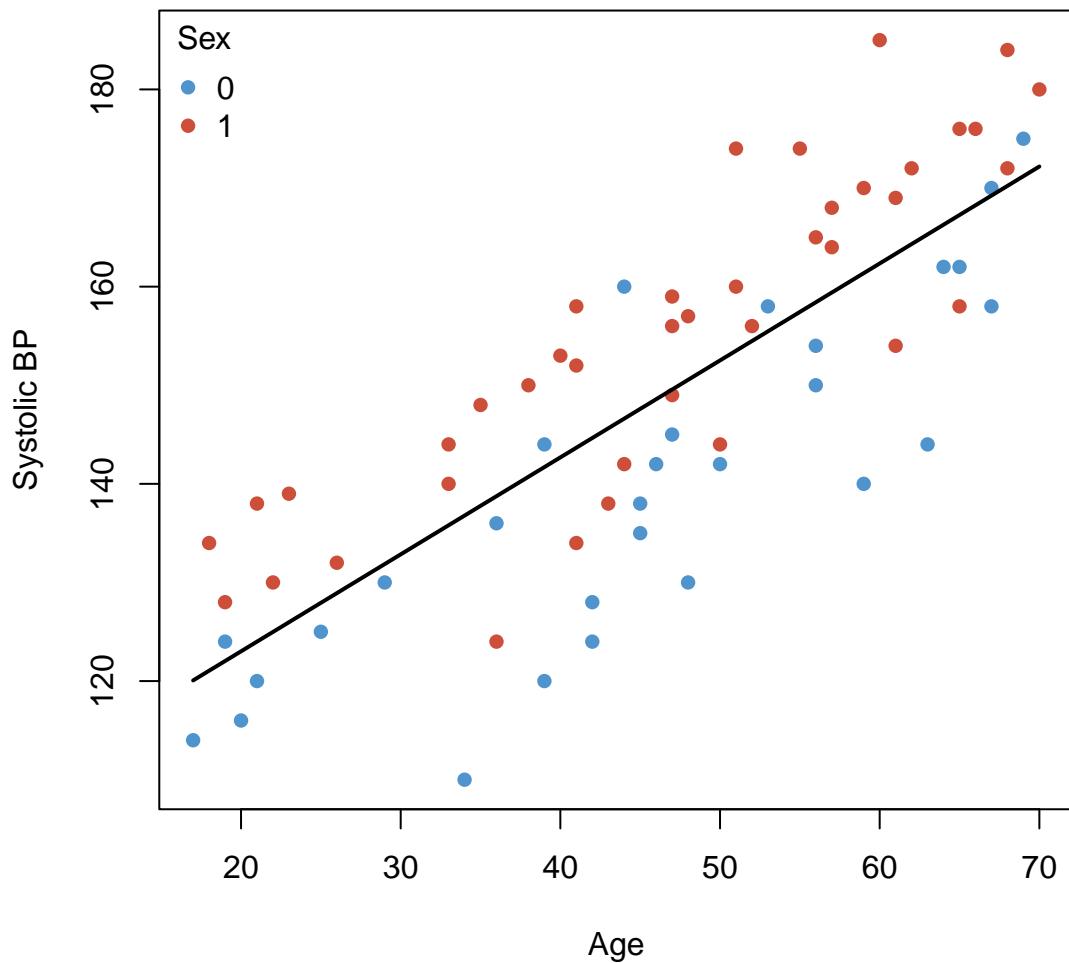
## Simple palette for the sex levels (works for 1-3 levels; expand if needed)
lev <- levels(sbpdata$sex)
cols <- setNames(c("steelblue3", "tomato3", "darkorchid3")[seq_along(lev)], lev)

## Scatter plot with colored points by sex
plot(sbp ~ age, data = sbpdata,
      col = cols[sbpdata$sex], pch = 16,
      xlab = "Age", ylab = "Systolic BP")

## Add predicted line
lines(new_age, pred, lwd = 2)

## Legend
legend("topleft", legend = lev, col = cols[lev], pch = 16, bty = "n", title = "Sex")
```

4 Multiple Linear Regression



```
data.frame(model.matrix(fit.age))
```

	X.Intercept.	age
1	1	39
2	1	45
3	1	47
4	1	65
5	1	46
6	1	67
7	1	42
8	1	67
9	1	56
10	1	64
11	1	56
12	1	59
13	1	34
14	1	42

4.7 Handling Categorical Variables with Dummy Variables

15	1	48
16	1	45
17	1	17
18	1	20
19	1	19
20	1	36
21	1	50
22	1	39
23	1	21
24	1	44
25	1	53
26	1	63
27	1	29
28	1	25
29	1	69
30	1	41
31	1	60
32	1	41
33	1	47
34	1	66
35	1	47
36	1	68
37	1	43
38	1	68
39	1	57
40	1	65
41	1	57
42	1	61
43	1	36
44	1	44
45	1	50
46	1	47
47	1	19
48	1	22
49	1	21
50	1	38
51	1	52
52	1	41
53	1	18
54	1	51
55	1	55
56	1	65
57	1	33
58	1	23
59	1	70

4 Multiple Linear Regression

```
60      1  56
61      1  62
62      1  51
63      1  48
64      1  59
65      1  40
66      1  35
67      1  33
68      1  26
69      1  61
```

```
print(anova(fit.age))
```

Analysis of Variance Table

```
Response: sbp
          Df  Sum Sq Mean Sq F value    Pr(>F)
age       1 14951.3 14951.3  121.27 < 2.2e-16 ***
Residuals 67  8260.5   123.3
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

4.7.1.2 Additive Effect Model (Age + Sex)

```
## Parallelism: H0: beta3=0 (Sex has additive effect)
fit.agePLUSsex <- lm(sbp ~ age + sex, data = sbpdata)

## Ensure sex is a factor for labeling/colors
sbpdata$sex <- factor(sbpdata$sex)

## Fit (additive: parallelism)
fit.agePLUSsex <- lm(sbp ~ age + sex, data = sbpdata)

## X-range and palette
ages <- seq(min(sbpdata$age, na.rm = TRUE),
            max(sbpdata$age, na.rm = TRUE),
            length.out = 200)
lev  <- levels(sbpdata$sex)
cols <- setNames(c("steelblue3", "tomato3", "darkorchid3") [seq_along(lev)], lev)

## Scatter with colored points by sex
plot(sbp ~ age, data = sbpdata,
```

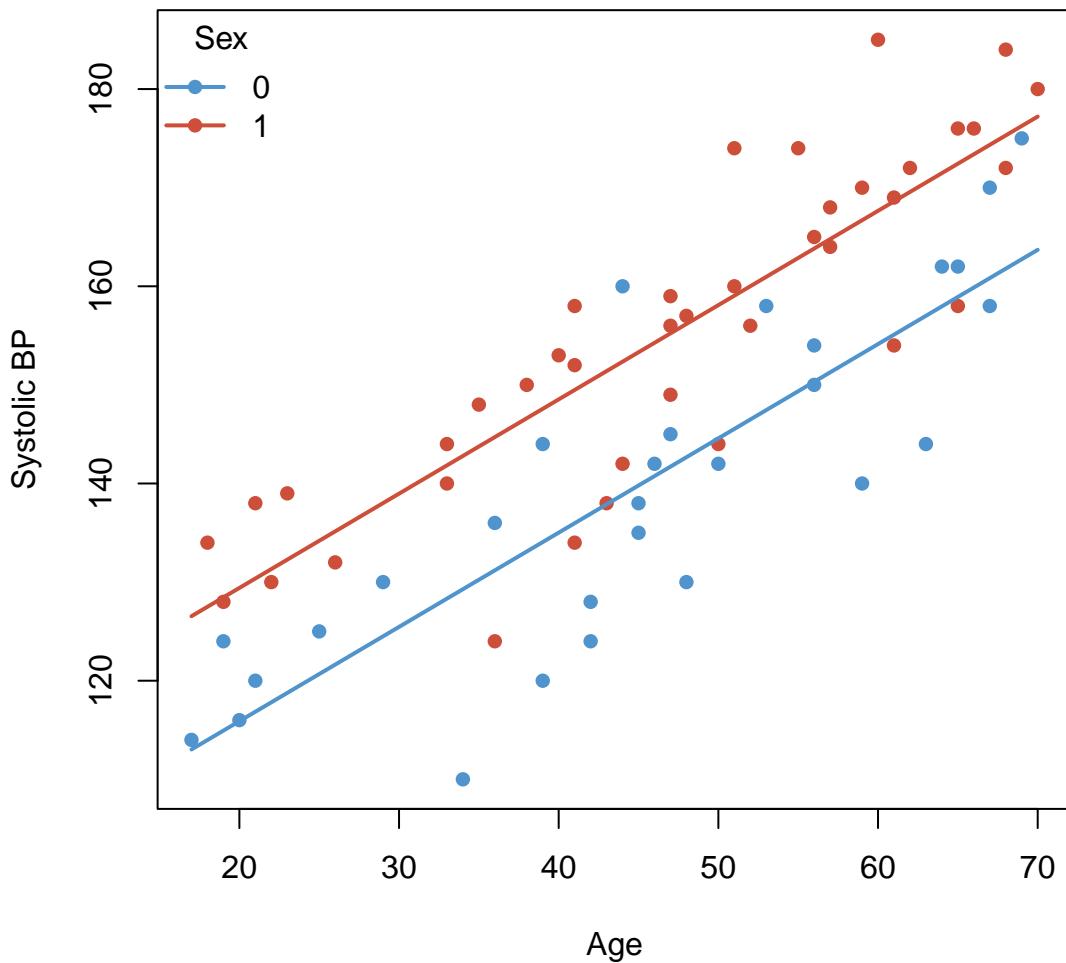
```

col = cols[sbpdata$sex], pch = 16,
xlab = "Age", ylab = "Systolic BP")

## Parallel fitted lines: one per sex (same slope, different intercepts)
for (sx in lev) {
  nd <- data.frame(age = ages, sex = factor(sx, levels = lev))
  yhat <- predict(fit.agePLUSsex, newdata = nd)
  lines(ages, yhat, col = cols[sx], lwd = 2)
}

## Legend
legend("topleft", legend = lev, col = cols[lev], pch = 16, lwd = 2, bty = "n", title = "Sex")

```



```
data.frame(model.matrix(fit.agePLUSsex))
```

```
X.Intercept. age sex1
```

4 Multiple Linear Regression

1	1	39	0
2	1	45	0
3	1	47	0
4	1	65	0
5	1	46	0
6	1	67	0
7	1	42	0
8	1	67	0
9	1	56	0
10	1	64	0
11	1	56	0
12	1	59	0
13	1	34	0
14	1	42	0
15	1	48	0
16	1	45	0
17	1	17	0
18	1	20	0
19	1	19	0
20	1	36	0
21	1	50	0
22	1	39	0
23	1	21	0
24	1	44	0
25	1	53	0
26	1	63	0
27	1	29	0
28	1	25	0
29	1	69	0
30	1	41	1
31	1	60	1
32	1	41	1
33	1	47	1
34	1	66	1
35	1	47	1
36	1	68	1
37	1	43	1
38	1	68	1
39	1	57	1
40	1	65	1
41	1	57	1
42	1	61	1
43	1	36	1
44	1	44	1
45	1	50	1

```

46      1  47    1
47      1  19    1
48      1  22    1
49      1  21    1
50      1  38    1
51      1  52    1
52      1  41    1
53      1  18    1
54      1  51    1
55      1  55    1
56      1  65    1
57      1  33    1
58      1  23    1
59      1  70    1
60      1  56    1
61      1  62    1
62      1  51    1
63      1  48    1
64      1  59    1
65      1  40    1
66      1  35    1
67      1  33    1
68      1  26    1
69      1  61    1

```

```
print(anova(fit.age, fit.agePLUSsex))
```

Analysis of Variance Table

```

Model 1: sbp ~ age
Model 2: sbp ~ age + sex
  Res.Df   RSS Df Sum of Sq    F    Pr(>F)
1     67 8260.5
2     66 5202.0  1    3058.5 38.805 3.701e-08 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

4.7.1.3 Varying Intercept and Varying Slope Model (Age + Sex + Age:Sex)

```

## Make sure sex is a factor (for colors/legend)
sbpdata$sex <- factor(sbpdata$sex)

```

4 Multiple Linear Regression

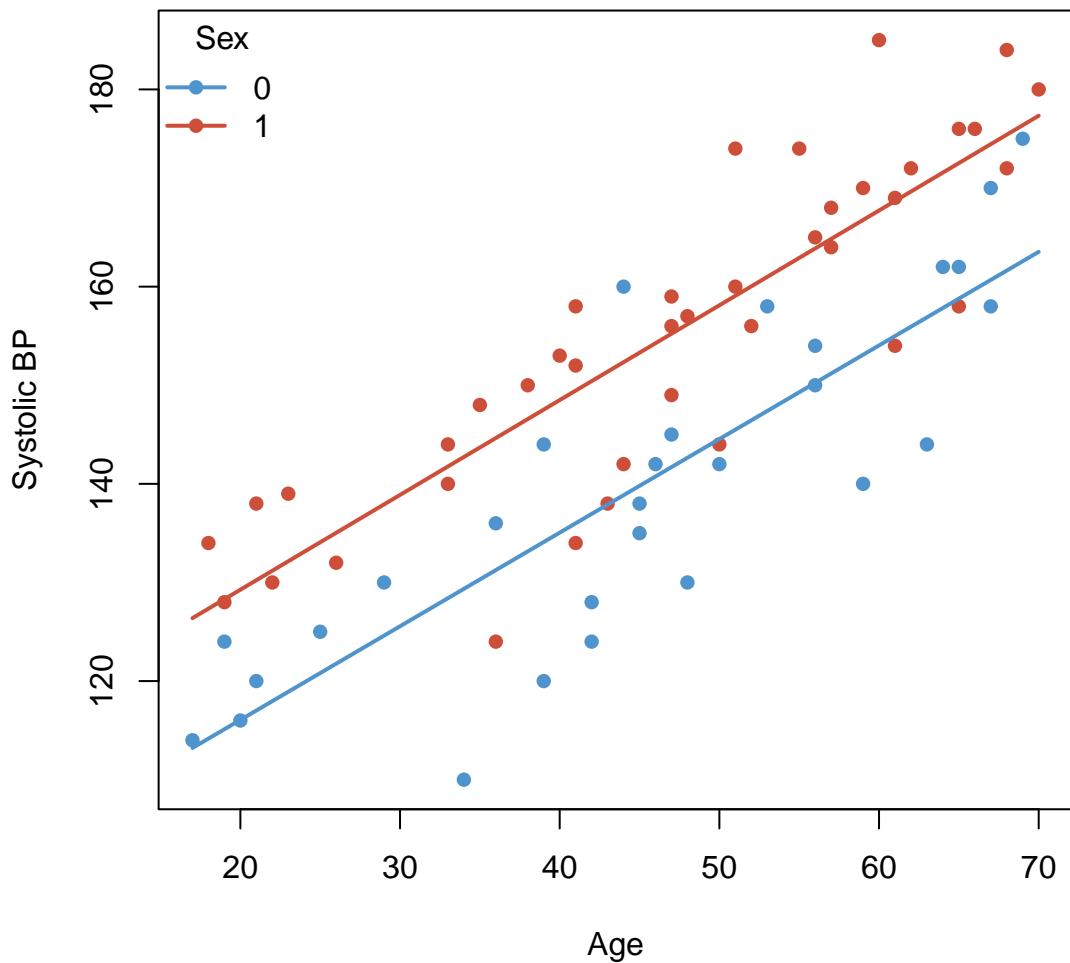
```
## Fit (interaction: different slopes by sex)
fit.age.TIMES.sex <- lm(sbp ~ age + sex + age:sex, data = sbpdata)

## Age grid and palette
ages <- seq(min(sbpdata$age, na.rm = TRUE),
             max(sbpdata$age, na.rm = TRUE),
             length.out = 200)
lev <- levels(sbpdata$sex)
cols <- setNames(c("steelblue3", "tomato3", "darkorchid3") [seq_along(lev)], lev)

## Scatter: color points by sex
plot(sbp ~ age, data = sbpdata,
      col = cols[sbpdata$sex], pch = 16,
      xlab = "Age", ylab = "Systolic BP")

## Fitted lines: one per sex (different slopes allowed)
for (sx in lev) {
  nd <- data.frame(age = ages, sex = factor(sx, levels = lev))
  yhat <- predict(fit.age.TIMES.sex, newdata = nd)
  lines(ages, yhat, col = cols[sx], lwd = 2)
}

## Legend
legend("topleft", legend = lev, col = cols[lev], pch = 16, lwd = 2, bty = "n", title = "Sex")
```



Model Matrix and ANOVA

```
data.frame(model.matrix(fit.age.TIMES.sex))
```

	X.Intercept.	age	sex1	age.sex1
1	1	39	0	0
2	1	45	0	0
3	1	47	0	0
4	1	65	0	0
5	1	46	0	0
6	1	67	0	0
7	1	42	0	0
8	1	67	0	0
9	1	56	0	0
10	1	64	0	0
11	1	56	0	0
12	1	59	0	0

4 Multiple Linear Regression

13	1	34	0	0
14	1	42	0	0
15	1	48	0	0
16	1	45	0	0
17	1	17	0	0
18	1	20	0	0
19	1	19	0	0
20	1	36	0	0
21	1	50	0	0
22	1	39	0	0
23	1	21	0	0
24	1	44	0	0
25	1	53	0	0
26	1	63	0	0
27	1	29	0	0
28	1	25	0	0
29	1	69	0	0
30	1	41	1	41
31	1	60	1	60
32	1	41	1	41
33	1	47	1	47
34	1	66	1	66
35	1	47	1	47
36	1	68	1	68
37	1	43	1	43
38	1	68	1	68
39	1	57	1	57
40	1	65	1	65
41	1	57	1	57
42	1	61	1	61
43	1	36	1	36
44	1	44	1	44
45	1	50	1	50
46	1	47	1	47
47	1	19	1	19
48	1	22	1	22
49	1	21	1	21
50	1	38	1	38
51	1	52	1	52
52	1	41	1	41
53	1	18	1	18
54	1	51	1	51
55	1	55	1	55
56	1	65	1	65
57	1	33	1	33

```

58      1 23   1    23
59      1 70   1    70
60      1 56   1    56
61      1 62   1    62
62      1 51   1    51
63      1 48   1    48
64      1 59   1    59
65      1 40   1    40
66      1 35   1    35
67      1 33   1    33
68      1 26   1    26
69      1 61   1    61

```

```
summary(fit.age.TIMES.sex)
```

```

Call:
lm(formula = sbp ~ age + sex + age:sex, data = sbpdata)

Residuals:
    Min      1Q  Median      3Q     Max 
-20.647 -3.410  1.254  4.314 21.153 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) 97.07708   5.17046 18.775 < 2e-16 ***
age          0.94932   0.10864  8.738 1.43e-12 ***
sex1         12.96144   7.01172  1.849  0.0691 .  
age:sex1     0.01203   0.14519  0.083  0.9342    
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 8.946 on 65 degrees of freedom
Multiple R-squared:  0.7759,    Adjusted R-squared:  0.7656 
F-statistic: 75.02 on 3 and 65 DF,  p-value: < 2.2e-16

```

```
print(anova(fit.age,fit.agePLUSsex,fit.age.TIMES.sex))
```

Analysis of Variance Table

```

Model 1: sbp ~ age
Model 2: sbp ~ age + sex
Model 3: sbp ~ age + sex + age:sex

```

4 Multiple Linear Regression

```

      Res.Df    RSS Df Sum of Sq      F    Pr(>F)
1       67 8260.5
2       66 5202.0  1   3058.52 38.2210 4.692e-08 ***
3       65 5201.4  1      0.55  0.0069     0.9342
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

4.7.1.4 Varying Slope, Equal Intercept Model (Age + Age:Sex)

```

## Make sure sex is a factor (for colors/legend)
sbpdata$sex <- factor(sbpdata$sex)

## Fit (interaction: different slopes by sex)
fit.equal.intercept <- lm(sbp ~ age + age:sex, data = sbpdata)

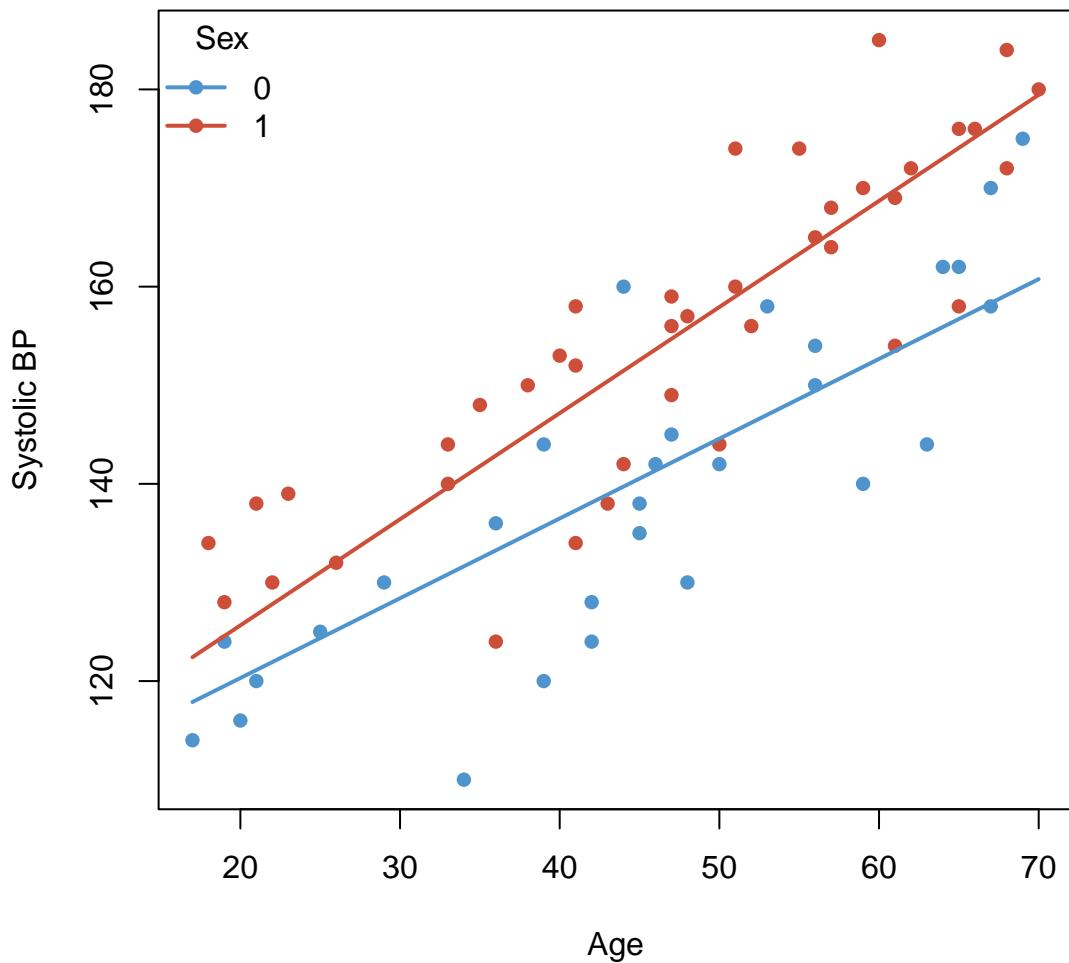
## Age grid and palette
ages <- seq(min(sbpdata$age, na.rm = TRUE),
             max(sbpdata$age, na.rm = TRUE),
             length.out = 200)
lev <- levels(sbpdata$sex)
cols <- setNames(c("steelblue3", "tomato3", "darkorchid3") [seq_along(lev)], lev)

## Scatter: color points by sex
plot(sbp ~ age, data = sbpdata,
      col = cols[sbpdata$sex], pch = 16,
      xlab = "Age", ylab = "Systolic BP")

## Fitted lines: one per sex (different slopes allowed)
for (sx in lev) {
  nd <- data.frame(age = ages, sex = factor(sx, levels = lev))
  yhat <- predict(fit.equal.intercept, newdata = nd)
  lines(ages, yhat, col = cols[sx], lwd = 2)
}

## Legend
legend("topleft", legend = lev, col = cols[lev], pch = 16, lwd = 2, bty = "n", title = "Sex")

```



4.7.2 Orders of Terms Matters in ANOVA and Warnings in Interpreting t-test Tables

```
fit.int <- lm(sbp ~ 1, data = sbpdata)
fit.sex <- lm(sbp ~ sex, data = sbpdata)

print(anova(fit.int, fit.age, fit.agePLUSsex, fit.age.TIMES.sex))
```

Analysis of Variance Table

Model	Term	Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
1	sbp ~ 1	68	23211.8				
2	sbp ~ age						
3	sbp ~ age + sex						
4	sbp ~ age + sex + age:sex						

4 Multiple Linear Regression

```
2      67  8260.5  1   14951.3 186.8390 < 2.2e-16 ***
3      66  5202.0  1    3058.5 38.2210 4.692e-08 ***
4      65  5201.4  1       0.5  0.0069     0.9342
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
print(anova(fit.int,fit.age,fit.equal.intercept, fit.age.TIMES.sex))
```

Analysis of Variance Table

```
Model 1: sbp ~ 1
Model 2: sbp ~ age
Model 3: sbp ~ age + age:sex
Model 4: sbp ~ age + sex + age:sex
  Res.Df   RSS Df Sum of Sq      F    Pr(>F)
1      68 23211.8
2      67  8260.5  1   14951.3 186.8390 < 2.2e-16 ***
3      66  5474.9  1    2785.6 34.8107 1.437e-07 ***
4      65  5201.4  1     273.4  3.4171  0.06907 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
print(anova(fit.int,fit.sex,fit.agePLUSsex, fit.age.TIMES.sex))
```

Analysis of Variance Table

```
Model 1: sbp ~ 1
Model 2: sbp ~ sex
Model 3: sbp ~ age + sex
Model 4: sbp ~ age + sex + age:sex
  Res.Df   RSS Df Sum of Sq      F    Pr(>F)
1      68 23211.8
2      67 19282.5  1    3929.2 49.1017 1.684e-09 ***
3      66  5202.0  1   14080.6 175.9583 < 2.2e-16 ***
4      65  5201.4  1       0.5  0.0069     0.9342
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(fit.age)
```

Call:

```

lm(formula = sbp ~ age, data = sbpdata)

Residuals:
    Min      1Q  Median      3Q     Max 
-26.782 -7.632   1.968   8.201  22.651 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) 103.34905   4.33190  23.86 <2e-16 ***  
age          0.98333   0.08929   11.01 <2e-16 ***  
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 11.1 on 67 degrees of freedom
Multiple R-squared:  0.6441, Adjusted R-squared:  0.6388 
F-statistic: 121.3 on 1 and 67 DF,  p-value: < 2.2e-16

```

```
summary(fit.equal.intercept)
```

Call:
`lm(formula = sbp ~ age + age:sex, data = sbpdata)`

Residuals:

Min	1Q	Median	3Q	Max
-21.6338	-4.3067	0.9922	4.9819	20.2753

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	104.12501	3.55578	29.283	< 2e-16 ***
age	0.80908	0.07918	10.219	3.14e-15 ***
age:sex1	0.26705	0.04608	5.795	2.09e-07 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 9.108 on 66 degrees of freedom
Multiple R-squared: 0.7641, Adjusted R-squared: 0.757
F-statistic: 106.9 on 2 and 66 DF, p-value: < 2.2e-16

```
summary(fit.agePLUSsex)
```

Call:

4 Multiple Linear Regression

```
lm(formula = sbp ~ age + sex, data = sbpdata)

Residuals:
    Min      1Q  Median      3Q     Max 
-20.705 -3.299  1.248  4.325 21.160 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) 96.77353   3.62085  26.727 < 2e-16 ***
age          0.95606   0.07153  13.366 < 2e-16 ***
sex1         13.51345  2.16932   6.229 3.7e-08 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 8.878 on 66 degrees of freedom
Multiple R-squared:  0.7759, Adjusted R-squared:  0.7691 
F-statistic: 114.2 on 2 and 66 DF,  p-value: < 2.2e-16
```

```
summary(fit.age.TIMES.sex)
```

```
Call:
lm(formula = sbp ~ age + sex + age:sex, data = sbpdata)

Residuals:
    Min      1Q  Median      3Q     Max 
-20.647 -3.410  1.254  4.314 21.153 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) 97.07708   5.17046 18.775 < 2e-16 ***
age          0.94932   0.10864  8.738 1.43e-12 ***
sex1         12.96144   7.01172  1.849  0.0691 .  
age:sex1     0.01203   0.14519  0.083  0.9342  
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 8.946 on 65 degrees of freedom
Multiple R-squared:  0.7759, Adjusted R-squared:  0.7656 
F-statistic: 75.02 on 3 and 65 DF,  p-value: < 2.2e-16
```

4.8 Model Building

```
library(olsrr)
## Note: Update this path to your local file location
wine <- read.csv("wine.csv")

model.wine <- lm(quality ~ ., data = wine)
```

4.8.1 All Possible Regression

```
ols_step_best_subset(model.wine)
```

Best Subsets Regression

Model Index	Predictors
1	flavor
2	flavor oakiness
3	aroma flavor oakiness
4	clarity aroma flavor oakiness
5	clarity aroma body flavor oakiness

Subsets Regression Summary

Model	Adj.		Pred		C(p)	AIC	SBIC	SBC	MSEP
	R-Square	R-Square	R-Square	R-Square					
1	0.6242	0.6137	0.5868	9.0436	130.0214	21.6859	134.9341	61.4102	
2	0.6611	0.6417	0.6058	6.8132	128.0901	20.1242	134.6404	57.0033	
3	0.7038	0.6776	0.6379	3.9278	124.9781	18.0702	133.1661	51.3383	
4	0.7147	0.6801	0.6102	4.6747	125.5480	19.2854	135.3736	50.9872	
5	0.7206	0.6769	0.587	6.0000	126.7552	21.0956	138.2183	51.5452	

AIC: Akaike Information Criteria

SBIC: Sawa's Bayesian Information Criteria

SBC: Schwarz Bayesian Criteria

MSEP: Estimated error of prediction, assuming multivariate normality

FPE: Final Prediction Error

HSP: Hocking's Sp

APC: Amemiya Prediction Criteria

4.8.2 Automated Stepwise Procedures

```
## Backward Elimination (alpha_out = 0.1)
ols_step_backward_p(model.wine, p_val = 0.1)
```

Stepwise Summary

Step	Variable	AIC	SBC	SBIC	R2	Adj. R2
0	Full Model	126.755	138.218	21.096	0.72060	0.67694
1	body	125.548	135.374	19.285	0.71471	0.68013
2	clarity	124.978	133.166	18.070	0.70377	0.67763

Final Model Output

Model Summary

R	0.839	RMSE	1.098
R-Squared	0.704	MSE	1.207
Adj. R-Squared	0.678	Coef. Var	9.338
Pred R-Squared	0.638	AIC	124.978
MAE	0.868	SBC	133.166

RMSE: Root Mean Square Error

MSE: Mean Square Error

MAE: Mean Absolute Error

AIC: Akaike Information Criteria

SBC: Schwarz Bayesian Criteria

ANOVA

	Sum of Squares	DF	Mean Square	F	Sig.
Regression	108.935	3	36.312	26.925	0.0000
Residual	45.853	34	1.349		
Total	154.788	37			

Parameter Estimates

model	Beta	Std. Error	Std. Beta	t	Sig	lower	upper
(Intercept)	6.467	1.333		4.852	0.000	3.759	9.176
aroma	0.580	0.262	0.307	2.213	0.034	0.047	1.113
flavor	1.200	0.275	0.603	4.364	0.000	0.641	1.758
oakiness	-0.602	0.264	-0.217	-2.278	0.029	-1.140	-0.065

```
## Forward Selection (alpha_in = 0.1)
ols_step_forward_p(model.wine, p_val = 0.1)
```

Stepwise Summary

Step	Variable	AIC	SBC	SBIC	R2	Adj. R2
0	Base Model	165.209	168.484	55.141	0.00000	0.00000
1	flavor	130.021	134.934	21.686	0.62417	0.61373
2	oakiness	128.090	134.640	20.124	0.66111	0.64175
3	aroma	124.978	133.166	18.070	0.70377	0.67763

Final Model Output

Model Summary

R	0.839	RMSE	1.098
R-Squared	0.704	MSE	1.207
Adj. R-Squared	0.678	Coef. Var	9.338
Pred R-Squared	0.638	AIC	124.978
MAE	0.868	SBC	133.166

RMSE: Root Mean Square Error

MSE: Mean Square Error

MAE: Mean Absolute Error

AIC: Akaike Information Criteria

SBC: Schwarz Bayesian Criteria

ANOVA

Sum of Squares	DF	Mean Square	F	Sig.

4 Multiple Linear Regression

Regression	108.935	3	36.312	26.925	0.0000
Residual	45.853	34	1.349		
Total	154.788	37			

Parameter Estimates

model	Beta	Std. Error	Std. Beta	t	Sig	lower	upper
(Intercept)	6.467	1.333		4.852	0.000	3.759	9.176
flavor	1.200	0.275	0.603	4.364	0.000	0.641	1.758
oakiness	-0.602	0.264	-0.217	-2.278	0.029	-1.140	-0.065
aroma	0.580	0.262	0.307	2.213	0.034	0.047	1.113

```
## Stepwise Regression (alpha_in = 0.1, alpha_out = 0.1)
ols_step_both_p(model.wine, p_enter = 0.1, p_remove = 0.1)
```

Stepwise Summary

Step	Variable	AIC	SBC	SBIC	R2	Adj. R2
0	Base Model	165.209	168.484	55.141	0.00000	0.00000
1	flavor (+)	130.021	134.934	21.686	0.62417	0.61373
2	oakiness (+)	128.090	134.640	20.124	0.66111	0.64175
3	aroma (+)	124.978	133.166	18.070	0.70377	0.67763

Final Model Output

Model Summary

R	0.839	RMSE	1.098
R-Squared	0.704	MSE	1.207
Adj. R-Squared	0.678	Coef. Var	9.338
Pred R-Squared	0.638	AIC	124.978
MAE	0.868	SBC	133.166

RMSE: Root Mean Square Error

MSE: Mean Square Error

MAE: Mean Absolute Error

AIC: Akaike Information Criteria

SBC: Schwarz Bayesian Criteria

ANOVA

	Sum of Squares	DF	Mean Square	F	Sig.
Regression	108.935	3	36.312	26.925	0.0000
Residual	45.853	34	1.349		
Total	154.788	37			

Parameter Estimates

model	Beta	Std. Error	Std. Beta	t	Sig	lower	upper
(Intercept)	6.467	1.333		4.852	0.000	3.759	9.176
flavor	1.200	0.275	0.603	4.364	0.000	0.641	1.758
oakiness	-0.602	0.264	-0.217	-2.278	0.029	-1.140	-0.065
aroma	0.580	0.262	0.307	2.213	0.034	0.047	1.113

4.9 Multicollinearity

4.9.1 A Simple Example

```
y <- c(19, 20, 37, 39, 36, 38)
x1 <- c(4, 4, 7, 7, 7.1, 7.1)
x2 <- c(16, 16, 49, 49, 50.4, 50.4)
cor(data.frame(x1, x2))
```

```
x1          x2
x1 1.0000000 0.9999713
x2 0.9999713 1.0000000
```

```
fit_multi <- lm(y ~ x1 + x2)
summary(fit_multi)
```

Call:

4 Multiple Linear Regression

```
lm(formula = y ~ x1 + x2)

Residuals:
 1   2   3   4   5   6 
-0.5  0.5 -1.0  1.0 -1.0  1.0 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) -156.056    117.158  -1.332   0.275    
x1           65.444     45.890   1.426   0.249    
x2          -5.389     4.152   -1.298   0.285    
                                                        
Residual standard error: 1.225 on 3 degrees of freedom
Multiple R-squared:  0.9897, Adjusted R-squared:  0.9829 
F-statistic: 144.3 on 2 and 3 DF,  p-value: 0.001043
```

```
fit1_multi <- lm(y ~ x1)
summary(fit1_multi)
```

```
Call:
lm(formula = y ~ x1)

Residuals:
 1   2   3   4   5   6 
-0.5260  0.4740 -0.1925  1.8075 -1.7814  0.2186 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) -4.0293    2.3332  -1.727   0.159    
x1           5.8888    0.3762  15.654 9.73e-05 ***  
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.325 on 4 degrees of freedom
Multiple R-squared:  0.9839, Adjusted R-squared:  0.9799 
F-statistic: 245.1 on 1 and 4 DF,  p-value: 9.725e-05
```

```
ols_vif_tol(fit_multi)
```

	Variables	Tolerance	VIF
1	x1	5.738191e-05	17427.09
2	x2	5.738191e-05	17427.09

4.9.2 VIFs in the Wine Quality Data

```
wine.x <- wine[, -ncol(wine)] # Assuming quality is the last column
cor(wine.x)
```

	clarity	aroma	body	flavor	oakiness
clarity	1.00000000	0.0619021	-0.3083783	-0.08515993	0.1832147
aroma	0.06190210	1.0000000	0.5489102	0.73656121	0.2016444
body	-0.30837826	0.5489102	1.0000000	0.64665917	0.1521059
flavor	-0.08515993	0.7365612	0.6466592	1.00000000	0.1797605
oakiness	0.18321471	0.2016444	0.1521059	0.17976051	1.0000000

```
## VIF using olsrr (data frame output)
ols_vif_tol(model.wine)
```

	Variables	Tolerance	VIF
1	clarity	0.7896462	1.266390
2	aroma	0.4199665	2.381143
3	body	0.4862649	2.056492
4	flavor	0.3728175	2.682277
5	oakiness	0.9118005	1.096731

4.9.3 VIFs in the Children Height Data

```
## Data: Weight, height and age of children
wgt <- c(64, 71, 53, 67, 55, 58, 77, 57, 56, 51, 76, 68)
hgt <- c(57, 59, 49, 62, 51, 50, 55, 48, 42, 42, 61, 57)
age <- c(8, 10, 6, 11, 8, 7, 10, 9, 10, 6, 12, 9)

fit_age_hgt <- lm(wgt ~ hgt + age, data = child.data)
ols_vif_tol(fit_age_hgt)
```

	Variables	Tolerance	VIF
1	hgt	0.6232021	1.604616
2	age	0.6232021	1.604616

5 Understanding the Leverage for Adjusting Residuals of OLS

A Simulation Illustration with R

5.1 Introduction

In statistical modeling, identifying data points that don't fit—the **outliers**—is a critical step. The most reliable tool for this job is the **externally studentized residual**. Its power comes from a simple, intuitive idea: to judge a point fairly, you shouldn't use that point when building your model. This is the core principle of **Leave-One-Out Cross-Validation (LOOCV)**.

This article provides a complete walkthrough of this essential concept. We'll start with the basic linear model, introduce the necessary notation, explore the flaws of simpler residuals, and then formally define and prove the equivalence of the conceptual and computational formulas for studentized residuals. Finally, we'll make it all concrete with a simple example.

5.2 The Linear Model

Our discussion is based on the standard multiple linear regression model. In matrix form, the relationship between a response vector \mathbf{Y} and a predictor matrix \mathbf{X} is:

$$\mathbf{Y} = \mathbf{X}\beta + \epsilon$$

where:

- \mathbf{Y} is an $n \times 1$ vector of the observed outcomes.
- \mathbf{X} is the $n \times p$ design matrix of predictor variables (where p is the number of coefficients, including the intercept).
- β is the $p \times 1$ vector of unknown true coefficients we want to estimate.
- ϵ is an $n \times 1$ vector of unobservable random errors, assumed to be independent and identically distributed with a mean of 0 and a variance of σ^2 .

5.3 Residuals for OLS

5.3.1 Our Notations

To discuss models fit with all data versus those with one point removed, we need clear notation.

Full Data Model (Using all n observations)

- $\hat{\beta}$: The estimated coefficient vector.
- \hat{y}_i : The predicted value for observation i from this model.
- e_i : The **ordinary residual** ($e_i = y_i - \hat{y}_i$).
- $\hat{\sigma}$: The estimated standard deviation of the errors (Residual Standard Error).
- h_{ii} : The **leverage** of observation i , a measure of how much its x-values influence the model.

Leave-One-Out (LOOCV) Model

- $\hat{\beta}_{-i}$: The coefficient vector estimated after **removing** observation i .
- $\hat{y}_{i,-i}$: The predicted value for observation i , from the model fit **without** observation i .
- $e_{i,-i}$: The **deleted residual** ($e_{i,-i} = y_i - \hat{y}_{i,-i}$).
- $\hat{\sigma}_{-i}$: The standard deviation of the errors estimated from the model fit **without** observation i .

5.3.2 Non-studentized Residuals

Before getting to the correct solution, it's crucial to understand why simpler methods of standardizing residuals are flawed.

5.3.2.1 The Ordinary Residual (e_i): Too Small and x_i Dependent

The most basic residual, e_i , is problematic for two key reasons.

An outlier has an undue influence on the model, pulling the regression line towards itself. This makes its own predicted value, \hat{y}_i , artificially close to its actual value, y_i . As a result, its residual, e_i , is **deceptively small** and doesn't reflect the true magnitude of the error.

The variance of an ordinary residual is not constant; it depends on the point's leverage. The variance can be derived from the hat matrix $H = X(X^\top X)^{-1}X^\top$. Since

$$\hat{y} = HY,$$

we have

$$e = (I - H)\epsilon. \quad (5.1)$$

Thus,

$$\text{Var}(e) = (I - H)\sigma^2(I - H)^\top = (I - H)\sigma^2. \quad (5.2)$$

Therefore, for the i th residual,

$$\text{Var}(e_i) = \sigma^2(1 - h_{ii}). \quad (5.3)$$

Since leverage (h_{ii}) is always greater than 0, the variance of an ordinary residual is always **less than the true error variance**, σ^2 . High-leverage points act as “anchors” for the line and have even smaller variance.

5.3.2.2 The LOOCV Residual ($e_{i,-i}$): Too large and x_i -Dependent Variance

The deleted residual, $e_{i,-i}$, solves the “too small” problem. Because the model isn’t influenced by the point it’s predicting, the residual is an honest measure of prediction error. However, its variance is still not constant. The variance of a deleted residual also depends on leverage, but in the opposite way.

$$\text{Var}(e_{i,-i}) = \frac{\sigma^2}{1 - h_{ii}} \quad (5.4)$$

From the key identity Equation 5.13,

$$e_{i,-i} = \frac{e_i}{1 - h_{ii}}. \quad (5.5)$$

Therefore,

$$\text{Var}(e_{i,-i}) = \frac{\text{Var}(e_i)}{(1 - h_{ii})^2} = \frac{\sigma^2(1 - h_{ii})}{(1 - h_{ii})^2} = \frac{\sigma^2}{1 - h_{ii}}. \quad (5.6)$$

Since $1 - h_{ii}$ is less than 1, the variance of a deleted residual is always **greater than the true error variance**, σ^2 . This is because it has two sources of randomness: the error in the point itself (y_i) and the error in the prediction ($\hat{y}_{i,-i}$).

5.3.3 Studentized Residuals

5.3.3.1 Studentized LOOCV (Deleted) Residual

The correct solution is to take the LOOCV residual and divide it by its true standard error, which properly accounts for its larger, x-dependent variance. This is the **externally studentized residual**, t_i , defined as follows:

$$t_i = \frac{e_{i,-i}}{\text{SE}(e_{i,-i})} = \frac{e_{i,-i}}{\frac{\hat{\sigma}_{-i}}{\sqrt{1-h_{ii}}}} \quad (5.7)$$

This final value is a reliable diagnostic. Under the null hypothesis that the observation is not an outlier, it follows a **Student’s t-distribution** with $n - p - 1$ degrees of freedom.

5 Understanding the Leverage for Adjusting Residuals of OLS

5.3.3.2 Studentized Full Data Residuals

Calculating the conceptual formula appears to require fitting n different regression models—a computationally expensive task. Fortunately, a mathematical identity allows us to calculate the exact same value using only the results from the single, full data model.

$$t_i = \frac{e_i}{\hat{\sigma}_{-i} \sqrt{1 - h_{ii}}} \quad (5.8)$$

This is not an approximation; it is an **exact algebraic rearrangement** of the conceptual definition.

5.3.3.3 Equivalence of Equation 5.8 and Equation 5.7

5.3.3.3.1 Proof of Equivalence

Let's start with the conceptual definition of the studentized LOOCV residuals Equation 5.7 and show how it transforms into Equation 5.8.

- Start with the conceptual LOOCV definition:

$$t_i = \frac{e_{i,-i}}{\text{SE}(e_{i,-i})} = \frac{e_{i,-i}}{\frac{\hat{\sigma}_{-i}}{\sqrt{1-h_{ii}}}} \quad (5.9)$$

- Substitute the key identity into the numerator:

$$t_i = \frac{\frac{e_i}{1-h_{ii}}}{\frac{\hat{\sigma}_{-i}}{\sqrt{1-h_{ii}}}} \quad (5.10)$$

- Simplify the complex fraction. We can do this by multiplying the numerator by the reciprocal of the denominator:

$$t_i = \frac{e_i}{1-h_{ii}} \cdot \frac{\sqrt{1-h_{ii}}}{\hat{\sigma}_{-i}} \quad (5.11)$$

- Cancel the terms. Since $1-h_{ii} = (\sqrt{1-h_{ii}})^2$, one of the $\sqrt{1-h_{ii}}$ terms in the denominator cancels with the term in the numerator. This leaves us with the computational shortcut formula:

$$t_i = \frac{e_i}{\hat{\sigma}_{-i} \sqrt{1-h_{ii}}} \quad (5.12)$$

This proves that the two formulas are mathematically identical. The computational shortcut is simply a clever algebraic rearrangement of the more intuitive LOOCV definition, allowing for efficient and accurate calculation.

□

Of course. Here is the modified .qmd file with the **standardized residual** (which you've labeled **STD-Full**) added to the table, the descriptions, and the plot.

The main changes include:

1. Adding the STD-Full column to the `residuals_df` data frame using R's `rstandard()` function.
2. Updating the list of calculated columns to include a description of **STD-Full**.
3. Modifying the plotting code to include **STD-Full** with its own distinct color and shape.

5.3.4 List of Residuals

In this article, we will compare the four residuals given as:

Table 5.1

Short Name	Full Name	Formula
NS-Full	Non-studentized Full-Data Residual	$\frac{e_i}{\hat{\sigma}}$
NS-LOO	Non-studentized LOOCV Residual	$\frac{e_{i,-i}}{\hat{\sigma}_{-i}}$
ST-LOO	Studentized LOOCV Residual	$\frac{e_{i,-i}}{\hat{\sigma}_{-i}/\sqrt{1-h_{ii}}}$
ST-Full	Studentized Full-Data Residual	$\frac{e_i}{\hat{\sigma}_{-i}\sqrt{1-h_{ii}}}$
STD-Full	Standardized (Internal Studentized) Residual	$\frac{e_i}{\hat{\sigma}\sqrt{1-h_{ii}}}$

5.3.5 Example of Various Residuals

5.3.5.1 The Linear Model

The simulation uses a **simple linear regression model** to describe the relationship between a single predictor variable, x_i , and a response variable, y_i . The underlying “true” model from which the data is generated is:

$$y_i = 2 + 3x_i + \epsilon_i$$

This means we have a true intercept of 2, a true slope of 3, and a random error term, ϵ_i , drawn from a normal distribution with a mean of 0 and a standard deviation of 5. One artificial outlier is added to this data to test the behavior of the different residual types. 5 unrelated predictors are added to the dataset.

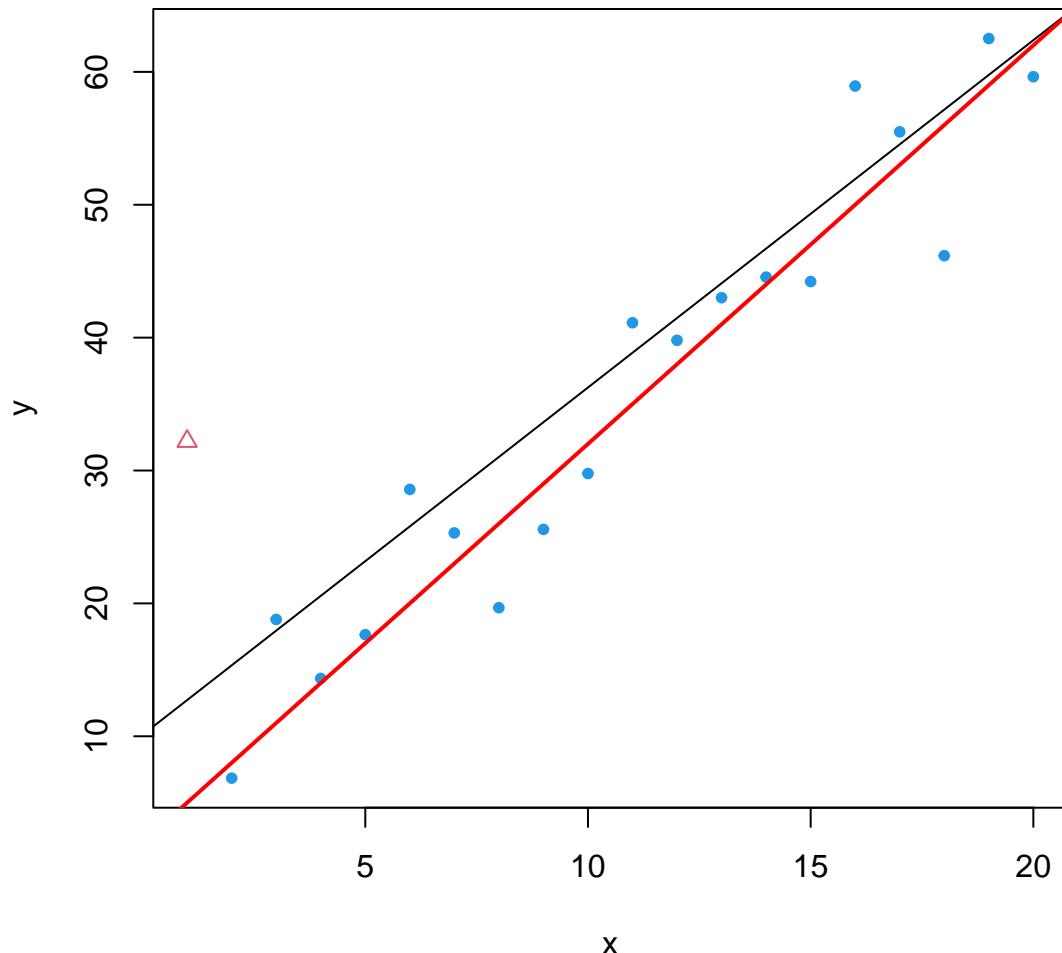
```
## Load libraries
library(dplyr)
library(knitr)

## -----
## 1) Data and full-model fit
## -----
set.seed(123)
n <- 20
x <- 1:n
```

5 Understanding the Leverage for Adjusting Residuals of OLS

```
y <- 2 + 3 * x + rnorm(n, mean = 0, sd = 5)
y[1] <- y[1] + 30
#y[11] <- y[11] - 30
o.index <- c(1)
flag.outlier <- rep(20, n)
flag.outlier[o.index] <- 2
full_data <- data.frame(x = x, replicate(5, rnorm (n)), y = y)

plot(y~x, data=full_data, pch= flag.outlier, col=flag.outlier)
fit <- lm(y~, data=full_data)
abline (fit)
abline (a=2, b=3, col="red", lwd=2)
```



5.3.5.2 Description of Calculated Columns

The final table compiles several important quantities calculated during the simulation. Here's what each column represents:

- x_i : The predictor variable, which is simply the index of the observation from 1 to 20.
- h_i : The **leverage** of the i -th observation. It measures how influential a point's x -value is in determining the model's fit. A higher value indicates a more influential point.
- e_i : The **ordinary residual**, calculated as the difference between the actual value (y_i) and the predicted value (\hat{y}_i) from the model fit on all data.
- $\hat{\sigma}$: The **residual standard error** (or Root Mean Square Error) of the full model, representing the typical size of an ordinary residual.
- $e_{i,-i}$: The **deleted (or LOOCV) residual**. This is the difference between the actual value (y_i) and the value predicted for it by a model that was fit on all other data *except* point i .
- $\hat{e}_{i,-i}$: This column shows the deleted residual calculated using the efficient algebraic shortcut ($e_i/(1 - h_{ii})$), verifying it's identical to the brute-force $e_{i,-i}$.
- $\hat{\sigma}_{-i}$: The **LOOCV residual standard error**, calculated from a model that was fit after removing observation i .
- $\tilde{\sigma}_{-i}$: The **LOOCV residual standard error**, calculated from the shortcut formula `?@eq-sigma_-i`.
- **NS-Full**: The **Non-studentized Full-Data Residual**, calculated as the ordinary residual divided by the full model's standard error ($e_i/\hat{\sigma}$).
- **NS-LOO**: The **Non-studentized LOOCV Residual**, calculated as the deleted residual divided by the corresponding LOOCV standard error ($e_{i,-i}/\hat{\sigma}_{-i}$).
- **STD-Full**: The **Standardized (or Internally Studentized) Residual**, calculated as the ordinary residual divided by its estimated standard error ($e_i/(\hat{\sigma}\sqrt{1 - h_{ii}})$). This is provided by R's `rstandard()` function.
- **ST-LOO**: The **Studentized LOOCV Residual**, calculated using the conceptual formula by dividing the deleted residual by its true standard error.
- **ST-Full**: The **Studentized Full-Data Residual**, calculated using the efficient shortcut formula, which is provided by R's `rstudent()` function.

```
library(kableExtra)

full_model <- lm(y ~ ., data = full_data)
p <- length(coef(full_model))
leverage     <- hatvalues(full_model)
e_full       <- resid(full_model)
sigma_hat_val <- summary(full_model)$sigma

rss_full <- sum(e_full^2)
df_loo <- n - p - 1
sigma_minus_i_shortcut <- sqrt((rss_full - (e_full^2 / (1 - leverage))) / df_loo)

## -----
## 2) LOOCV quantities (refit n times)
```

5 Understanding the Leverage for Adjusting Residuals of OLS

```

## -----
e_del_val <- numeric(n)
sigma_minus_i_val <- numeric(n)

for (i in 1:n) {
  loocv_model <- lm(y ~ ., data = full_data[-i, ])
  yhat_minus <- predict(loocv_model, newdata = full_data[i, , drop = FALSE])
  e_del_val[i] <- full_data$y[i] - yhat_minus
  sigma_minus_i_val[i] <- summary(loocv_model)$sigma
}

## -----
## 3) Assemble and round results
## -----
residuals_df <- data.frame(
  x = full_data$x,
  h = as.numeric(leverage),
  e_i = as.numeric(e_full),
  sigma_hat = as.numeric(sigma_hat_val),
  e_i_minus_i = as.numeric(e_del_val),
  e_i_minus_i_2 = e_full/(1-leverage),
  sigma_minus_i = as.numeric(sigma_minus_i_val),
  sigma_minus_i_shortcut = as.numeric(sigma_minus_i_shortcut),
  `NS-Full` = e_full / sigma_hat_val,
  `NS-LOO` = e_del_val / sigma_minus_i_val,
  `STD-Full` = rstandard(full_model), # <-- ADDED STANDARDIZED RESIDUAL
  `ST-LOO` = e_del_val / (sigma_minus_i_val / sqrt(1 - leverage)),
  `ST-Full` = rstudent(full_model)
) %>%
  mutate(across(where(is.numeric), ~ round(.x, 3)))

## 4) Create simple display names
display_names <- c("$x_i$", "$h_i$", "$e_i$", "$\hat{\sigma}$",
                  "$e_{i,-i}$", "$\hat{e}_{i,-i}$",
                  "$\hat{\sigma}_{-i}$", "$\tilde{\sigma}_{-i}$",
                  "NS-Full", "NS-LOO", "STD-Full", "ST-LOO", "ST-Full") # <-- ADDED LABEL

## 5) Display the table
## Conditional check for output format
if (knitr::is_html_output()) {
  ## --- Code for HTML Output (using kableExtra) ---
  knitr::kable(
    residuals_df,

```

```

caption = "Residual variants",
col.names = display_names,
align = "r",
#format="html",
escape = FALSE # Allows LaTeX and <br/> to render
)
} else {
## --- Code for PDF/Other Output (using kableExtra) ---
knitr::kable(
  residuals_df,
  caption = "Residual variants.",
  col.names = display_names,
  align = "r",
  format = "latex",
  booktabs = TRUE,
  escape = FALSE # Allows LaTeX and \\ to render
) %>%
  kable_styling(
    latex_options = "scale_down"
)
}
}

```

```

## Load libraries
library(dplyr)
library(tidyr)
library(ggplot2)
library(knitr)

## -----
## 3) Plotting Code with Updated Names
## -----


## Prepare data for plotting
plot_df <- residuals_df %>%
  ## Use the new, simple column names (R converts '-' to '.')
  select(
    x,
    NS.Full,
    NS.LOO,
    STD.Full, # <-- ADDED FOR PLOTTING
    ST.LOO,
    ST.Full
  ) %>%

```

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Table 5.2: Residual variants.

x_i	h_i	e_i	$\hat{\sigma}$	$e_{i,-i}$	$\hat{e}_{i,-i}$	$\hat{\sigma}_{-i}$	$\tilde{\sigma}_{-i}$	NS-Full	NS-LOO	STD-Full	ST-LOO	ST-Full
1	0.247	17.638	7.57	23.434	23.434	5.257	5.257	2.330	4.457	2.686	3.867	3.867
2	0.241	-7.909	7.57	-10.418	-10.418	7.431	7.431	-1.045	-1.402	-1.199	-1.222	-1.222
3	0.364	-3.271	7.57	-5.147	-5.147	7.790	7.790	-0.432	-0.661	-0.542	-0.527	-0.527
4	0.555	1.553	7.57	3.490	3.490	7.851	7.851	0.205	0.445	0.308	0.297	0.297
5	0.257	-1.515	7.57	-2.038	-2.038	7.863	7.863	-0.200	-0.259	-0.232	-0.223	-0.223
6	0.400	-0.400	7.57	-0.666	-0.666	7.878	7.878	-0.053	-0.085	-0.068	-0.066	-0.066
7	0.253	0.247	7.57	0.331	0.331	7.879	7.879	0.033	0.042	0.038	0.036	0.036
8	0.303	-8.972	7.57	-12.871	-12.871	7.243	7.243	-1.185	-1.777	-1.419	-1.484	-1.484
9	0.347	-8.394	7.57	-12.852	-12.852	7.287	7.287	-1.109	-1.764	-1.372	-1.425	-1.425
10	0.573	-5.696	7.57	-13.342	-13.342	7.467	7.467	-0.752	-1.787	-1.152	-1.168	-1.168
11	0.117	7.175	7.57	8.127	8.127	7.565	7.565	0.948	1.074	1.009	1.009	1.009
12	0.441	0.998	7.57	1.786	1.786	7.870	7.870	0.132	0.227	0.176	0.170	0.170
13	0.359	1.298	7.57	2.026	2.026	7.865	7.865	0.171	0.258	0.214	0.206	0.206
14	0.395	0.698	7.57	1.153	1.153	7.875	7.875	0.092	0.146	0.119	0.114	0.114
15	0.228	-1.221	7.57	-1.583	-1.583	7.869	7.869	-0.161	-0.201	-0.184	-0.177	-0.177
16	0.402	7.998	7.57	13.365	13.365	7.292	7.292	1.057	1.833	1.366	1.418	1.418
17	0.433	3.996	7.57	7.048	7.048	7.729	7.729	0.528	0.912	0.701	0.687	0.687
18	0.414	-3.369	7.57	-5.746	-5.746	7.776	7.776	-0.445	-0.739	-0.581	-0.566	-0.566
19	0.258	3.073	7.57	4.141	4.141	7.812	7.812	0.406	0.530	0.471	0.457	0.457
20	0.414	-3.930	7.57	-6.707	-6.707	7.739	7.739	-0.519	-0.867	-0.678	-0.663	-0.663

```

pivot_longer(
  cols = -x,
  names_to = "residual_type",
  values_to = "residual_value"
)

## Update the names in the mapping vectors
shape_map <- c(
  NS.Full    = 16,    # solid circle
  NS.LOO     = 1,     # hollow circle
  STD.Full   = 2,     # hollow triangle <-- ADDED
  ST.LOO     = 6,     # asterisk
  ST.Full    = 10     # asterisk
)

labels_map <- c(
  NS.Full    = "NS-Full",
  NS.LOO     = "NS-LOO",
  STD.Full   = "STD-Full", # <-- ADDED
  ST.LOO     = "ST-LOO",
  ST.Full    = "ST-Full"
)

color_map <- c(
  NS.Full    = "#1f77b4",  # blue
  NS.LOO     = "#ff7f0e",  # orange
  STD.Full   = "#9467bd",  # purple <-- ADDED
  ST.LOO     = "#2ca02c",  # green
  ST.Full    = "#d62728"   # red
)

## Generate the plot
ggplot(
  plot_df,
  aes(x = x, y = residual_value,
      shape = residual_type, color = residual_type, group = residual_type)
) +
  geom_hline(yintercept = 0, linetype = "dashed") +
  geom_point(size = 3, stroke = 1.2) + # Increased stroke for visibility
  scale_shape_manual(
    values = shape_map,
    breaks = names(labels_map),
    labels = unname(labels_map),
    name = "Residual Type"
)

```

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```
) +
scale_color_manual(
  values = color_map,
  breaks = names(labels_map),
  labels = unname(labels_map),
  name = "Residual Type"
) +
labs(
  title = "Five Residual Variants vs x",
  x = "x_i",
  y = "Residual value"
) +
theme_bw() +
theme(
  legend.position = "right",
  legend.title = element_text(face = "bold")
)
```

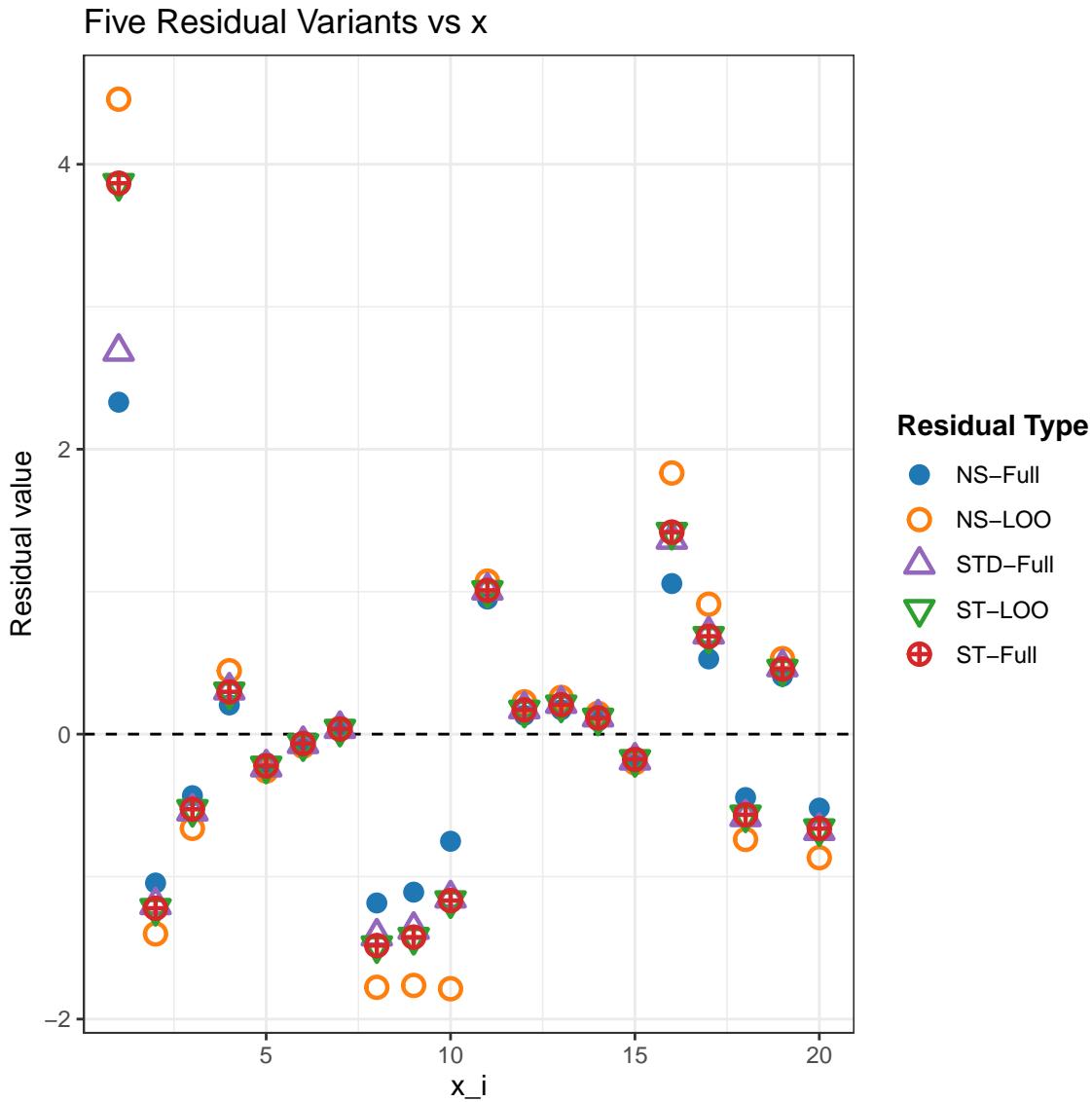


Figure 5.1: Five residual variants plotted against the predictor variable x.

From the above simulation results, we observe the following important facts:

- **Leverage and Influence:** The simulation confirms that leverage (h_{ii}) measures an observation's influence on the model's coefficients. It shows that points with higher leverage pull the regression line toward them, resulting in smaller, deceptively conservative full-data residuals (e_i).
- **Conservative Residuals:** The study highlights that the ordinary residual (e_i) is a “conservative” measure of error because its value for an outlier is systematically reduced by that same outlier’s influence on the model.
- **Identity Verification:** The numerical results validated the key algebraic identity that connects the full-data residual (e_i) to the leave-one-out (deleted) residual ($e_{i,-i}$), as well as the identity for calculating the

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LOOCV standard error ($\hat{\sigma}_{-i}$) from the full model's statistics. This demonstrates that all key LOOCV errors can be calculated efficiently from a single model fit.

- **Effective Studentization:** The final step of studentization, which uses leverage to properly scale the residuals, is shown to be crucial. It successfully transforms the residuals into a reliable diagnostic tool with a constant variance across all predictor values (x_i), causing them to behave much more like a standard normal or t-distribution.

5.4 Cook's Distance

5.4.1 Definition from the change in coefficients

Let $\hat{\beta}$ be the OLS estimate on all n cases and $\hat{\beta}_{(-i)}$ the estimate after deleting case i . With p parameters (including intercept) and $\hat{\sigma}^2 = \text{MSE}$,

$$D_i = \frac{(\hat{\beta} - \hat{\beta}_{(-i)})^\top (X^\top X) (\hat{\beta} - \hat{\beta}_{(-i)})}{p \hat{\sigma}^2}.$$

This measures how far the whole coefficient vector moves (in the $X^\top X$ metric) when case i is removed, scaled **per parameter**.

5.4.1.1 Express D_i via the studentized LOOCV residual: t_i

Let h_{ii} be the leverage and define the LOOCV quantities $e_{i,-i}$ and $\hat{\sigma}_{-i}$ from the model refit **without** case i . The externally studentized residual is

$$t_i = \frac{e_i}{\hat{\sigma}_{-i} \sqrt{1 - h_{ii}}} = \frac{e_{i,-i} \sqrt{1 - h_{ii}}}{\hat{\sigma}_{-i}}, \quad \text{since } e_{i,-i} = \frac{e_i}{1 - h_{ii}}.$$

Then Cook's distance can be written as

$$D_i = \frac{n-p}{p} \frac{h_{ii}}{1-h_{ii}} \frac{t_i^2}{(n-p-1) + t_i^2}.$$

5.4.1.2 Exact null distribution

Under the classical linear model,

$$t_i^2 \sim F_{1, \nu}, \quad \nu = n - p - 1.$$

Let

$$c_i = \frac{n-p}{p} \cdot \frac{h_{ii}}{1-h_{ii}}, \quad W_i = \frac{t_i^2}{\nu + t_i^2}.$$

Because $t_i^2 \sim F_{1,\nu}$,

$$W_i \sim \text{Beta}\left(\frac{1}{2}, \frac{\nu}{2}\right), \quad \frac{D_i}{c_i} = W_i \in [0, 1].$$

This yields exact, per-case p -values and critical values:

$$p_i = \Pr\left(W_i \geq \frac{D_i}{c_i}\right) = S_{\text{Beta}}\left(\frac{D_i}{c_i}; \frac{1}{2}, \frac{n-p-1}{2}\right),$$

$$d_{i,\alpha} = c_i q_{\text{Beta}}\left(1 - \alpha; \frac{1}{2}, \frac{n-p-1}{2}\right).$$

where S_{Beta} and q_{Beta} stand for the survival and quantile functions of Beta distribution.

5.4.1.3 The rough $4/n$ rule (average-leverage simplification)

Approximating a “typical” case by **average leverage** $h_{ii} \approx p/n$ gives

$$c_i = \frac{n-p}{p} \cdot \frac{p/n}{1-p/n} \approx 1.$$

The 95th percentile of W_i is

$$\text{qbeta}\left(0.95; \frac{1}{2}, \frac{n-p-1}{2}\right) \approx \frac{F_{1,\nu, 0.95}}{\nu + F_{1,\nu, 0.95}} \approx \frac{3.84}{n-p-1} \approx \frac{4}{n} \quad (\text{when } p \ll n).$$

So $4/n$ is a **rule-of-thumb** 95% cutoff for an **average-leverage** point; the exact leverage-aware cutoff is $d_{i,\alpha}$ above (larger for high h_{ii} , smaller for low h_{ii}).

5.4.1.4 Comparing $4/n$ rules with the actual critical values

```

library(dplyr)
library(tidyr)
library(knitr)
library(kableExtra)

## Exact 95% Cook's D cutoff under average leverage  $h_{ii} = p/n$  (so  $c_i = 1$ ):
##  $d_{\{i, 0.95\}} = qbeta(0.95; 1/2, (n - p - 1)/2)$ , valid when  $nu = n - p - 1 > 0$ 
cook_crit_avg <- function(n, p, alpha = 0.05) {
  nu <- n - p - 1
  if (nu <= 0) return(NA_real_)
  stats::qbeta(1 - alpha, shape1 = 0.5, shape2 = nu / 2)
}

## Grids (edit as needed)
n_vals <- c(20, 30, 50, 80, 100, 150, 200, 500)
p_vals <- c(2, 3, 5, 10, 15, 20, 30, 50)

df <- tidyverse::crossing(n = n_vals, p = p_vals) %>%
  mutate(valid = p <= n - 2,
        nu      = n - p - 1L) %>%
  rowwise() %>%
  mutate(
    cook_crit_95 = if (valid) cook_crit_avg(n, p, 0.05) else NA_real_,
    `4/n`         = 4 / n,
    ratio         = cook_crit_95 / `4/n`,
    `p/n`         = p / n
  ) %>%
  ungroup() %>%
  filter(valid) %>%
  select(n, p, `p/n`, nu, cook_crit_95, `4/n`, ratio) %>%
  mutate(
    `p/n`         = round(`p/n`, 3),
    cook_crit_95 = round(cook_crit_95, 6),
    `4/n`         = round(`4/n`, 6),
    ratio         = round(ratio, 4)
  )

if (knitr::is_html_output()) {
  ## HTML → Quarto prints `df` as a paged table and uses tbl-cap
  library(DT)
  DT::datatable(

```

```

df,
rownames = FALSE,
options = list(pageLength = 10, scrollX = TRUE),
caption = htmltools::tags$caption(
  style = 'caption-side: top; text-align: left;',
  htmltools::HTML("Exact 95% Cook's D critical value (average leverage $h_{ii}=p/n \\\Rightarrow c_i=1$"))
)
}
} else {
## Non-HTML (PDF, DOCX) → fall back to kable

knitr::kable(
  df,
  align = "r",
  booktabs = TRUE,
  caption = "Exact 95% Cook's D critical value (average leverage $h_{ii}=p/n \\\Rightarrow c_i=1$")
)
}
}

```

Table 5.3: Exact 95% Cook's D critical value (average leverage $h_{ii} = p/n \Rightarrow c_i = 1$) vs heuristic $4/n$.

n	p	p/n	nu	cook_crit_95	4/n	ratio
20	2	0.100	17	0.207508	0.200000	1.0375
20	3	0.150	16	0.219284	0.200000	1.0964
20	5	0.250	14	0.247316	0.200000	1.2366
20	10	0.500	9	0.362487	0.200000	1.8124
20	15	0.750	4	0.658372	0.200000	3.2919
30	2	0.067	27	0.134893	0.133333	1.0117
30	3	0.100	26	0.139791	0.133333	1.0484
30	5	0.167	24	0.150733	0.133333	1.1305
30	10	0.333	19	0.187366	0.133333	1.4052
30	15	0.500	14	0.247316	0.133333	1.8549
30	20	0.667	9	0.362487	0.133333	2.7187
50	2	0.040	47	0.079282	0.080000	0.9910
50	3	0.060	46	0.080951	0.080000	1.0119
50	5	0.100	44	0.084510	0.080000	1.0564
50	10	0.200	39	0.094944	0.080000	1.1868
50	15	0.300	34	0.108314	0.080000	1.3539
50	20	0.400	29	0.126058	0.080000	1.5757
50	30	0.600	19	0.187366	0.080000	2.3421
80	2	0.025	77	0.048973	0.050000	0.9795
80	3	0.038	76	0.049605	0.050000	0.9921
80	5	0.062	74	0.050920	0.050000	1.0184
80	10	0.125	69	0.054533	0.050000	1.0907

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n	p	p/n	nu	cook_crit_95	4/n	ratio
80	15	0.188	64	0.058698	0.050000	1.1740
80	20	0.250	59	0.063551	0.050000	1.2710
80	30	0.375	49	0.076141	0.050000	1.5228
80	50	0.625	29	0.126058	0.050000	2.5212
100	2	0.020	97	0.039025	0.040000	0.9756
100	3	0.030	96	0.039425	0.040000	0.9856
100	5	0.050	94	0.040251	0.040000	1.0063
100	10	0.100	89	0.042476	0.040000	1.0619
100	15	0.150	84	0.044961	0.040000	1.1240
100	20	0.200	79	0.047756	0.040000	1.1939
100	30	0.300	69	0.054533	0.040000	1.3633
100	50	0.500	49	0.076141	0.040000	1.9035
150	2	0.013	147	0.025880	0.026667	0.9705
150	3	0.020	146	0.026056	0.026667	0.9771
150	5	0.033	144	0.026414	0.026667	0.9905
150	10	0.067	139	0.027355	0.026667	1.0258
150	15	0.100	134	0.028364	0.026667	1.0637
150	20	0.133	129	0.029452	0.026667	1.1044
150	30	0.200	119	0.031897	0.026667	1.1961
150	50	0.333	99	0.038248	0.026667	1.4343
200	2	0.010	197	0.019359	0.020000	0.9680
200	3	0.015	196	0.019457	0.020000	0.9729
200	5	0.025	194	0.019657	0.020000	0.9828
200	10	0.050	189	0.020173	0.020000	1.0086
200	15	0.075	184	0.020717	0.020000	1.0358
200	20	0.100	179	0.021291	0.020000	1.0645
200	30	0.150	169	0.022540	0.020000	1.1270
200	50	0.250	149	0.025536	0.020000	1.2768
500	2	0.004	497	0.007707	0.008000	0.9634
500	3	0.006	496	0.007723	0.008000	0.9653
500	5	0.010	494	0.007754	0.008000	0.9692
500	10	0.020	489	0.007833	0.008000	0.9791
500	15	0.030	484	0.007914	0.008000	0.9892
500	20	0.040	479	0.007996	0.008000	0.9995
500	30	0.060	469	0.008166	0.008000	1.0207
500	50	0.100	449	0.008529	0.008000	1.0661

5.4.2 Example for Cook's Distance:

```
library(dplyr)
library(ggplot2)
```

```

library(knitr)

## --- 1) Data and full-model fit (your setup)

n <- 20
x <- 1:n
y <- 2 + 3 * x + rnorm(n, mean = 0, sd = 5)
y[1] <- y[1] + 30 # add an outlier at i = 1
y[11] <- y[11] + 30
full_data <- data.frame(x = x, replicate(5, rnorm(n)), y = y)

fit <- lm(y ~ ., data = full_data)

## --- 2) Ingredients for Cook's D and thresholds
p      <- length(coef(fit))          # includes intercept
h      <- hatvalues(fit)             # leverage h_ii
D      <- cooks.distance(fit)        # Cook's D_i
nu    <- n - p - 1                 # df for deleted-studentized residual
alpha <- 0.05

## Per-case scaling factor: c_i = ((n-p)/p) * (h_ii/(1-h_ii))
c_i    <- ((n - p) / p) * (h / (1 - h))

## Exact per-case Beta 95% critical values:
## D_i / c_i ~ Beta(1/2, (n-p-1)/2) => D_crit_i = c_i * qbeta(0.95, 1/2, (n-p-1)/2)
crit_beta_i <- c_i * qbeta(1 - alpha, shape1 = 0.5, shape2 = nu / 2)

## Average-leverage Beta 95% critical value:
## If h_ii = p/n (average leverage), then c_i = 1 exactly
crit_beta_avg <- qbeta(1 - alpha, shape1 = 0.5, shape2 = nu / 2)

## Heuristic 4/n line
crit_heur <- 4 / n

## --- 3) Assemble results table
df_cook <- tibble(
  i           = seq_len(n),
  h_ii        = as.numeric(h),
  D_i         = as.numeric(D),
  c_i         = as.numeric(c_i),
  crit_beta_i = as.numeric(crit_beta_i),
  crit_beta_avg = crit_beta_avg,
  crit_heur   = crit_heur
)

```

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```
## Print a compact table
knitr::kable(
  df_cook %>% mutate(across(where(is.numeric), ~ round(.x, 5))),
  caption = "Cook's D, leverage, and thresholds: per-case Beta 95%, average-leverage Beta 95%",
)
```

Table 5.4: Cook's D, leverage, and thresholds: per-case Beta 95%, average-leverage Beta 95%, and 4/n.

i	h_ii	D_i	c_i	crit_beta_i	crit_beta_avg	crit_heur
1	0.67204	1.62738	3.80555	1.07873	0.28346	0.2
2	0.31296	0.07715	0.84595	0.23979	0.28346	0.2
3	0.49722	0.08784	1.83660	0.52061	0.28346	0.2
4	0.61111	0.23875	2.91831	0.82724	0.28346	0.2
5	0.21633	0.02983	0.51265	0.14532	0.28346	0.2
6	0.14309	0.00469	0.31011	0.08790	0.28346	0.2
7	0.47629	0.07632	1.68900	0.47877	0.28346	0.2
8	0.41204	0.00004	1.30148	0.36892	0.28346	0.2
9	0.40499	0.29801	1.26407	0.35832	0.28346	0.2
10	0.17593	0.00026	0.39648	0.11239	0.28346	0.2
11	0.39917	0.73199	1.23380	0.34974	0.28346	0.2
12	0.10715	0.00088	0.22287	0.06318	0.28346	0.2
13	0.21158	0.01277	0.49837	0.14127	0.28346	0.2
14	0.30757	0.00026	0.82491	0.23383	0.28346	0.2
15	0.26786	0.04549	0.67944	0.19260	0.28346	0.2
16	0.71261	0.48354	4.60490	1.30532	0.28346	0.2
17	0.20630	0.01202	0.48271	0.13683	0.28346	0.2
18	0.27965	0.00082	0.72098	0.20437	0.28346	0.2
19	0.29482	0.03388	0.77642	0.22009	0.28346	0.2
20	0.29132	0.00775	0.76341	0.21640	0.28346	0.2

Cook's D by case with heuristic 4/n (red dotted), per-case Beta 95% critical values (blue dashed), and average-leverage Beta 95% line (purple dot-dash).

```
## --- 4) Plot D_i with thresholds
thresh_df <- bind_rows(
  df_cook %>% transmute(i, value = crit_beta_i, Type = "Beta 95% (per-case)"),
  tibble(i = seq_len(n), value = crit_beta_avg, Type = "Beta 95% (avg leverage)"),
  tibble(i = seq_len(n), value = crit_heur, Type = "4/n rule")
)

ggplot(df_cook, aes(x = i, y = D_i)) +
  geom_point(size = 2) +
```

```
geom_line(data = thresh_df,
          aes(y = value, color = Type, linetype = Type),
          linewidth = 0.9) +
scale_color_manual(values = c(
  "Beta 95% (per-case)"      = "#1f77b4",
  "Beta 95% (avg leverage)" = "#7f3c8d",
  "4/n rule"                 = "#d62728"
)) +
scale_linetype_manual(values = c(
  "Beta 95% (per-case)"      = "dashed",
  "Beta 95% (avg leverage)" = "dotdash",
  "4/n rule"                 = "dotted"
)) +
labs(x = "Observation i", y = "Cook's D_i") +
theme_bw() +
theme(legend.title = element_blank())
```

5 Understanding the Leverage for Adjusting Residuals of OLS

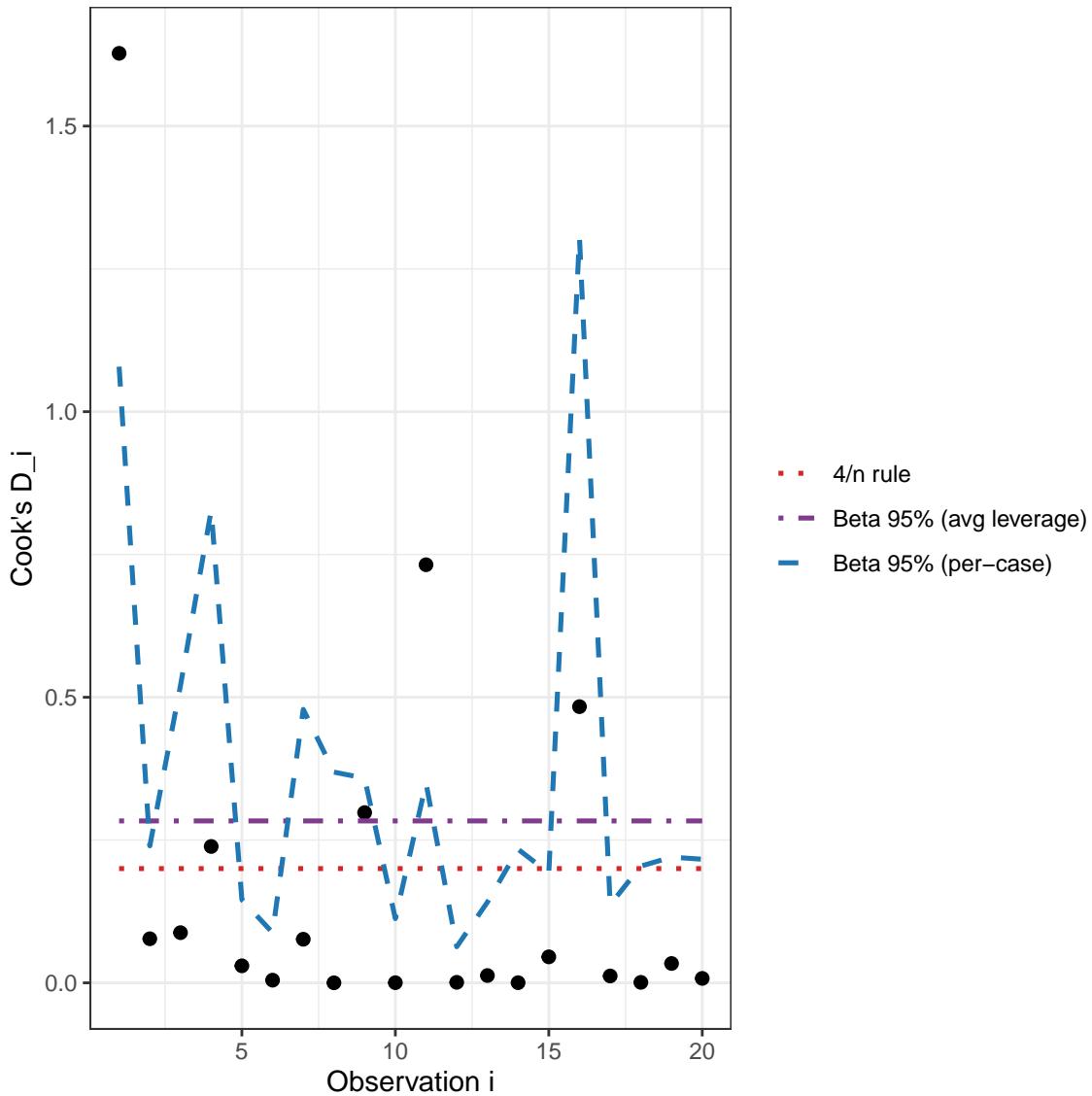


Figure 5.2: Cook's D by case with heuristic $4/n$ (red dotted), per-case Beta 95% critical values (blue dashed), and average-leverage Beta 95% line (purple dot-dash).

Appendix: Key Identities

The power of modern regression diagnostics comes from algebraic shortcuts that allow us to find the results of a leave-one-out process without the computational cost of refitting the model n times. The following two identities are fundamental to this efficiency.

Finding the LOOCV Residual ($e_{i,-i}$) from the Ordinary Residual (e_i)

This identity shows that we can find the “pure” leave-one-out residual using only the results from the single model fit on all data.

$$e_{i,-i} = \frac{e_i}{1 - h_{ii}} \quad (5.13)$$

Finding the LOOCV Standard Error from the Full-Model Standard Error

Similarly, this formula provides an efficient shortcut to see how the model’s overall error changes when a single point is removed.

$$\hat{\sigma}_{-i} = \sqrt{\frac{(n-p)\hat{\sigma}^2 - \frac{e_i^2}{1-h_{ii}}}{n-p-1}} \quad (5.14)$$

The derivation of this formula relies on first proving the relationship between the full model’s Residual Sum of Squares (RSS) and the leave-one-out version (RSS_{-i}).

1. Start with the definition of the leave-one-out residual sum of squares:

$$RSS_{-i} = \sum_{k \neq i} (y_k - \mathbf{x}_k^T \hat{\beta}_{-i})^2$$

2. Introduce the key identity that relates the leave-one-out coefficient vector ($\hat{\beta}_{-i}$) to the full model’s coefficient vector ($\hat{\beta}$):

$$\hat{\beta}_{-i} = \hat{\beta} - (X^T X)^{-1} \mathbf{x}_i \frac{e_i}{1 - h_{ii}}$$

3. Substitute this identity into the expression for a generic leave-one-out residual, $e_{k,-i} = y_k - \mathbf{x}_k^T \hat{\beta}_{-i}$. After simplification, this yields:

$$e_{k,-i} = e_k + h_{ki} \frac{e_i}{1 - h_{ii}}$$

where e_k is the ordinary residual and h_{ki} is the (k, i) -th element of the hat matrix.

4. Substitute this back into the definition of RSS_{-i} . After expanding the squared term and performing the summation (which involves considerable but standard matrix algebra), the expression simplifies to the elegant result:

$$RSS_{-i} = RSS - \frac{e_i^2}{1 - h_{ii}}$$

5. Finally, derive the formula for $\hat{\sigma}_{-i}$. We know that $\hat{\sigma}_{-i}^2 = \frac{RSS_{-i}}{n-p-1}$ and that $RSS = (n-p)\hat{\sigma}^2$. By substituting the result from Step 4, we arrive at the formula for the variance, and taking the square root gives us the standard error. \square

6 Logistic Regression

6.1 Odds as a Function of Probability

For an event with probability p , the odds is

$$\text{odds}(p) = \frac{p}{1-p}$$

and the log-odds (logit) is

$$\text{logit}(p) = \log\left(\frac{p}{1-p}\right)$$

```
## Plot odds(p) with a right-hand axis for log(odds(p)),
## using different line colors for the two curves.
## Defaults: p in [0.01, 0.99].
## Args:
##   p_min, p_max : endpoints for p-grid (0 < p_min < p_max < 1)
##   n            : number of grid points
##   annotate     : add reference lines/labels if TRUE
##   odds_col     : color for odds(p)
##   logit_col    : color for log(odds(p))
##   lwd1, lwd2   : line widths for the two curves

plot_odds <- function(p_min = 0.01, p_max = 0.99, n = 400,
                      annotate = TRUE,
                      odds_col = "steelblue",
                      logit_col = "firebrick",
                      lwd1 = 2, lwd2 = 2) {
  stopifnot(p_min > 0, p_max < 1, p_min < p_max, n >= 10)
  p <- seq(p_min, p_max, length.out = n)
  odds <- p / (1 - p)
  logit <- log(odds)

  ## Left y-axis: odds(p)
  plot(p, odds, type = "l", lwd = lwd1, col = odds_col,
       xlab = "Probability p",
```

6 Logistic Regression

```
ylab = "odds(p) = p / (1 - p)"
if (annotate) {
  abline(h = 1, v = 0.5, lty = 2)
  text(0.52, 1.05, "p = 0.5 → odds = 1", adj = 0)
}

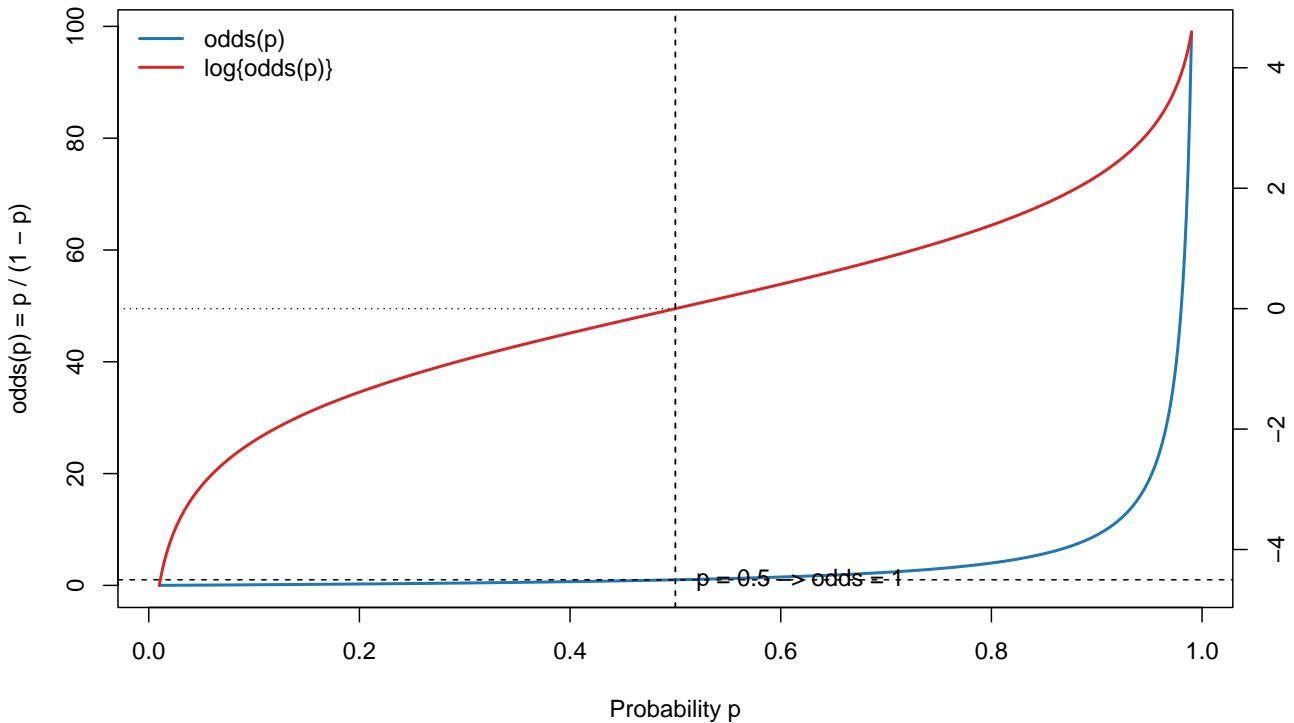
## Right y-axis: logit(p) = log(odds)
op <- par(new = TRUE)
on.exit(par(op), add = TRUE)
plot(p, logit, type = "l", lwd = lwd2, col = logit_col,
      axes = FALSE, xlab = "", ylab = "")
axis(4)
mtext("log{odds(p)} = log{p/(1 - p)}", side = 4, line = 3)

if (annotate) {
  abline(v = 0.5, lty = 2)
  # logit(0.5) = 0 reference (horizontal) on the right-axis scale
  usr <- par("usr")
  segments(x0 = usr[1], y0 = 0, x1 = 0.5, y1 = 0, lty = 3)
}

legend("topleft",
       legend = c("odds(p)", "log{odds(p)}"),
       col = c(odds_col, logit_col),
       lwd = c(lwd1, lwd2), bty = "n")

invisible(list(p = p, odds = odds, logit = logit))
}

## Example usage:
## plot_odds() # defaults: steelblue for odds, firebrick for log-odds (right axis)
plot_odds(odds_col = "#1f77b4", logit_col = "#d62728", n = 600)
```



Logistic regression models **log-odds** linearly in predictors, which both keeps fitted probabilities in $(0, 1)$ and turns multiplicative effects on odds into **additive** effects on the linear predictor.

6.2 A Simulated Data

We simulate data from a logistic model where the **logit** is a linear function of x :

$$\text{logit } p(x) = \log \left(\frac{p(x)}{1 - p(x)} \right) = \beta_0 + \beta_1 x,$$

so that

$$p(x) = \text{logit}^{-1}(\beta_0 + \beta_1 x) = \frac{1}{1 + \exp^{-(\beta_0 + \beta_1 x)}}.$$

We then display the observed y_i (binary outcomes) and the true probability curve $p(x)$ in red.

6 Logistic Regression

```
set.seed(123)

## -- Truth (edit as desired) --
n      <- 200
beta0 <- 0
beta1 <- 4

## -- Simulate --
x      <- runif(n, -1, 1)           # predictor
eta   <- beta0 + beta1 * x
p     <- plogis(eta)              # true p(x)
y     <- rbinom(n, size = 1, prob = p) # outcomes

sim.data <- data.frame(x = x, y = y, p = p)
```

6.2.1 Fit a logistic model to the simulated data

```
## -- Optional: fit a model to the simulated data --
sim.fit <- glm(y ~ x, data = sim.data, family = binomial())
p_fit <- predict(sim.fit, newdata = data.frame(x = x), type = "response")

## -- Plot: points for  $y_i$  (jittered), red line for true  $p(x)$  --
## Define jitter amount
jit <- 0.05
## jitter to separate 0/1 visually
yj <- jitter(sim.data$y, amount = jit)

plot(sim.data$x, yj,
      pch = 16, col = rgb(0, 0, 0, 0.45),
      xlab = "x",
      ylab = "Observed y (points) & p(x) (curves)",
      ylim = c(-0.1, 1.1))

## True probability curve (red)
xg <- seq(min(x), max(x), length.out = 500)
lines(xg, plogis(beta0 + beta1 * xg), col = "red", lwd = 2)

## Optional: add fitted probability curve (dashed dark red)
lines(xg, predict(sim.fit, newdata = data.frame(x = xg), type = "response"),
      col = "darkred", lwd = 2, lty = 2)

legend("topleft",
```

```

legend = c("y (jittered points)", "true p(x)", "fitted p(x)",  

  pch = c(16, NA, NA),  

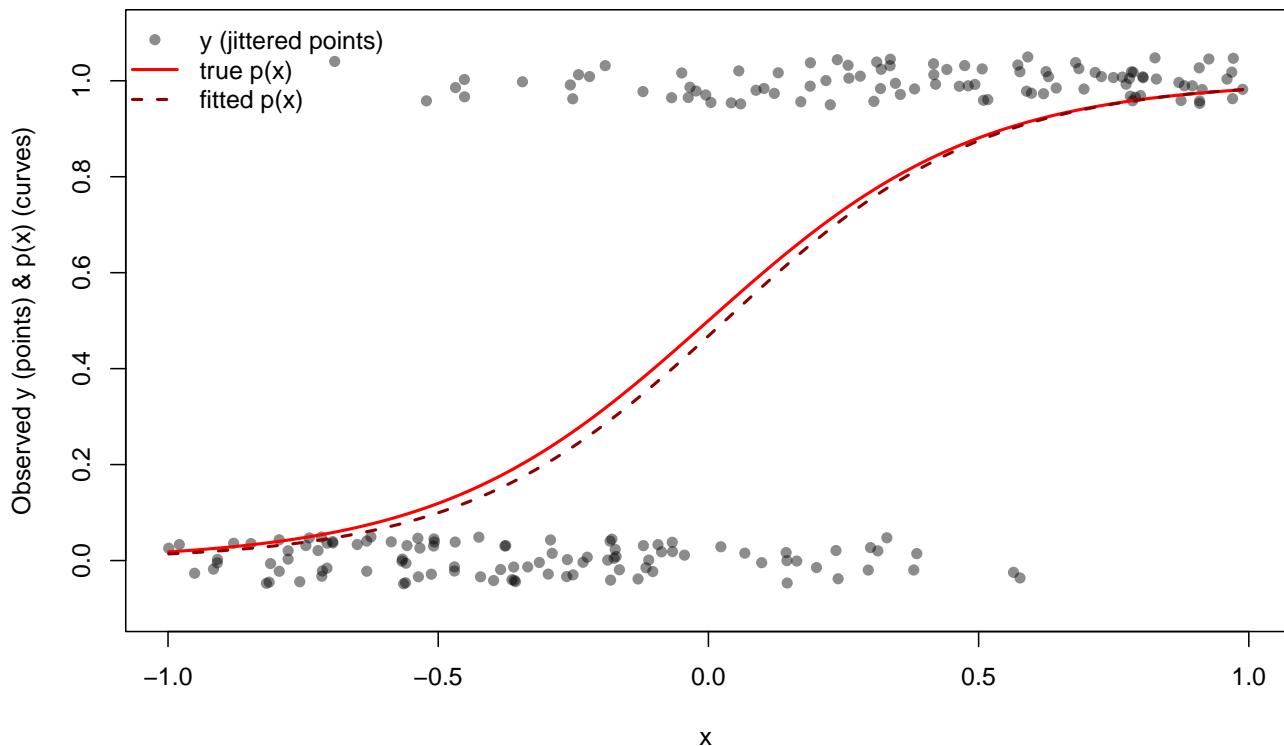
  lty = c(NA, 1, 2),  

  col = c(rgb(0,0,0,0.45), "red", "darkred"),  

  lwd = c(NA, 2, 2),  

  bty = "n")

```



6.3 Example of Coronary Heart Disease Data

6.3.1 Load a dataset

This dataset is about a follow-up study to determine the development of coronary heart disease (CHD) over 9 years of follow-up of 609 white males from Evans County, Georgia.

Variable meanings (as provided):

- chd: 1 if a person has the disease, 0 otherwise.
- smk: 1 if smoker, 0 if not.
- cat: 1 if catecholamine level is high, 0 if low.
- sbp: systolic blood pressure (continuous).
- age: age in years (continuous).
- chl: cholesterol level (continuous).

6 Logistic Regression

- `ecg`: 1 if electrocardiogram is abnormal, 0 if normal.
- `hpt`: 1 if high blood pressure, 0 if normal.

```
## Adjust the path if needed. The default is your original V: drive path.
data_path <- "evans.dat"

## Read data (expects a header row)
CHD.data <- read.table(data_path, header = TRUE)
if (knitr:::is_html_output()){
  CHD.data
} else{
  CHD.data[1:20,]
}
```

	id	chd	age	cat	chl	dbp	ecg	sbp	smk	hpt
1	21	0	56	0	270	80	0	138	0	0
2	31	0	43	0	159	74	0	128	1	0
3	51	1	56	1	201	112	1	164	1	1
4	71	0	64	1	179	100	0	200	1	1
5	74	0	49	0	243	82	0	145	1	0
6	91	0	46	0	252	88	0	142	1	0
7	111	1	52	0	179	80	1	128	1	0
8	131	0	63	0	217	92	0	135	0	0
9	141	0	42	0	176	76	0	114	1	0
10	191	0	55	0	250	114	1	182	0	1
11	201	0	74	0	293	100	0	166	0	1
12	241	0	53	0	179	90	0	158	0	0
13	251	0	58	0	201	86	0	142	1	0
14	261	0	56	0	206	85	0	120	1	0
15	271	0	69	0	225	84	0	168	0	1
16	283	1	51	1	259	102	1	135	0	1
17	291	0	43	0	193	78	0	118	1	0
18	311	0	64	1	185	100	1	180	0	1
19	312	0	44	0	150	108	0	160	0	1
20	331	0	42	0	211	86	1	122	0	0

6.3.2 Fit Logistic Regression Model for a Single Variable

```
vars <- c("smk", "sbp", "age", "chl")
#jit <- 0.01 # global jitter amount for y

## par(mfrow = c(2, 2), mar = c(4, 4, 2, 4) + 0.1) # extra right margin for axis(4)
```

```

for (v in vars) {
  ## Univariate logistic regression using ORIGINAL variable name in the formula
  fit <- glm(
    formula = reformulate(v, response = "chd"),
    data    = CHD.data,
    family  = binomial()
  )
  print(summary(fit))

  ## Base scatter of chd with small jitter (left axis: probability scale)
  plot(
    CHD.data[[v]],
    jitter(CHD.data$chd, amount = jit),
    pch  = 16, col = rgb(0, 0, 0, 0.45),
    xlab = v, ylab = "chd (jittered)",
    main = paste("chd vs", v),
    ylim = c(-0.1, 1.1)
  )

  ## Fitted (x) in red (left axis)
  if (length(unique(CHD.data[[v]])) == 2) {
    # binary predictor
    xcat <- sort(unique(CHD.data[[v]]))
    nd   <- setNames(data.frame(xcat), v)
    pcat <- predict(fit, newdata = nd, type = "response")
    points(xcat, pcat, pch = 19, col = "red")
    lines(xcat, pcat, col = "red", lwd = 2)

    # Right-axis: logit{ (x) } with fixed y-limits
    logit_p <- log(pcat / (1 - pcat))
    par(new = TRUE)
    plot(
      xcat, logit_p, type = "l", lwd = 2, col = "blue",
      axes = FALSE, xlab = "", ylab = "",
      xlim = range(CHD.data[[v]]), ylim = c(-2.5, 0)
    )
    axis(4)
    mtext("logit(p(x))", side = 4, line = 3)
    par(new = FALSE)
  } else {
    # continuous predictor
    xg <- seq(min(CHD.data[[v]]), max(CHD.data[[v]]), length.out = 400)
    nd <- setNames(data.frame(xg), v)
  }
}

```

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```
pg <- predict(fit, newdata = nd, type = "response")
lines(xg, pg, col = "red", lwd = 2)

# Right-axis: logit{ (x) } with fixed y-limits
logit_pg <- log(pg / (1 - pg))
par(new = TRUE)
plot(
  xg, logit_pg, type = "l", lwd = 2, col = "blue",
  axes = FALSE, xlab = "", ylab = "",
  xlim = range(xg), ylim = c(-2.5, 0)
)
axis(4)
mtext("logit(p(x))", side = 4, line = 3)
par(new = FALSE)
}
}
```

Call:

```
glm(formula = reformulate(v, response = "chd"), family = binomial(),
  data = CHD.data)
```

Coefficients:

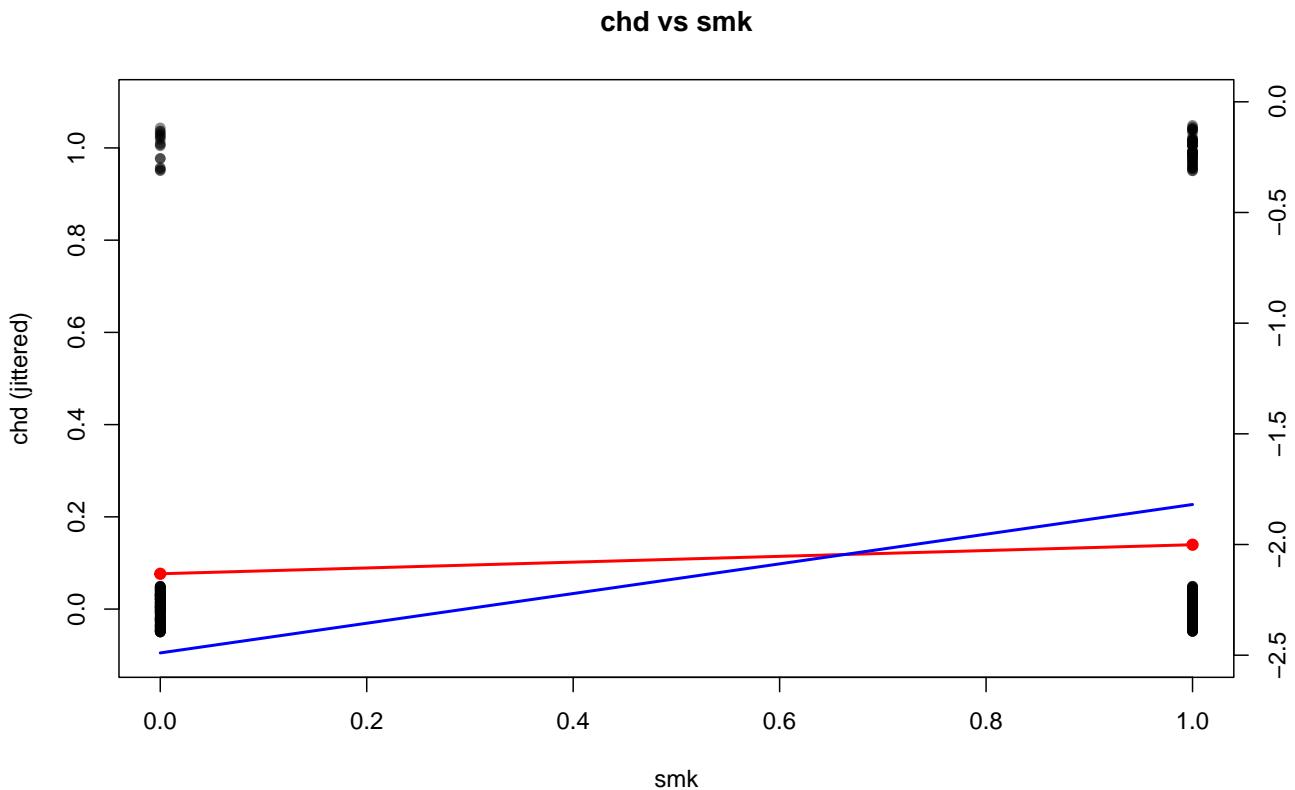
	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-2.4898	0.2524	-9.865	<2e-16 ***
smk	0.6706	0.2919	2.297	0.0216 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 438.56 on 608 degrees of freedom
Residual deviance: 432.81 on 607 degrees of freedom
AIC: 436.81

Number of Fisher Scoring iterations: 5



Call:

```
glm(formula = reformulate(v, response = "chd"), family = binomial(),
  data = CHD.data)
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-3.837912	0.629805	-6.094	1.1e-09 ***
sbp	0.012154	0.004036	3.011	0.0026 **

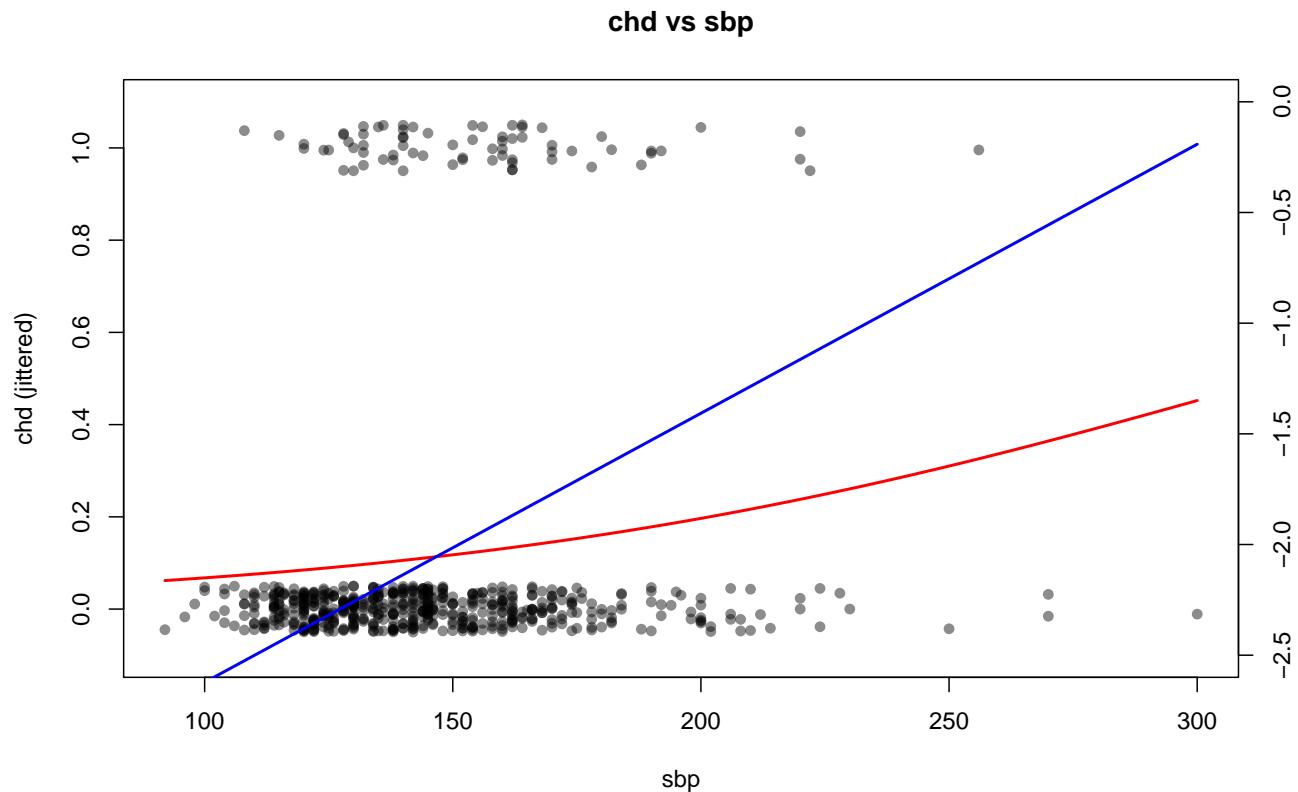
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 438.56 on 608 degrees of freedom
 Residual deviance: 430.06 on 607 degrees of freedom
 AIC: 434.06

Number of Fisher Scoring iterations: 4

6 Logistic Regression



Call:

```
glm(formula = reformulate(v, response = "chd"), family = binomial(),
    data = CHD.data)
```

Coefficients:

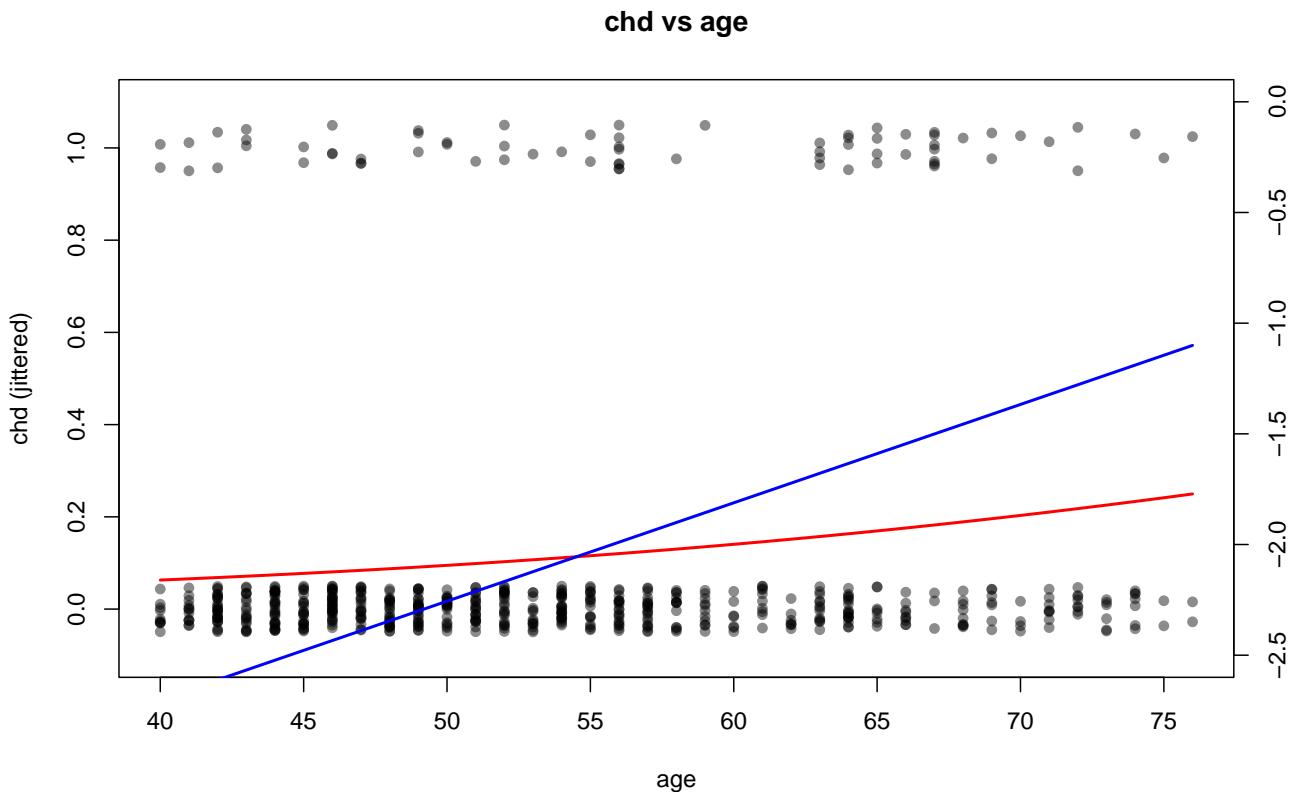
	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-4.47833	0.75610	-5.923	3.16e-09 ***
age	0.04445	0.01315	3.381	0.000723 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 438.56 on 608 degrees of freedom
 Residual deviance: 427.22 on 607 degrees of freedom
 AIC: 431.22

Number of Fisher Scoring iterations: 5



Call:

```
glm(formula = reformulate(v, response = "chd"), family = binomial(),
  data = CHD.data)
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-3.538260	0.686879	-5.151	2.59e-07 ***
chl	0.007004	0.003064	2.286	0.0223 *

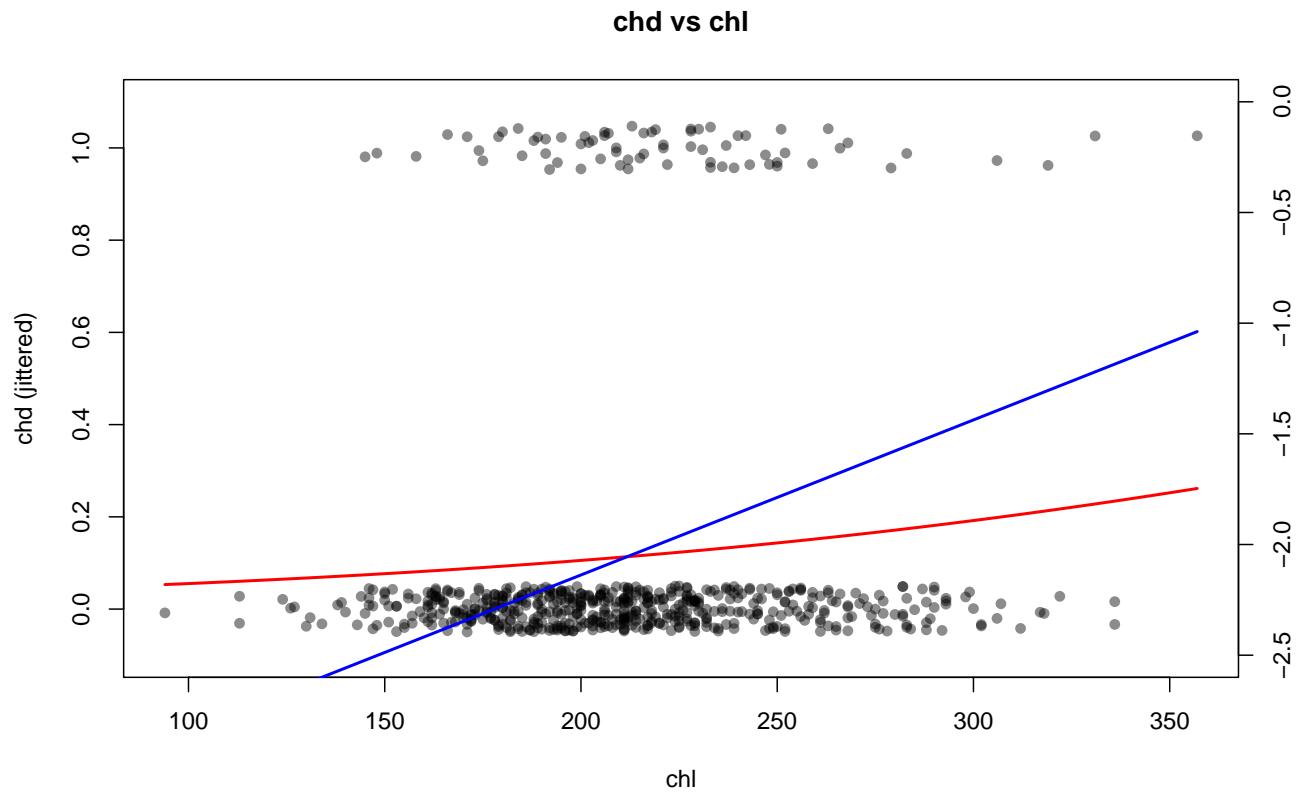
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 438.56 on 608 degrees of freedom
 Residual deviance: 433.42 on 607 degrees of freedom
 AIC: 437.42

Number of Fisher Scoring iterations: 4

6 Logistic Regression



6.3.3 Fit Logistic Regression Model with all variables

We fit a logistic regression with a logit link:

```
fit1_chd <- glm(  
  chd ~ smk + cat + sbp + age + chl + ecg + hpt,  
  data = CHD.data,  
  family = binomial(link = "logit")  
)  
summary(fit1_chd)
```

Call:
glm(formula = chd ~ smk + cat + sbp + age + chl + ecg + hpt,
 family = binomial(link = "logit"), data = CHD.data)

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-6.048892	1.345165	-4.497	6.9e-06 ***
smk	0.855951	0.306505	2.793	0.00523 **
cat	0.732763	0.376129	1.948	0.05139 .

6.4 Inference for Coefficients: Confidence Intervals and Covariance Matrix

```

sbp      -0.006995  0.006976 -1.003  0.31600
age       0.033956  0.015344  2.213  0.02690 *
chl       0.008970  0.003274  2.740  0.00615 **
ecg       0.417776  0.295553  1.414  0.15750
hpt       0.655498  0.359976  1.821  0.06861 .

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

(Dispersion parameter for binomial family taken to be 1)

```

Null deviance: 438.56 on 608 degrees of freedom
Residual deviance: 399.35 on 601 degrees of freedom
AIC: 415.35

```

Number of Fisher Scoring iterations: 5

Notes for interpretation:

- Positive coefficients increase the log-odds of CHD; negative coefficients decrease it.
- For indicator variables (e.g., smk), $\exp(\beta)$ is the adjusted odds ratio comparing the group with value 1 versus 0, holding others fixed.
- For continuous predictors (e.g., sbp, age), $\exp(\beta)$ is the multiplicative change in the odds for a one-unit increase. For a d -unit increase, the OR is $\exp(d * \beta)$.

6.4 Inference for Coefficients: Confidence Intervals and Covariance Matrix

We extract profile likelihood CIs and the covariance matrix to confirm standard errors.

```

ci_95 <- confint(fit1_chd, level = 0.95)      # profile-likelihood CI
vcov_mat <- vcov(fit1_chd)                      # covariance matrix of coefficients
se_vec   <- sqrt(diag(vcov_mat))                # standard errors

ci_95

```

	2.5 %	97.5 %
(Intercept)	-8.718003347	-3.427904298
smk	0.275699158	1.483333169
cat	-0.006873216	1.471885644
sbp	-0.021166144	0.006266328
age	0.003687290	0.064005215
chl	0.002533226	0.015404292
ecg	-0.171584621	0.990632546

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```
hpt      -0.050184520 1.364993401
```

```
vcov_mat
```

	(Intercept)	smk	cat	sbp
(Intercept)	1.809468553	-1.014526e-01	0.1391440386	-4.908229e-03
smk	-0.101452600	9.394560e-02	-0.0032961000	-1.653230e-04
cat	0.139144039	-3.296100e-03	0.1414730484	-9.299960e-04
sbp	-0.004908229	-1.653230e-04	-0.0009299960	4.866901e-05
age	-0.011142995	7.738971e-04	-0.0017879998	-1.311191e-05
chl	-0.002111134	3.161443e-05	0.0003146354	-1.821907e-06
ecg	0.003442546	9.255483e-03	-0.0204455233	-2.982539e-04
hpt	0.139817180	6.954592e-03	-0.0044220690	-1.486400e-03
	age	chl	ecg	hpt
(Intercept)	-1.114300e-02	-2.111134e-03	3.442546e-03	1.398172e-01
smk	7.738971e-04	3.161443e-05	9.255483e-03	6.954592e-03
cat	-1.788000e-03	3.146354e-04	-2.044552e-02	-4.422069e-03
sbp	-1.311191e-05	-1.821907e-06	-2.982539e-04	-1.486400e-03
age	2.354442e-04	-1.480501e-06	-4.972374e-05	4.044434e-04
chl	-1.480501e-06	1.071766e-05	5.040548e-05	-6.046197e-05
ecg	-4.972374e-05	5.040548e-05	8.735130e-02	9.506863e-04
hpt	4.044434e-04	-6.046197e-05	9.506863e-04	1.295828e-01

```
se_vec # should match the SE column in summary(fit1_chd)
```

	(Intercept)	smk	cat	sbp	age	chl
1.345164879	0.306505459	0.376129032	0.006976318	0.015344190	0.003273784	
	ecg	hpt				
0.295552531	0.359976081					

6.5 Inference for Odds Ratios

6.5.1 Interpretation of Odds Ratios in Logistic Regression

A multiple logistic regression model expresses the log-odds (logit) of an event as a linear function of predictors:

$$\log \left(\frac{p}{1-p} \right) = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \cdots + \beta_k x_k.$$

Here,

- $p = \Pr(Y = 1 | x_1, x_2, \dots, x_k)$ is the probability of the event,
- β_0 is the intercept, and
- each β_j represents the **change in the log-odds** of the event per one-unit increase in x_j , *holding all other variables constant*.

Exponentiating both sides gives the model in odds form:

$$\frac{p}{1-p} = \exp(\beta_0) \times \exp(\beta_1 x_1) \times \exp(\beta_2 x_2) \times \dots \times \exp(\beta_k x_k).$$

An R function for OR at two Profiles

The or_from_predict R function is a utility designed to calculate the Odds Ratio (OR) and its 95% confidence interval (CI) between two specific covariate profiles (new1 and new0) for a given logistic regression model (fit). The calculation is performed on the link (logit) scale. For a logistic model $\text{logit}(p) = \eta = \mathbf{X}\beta$, the log-Odds Ratio (logOR) is the difference between the linear predictors (η_1, η_0) for the two profiles:

$$\widehat{\text{logOR}} = \eta_1 - \eta_0 = (\mathbf{x}_1^T - \mathbf{x}_0^T)\beta = \mathbf{c}^T\beta \quad (6.1)$$

Here, $\mathbf{c} = \mathbf{x}_1 - \mathbf{x}_0$ is the linear contrast vector derived from the model matrices of the two profiles. The function estimates the variance of this contrast as $\text{Var}(\widehat{\text{logOR}}) = \mathbf{c}^T \mathbf{V} \mathbf{c}$, where \mathbf{V} is the model's variance-covariance matrix (vcov(fit)). The standard error $SE = \sqrt{\mathbf{c}^T \mathbf{V} \mathbf{c}}$ is used to compute the $100(1 - \alpha)\%$ confidence interval for the logOR:

$$\widehat{\text{logOR}} \pm z_{1-\alpha/2} \times SE.$$

These values (estimate and CI bounds) are then exponentiated to produce the final $\widehat{\text{OR}} = \exp(\widehat{\text{logOR}})$ and its 95% CI. The function also prints two helpful summaries to the console: a data frame showing only the variables that differ between the new0 and new1 profiles, and a 2x3 table presenting the estimates and CIs for both the OR and the logOR.

The R function to find ORs

```
## Compute OR and 95% CI via predict() on the LINK scale
## OR = exp( eta(new1) - eta(new0) ), where eta(.) = logit{(.)}
## Compute OR via predict() contrast on the LINK scale, also:
## (ii) print a 2-row data.frame of only variables that differ between new0 and new1
## (iii) print a 2x3 table (rows: OR, logOR; cols: Estimate, CI_low, CI_up)
or_from_predict <- function(fit, new1, new0, level = 0.95, digits = 4, tol = 1e-12) {
  stopifnot(is.data.frame(new1), is.data.frame(new0))

  ## --- REFACTORED SECTION START ---
  ## ---- (ii) Two-row data.frame with only changed variables ----

  ## Helper function to find differing variables between two profiles
  ## This is defined *inside* or_from_predict for encapsulation
  get_changed_vars <- function(d0, d1, tolerance) {
```

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```
common <- intersect(names(d0), names(d1))
diffv <- vapply(common, function(nm) {
  x0 <- d0[[nm]]; x1 <- d1[[nm]]
  if (is.numeric(x0) && is.numeric(x1)) {
    !isTRUE(all.equal(as.numeric(x0), as.numeric(x1), tolerance = tolerance))
  } else {
    !identical(x0, x1)
  }
}, logical(1))

keep <- common[diffv]
if (length(keep) == 0L) {
  out <- data.frame(`_no_changes_` = "no differences")
  rownames(out) <- c("new0", "new1")
  return(out)
}
out <- rbind(d0[keep], d1[keep])
rownames(out) <- c("new0", "new1")
out
}

## Call the helper function
changes_df <- get_changed_vars(new0, new1, tol)
## --- REFACTORED SECTION END ---

## ---- Linear contrast for log-OR and its variance ----

## (i) Calculate logOR estimate using predict(type="link")
## eta(.) = logit{p(.)}
eta1 <- predict(fit, newdata = new1, type = "link")
eta0 <- predict(fit, newdata = new0, type = "link")
logOR_hat <- as.numeric(eta1 - eta0) # logOR = eta1 - eta0

## (ii) Calculate standard error using the contrast vector 'cvec'
X1 <- model.matrix(delete.response(terms(fit)), data = new1)
X0 <- model.matrix(delete.response(terms(fit)), data = new0)
cvec      <- as.numeric(X1 - X0)
V         <- vcov(fit)
se_logOR <- sqrt(as.numeric(t(cvec) %*% V %*% cvec))

alpha   <- 1 - level
z       <- qnorm(1 - alpha / 2)
ci_log <- c(logOR_hat - z * se_logOR, logOR_hat + z * se_logOR)
```

```

## ---- 2x3 table: rows OR and logOR; columns Estimate, CI_low, CI_up ----
res_tab <- data.frame(
  Estimate = c(exp(logOR_hat), logOR_hat),
  CI_low   = c(exp(ci_log[1L]), ci_log[1L]),
  CI_up    = c(exp(ci_log[2L]), ci_log[2L]),
  row.names = c("OR", "logOR")
)

## ---- Print requested items ----
cat("\nVariables that differ between new0 and new1:\n")
print(changes_df)
cat("\nOdds Ratio summary:\n")
print(round(res_tab, digits = digits)) # Added rounding for neatness

## ---- Return (invisibly) ----
invisible(list(
  OR      = exp(logOR_hat),
  CI_OR   = exp(ci_log),
  logOR   = logOR_hat,
  CI_logOR = ci_log,
  se_logOR = se_logOR,
  changes  = changes_df,
  table    = res_tab
))
}

## --- Example usage ---
## Suppose 'fit1_chd' is your fitted model and 'CHD.data' is your data
## base_prof <- as.data.frame(lapply(CHD.data, function(col) if (is.numeric(col)) mean(col) else
## new0 <- base_prof; new0$smk <- 0
## new1 <- base_prof; new1$smk <- 1
## or_from_predict(fit1_chd, new1 = new1, new0 = new0)

mean_profile <- function(data, vars_binary_as = c(0,1)) {
  ## Build a single-row data.frame of typical values:
  out <- lapply(data, function(col) {
    if (is.numeric(col)) {
      # If strictly 0/1, keep mean (works fine for GLM prediction),
      # or switch to mode if you prefer.
      if (all(col %in% c(0,1))) mean(col) else mean(col, na.rm = TRUE)
    } else {
      # Fallback to first level for factors/characters
      if (is.factor(col)) levels(col)[1] else unique(col)[1]
    }
  })
}

```

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```
    }
  })
  as.data.frame(out)
}
```

6.5.2 Examples of Finding ORs and Their CIs for the CHD Dataset

6.5.2.1 OR Smoking (smk) (1 vs 0)

```
### 1) Smoking OR: smk = 1 vs 0 (other vars at their means)
## Example profiles at sample means (adjust as you like)
base_prof <- mean_profile(CHD.data)
new0 <- base_prof; new0$smk <- 0
new1 <- base_prof; new1$smk <- 1

res_smk <- or_from_predict(fit1_chd, new1 = new1, new0 = new0)
```

Variables that differ between new0 and new1:

```
  smk
new0   0
new1   1
```

Odds Ratio summary:

	Estimate	CI_low	CI_up
OR	2.3536	1.2907	4.2917
logOR	0.8560	0.2552	1.4567

How to read this:

- $OR_{smk} > 1$ suggests higher odds of CHD among smokers (adjusted for other variables). If the 95% CI excludes 1, the association is statistically significant at the 5% level.

6.5.2.2 OR for Systolic Blood Pressure (sbp): from 120 to 160

We compute the adjusted OR for a 40-unit increase in sbp (from 120 to 160):

```
### 2) SBP OR: 160 vs 120 (other vars at their means)
new0 <- base_prof; new0$sbp <- 120
new1 <- base_prof; new1$sbp <- 160

res_sbp <- or_from_predict(fit1_chd, new1 = new1, new0 = new0)
```

Variables that differ between new0 and new1:

```
sbp
new0 120
new1 160
```

Odds Ratio summary:

	Estimate	CI_low	CI_up
OR	0.7559	0.4375	1.3062
logOR	-0.2798	-0.8267	0.2671

6.5.2.3 OR for Combined Effects of Two Variables: Smoking with an Age Difference

Suppose we compare two groups that differ in **smoking status** and **age**:

- **Group A:** smk = 1, age = 50 (all other covariates equal)
- **Group B:** smk = 0, age = 30

The log \square odds contrast is ($A = \beta_{smk} + (50 - 20)\beta_{age}$), so the OR is ($\exp(A)$).

```
new0 <- base_prof; new0$age <- 30; new0$smk <- 0
new1 <- base_prof; new1$age <- 50; new1$smk <- 1

res_ageAsmk <- or_from_predict(fit1_chd, new1 = new1, new0 = new0)
```

Variables that differ between new0 and new1:

```
age smk
new0 30 0
new1 50 1
```

Odds Ratio summary:

	Estimate	CI_low	CI_up
OR	4.6417	1.8546	11.6168
logOR	1.5351	0.6177	2.4525

6.6 Assessing Statistical Significance with Wilks' Theorem (Analogue of F-test for OLS)

In the context of logistic regression, Wilks' theorem provides the basis for the Likelihood Ratio Test (LRT) used to assess the significance of predictor variables. The theorem states that when comparing a full model (M_1) to a nested null model (M_0), the test statistic, Λ , asymptotically follows a chi-squared (χ^2) distribution under the null hypothesis (i.e., that the simpler model M_0 is correct).

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The statistic Λ is calculated as the difference in the maximized log-likelihoods:

$$\Lambda = -2(\log L_0 - \log L_1) \quad (6.2)$$

where $\log L_0$ and $\log L_1$ are the log-likelihoods of the null and full models, respectively. In logistic regression, this is equivalent to the difference in the deviances: $\Lambda = \text{Deviance}_0 - \text{Deviance}_1$. This test statistic Λ represents the reduction in deviance (a measure of badness-of-fit) achieved by adding the extra predictors to the model.

The following R code chunk generates a conceptual plot of this relationship:

```
#| label: plot-lrt-concept
#| echo: false
#| fig-cap: "Conceptual plot of Deviance versus Number of Parameters, illustrating the Likelihood Principle"

library(ggplot2)

## 1. Create conceptual data for the plot
## These are just for illustration
n_obs <- 60 # Number of observations
p0 <- 1      # Parameters in null model (intercept)
p1 <- 21     # Parameters in full model (e.g., intercept + 7 predictors)
psat <- n_obs # Parameters in saturated model (1 per observation)

D0 <- 41 # Null deviance
D1 <- 20 # Full model deviance (residual deviance of M1)
D_sat <- 0 # Saturated model deviance

## Data frame for the three points
plot_data <- data.frame(
  model = c("M_0 (Null)", "M_1 (Full)", "M_Sat (Saturated)"),
  params = c(p0, p1, psat),
  deviance = c(D0, D1, D_sat),
  ## Add custom justification and nudges for labels
  hjust_val = c(0.5, 0.5, 1.1), # Right-align the last label
  nudge_x_val = c(0, 0, 0)
)

## 2. Create the ggplot
ggplot(plot_data, aes(x = params, y = deviance)) +
  ## Draw dashed guide lines for D0 and D1
  geom_segment(aes(x = p0, y = D0, xend = p1, yend = D0), linetype = "dashed", color = "grey70")
  geom_segment(aes(x = p1, y = D1, xend = psat, yend = D1), linetype = "dashed", color = "grey70")

  ## Connect the points with lines
  geom_line(color = "black", linetype = "solid", linewidth = 0.5) +
```

6.6 Assessing Statistical Significance with Wilks' Theorem (Analogue of F-test for OLS)

```

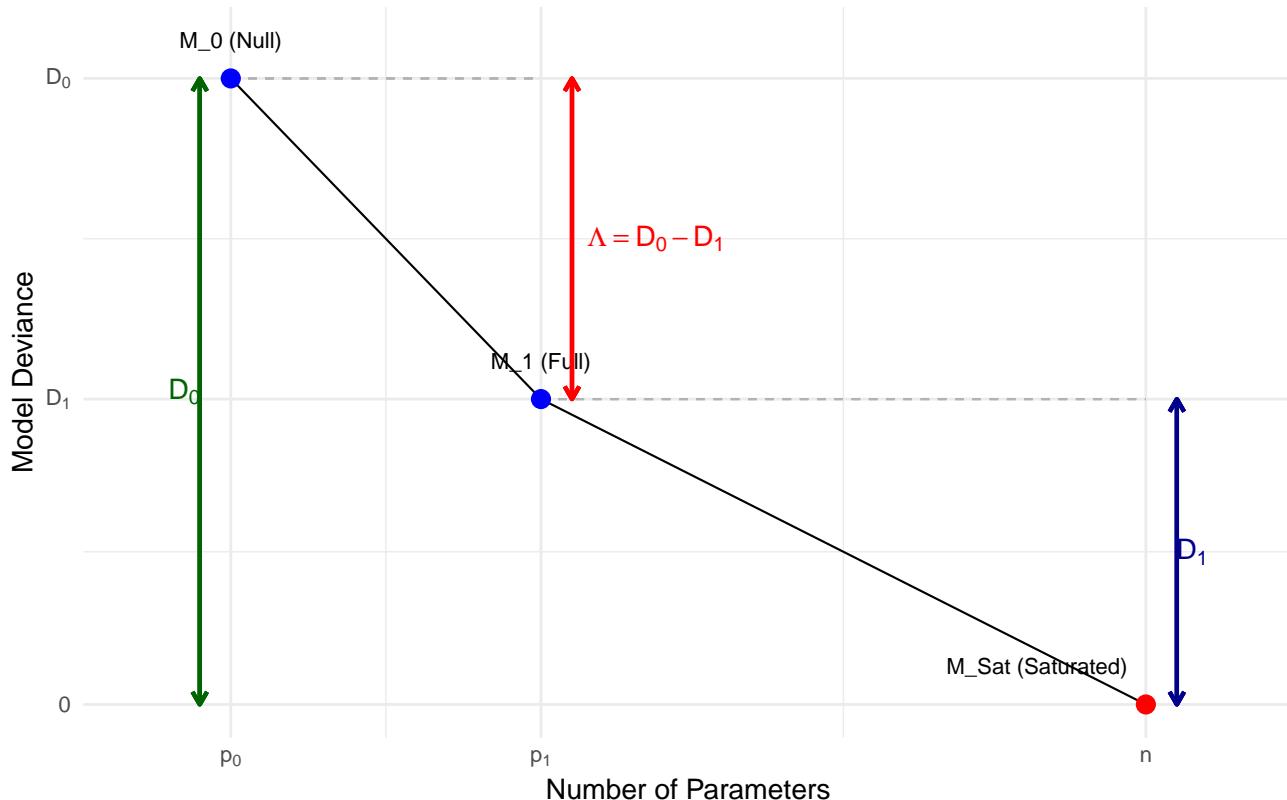
## Draw the main points
geom_point(size = 4, aes(color = model)) +
  ## --- MODIFIED LABEL PLACEMENT ---
  ## Label the points using custom nudge/justification
  geom_text(
    aes(label = model, hjust = hjust_val, nudge_x = nudge_x_val),
    nudge_y = 2.5, # Use a much smaller vertical nudge
    size = 4
  ) +
  ## --- ADDED BACK D0 and D1 ANNOTATIONS ---
  ## D0 (Null Deviance)
  geom_segment(
    aes(x = p0 - 2, y = D0, xend = p0 - 2, yend = D_sat), # Nudged left
    arrow = arrow(ends = "both", length = unit(0.1, "inches")),
    color = "darkgreen",
    linewidth = 1
  ) +
  annotate(
    "text",
    x = p0 - 3, y = D0 / 2, # Nudged left
    label = "D[0]", parse = TRUE,
    color = "darkgreen", hjust = 0.5, size = 5
  ) +
  ## D1 (Residual Deviance of Full Model)
  geom_segment(
    aes(x = psat + 2, y = D1, xend = psat + 2, yend = D_sat), # Nudged right
    arrow = arrow(ends = "both", length = unit(0.1, "inches")),
    color = "darkblue",
    linewidth = 1
  ) +
  annotate(
    "text",
    x = psat + 3, y = D1 / 2, # Nudged right
    label = "D[1]", parse = TRUE,
    color = "darkblue", hjust = 0.5, size = 5
  ) +
  ## LRT statistic  $\Lambda = D0 - D1$ 
  geom_segment(
    aes(x = p1 + 2, y = D0, xend = p1 + 2, yend = D1), # Nudged right
    arrow = arrow(ends = "both", length = unit(0.1, "inches")),

```

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```
color = "red",
lineWidth = 1
) +
annotate(
  "text",
  x = p1 + 3, y = D1 + (D0 - D1) / 2, # Nudged right
  label = "Lambda == D[0] - D[1]",
  parse = TRUE,
  color = "red", hjust = 0, size = 5
) +
## Customize axes to show the symbolic labels
scale_x_continuous(
  breaks = c(p0, p1, psat),
  labels = c(expression(p[0]), expression(p[1]), expression(n)),
  expand = expansion(mult = 0.1) # Add some padding
) +
scale_y_continuous(
  breaks = c(D_sat, D1, D0),
  labels = c(expression(0), expression(D[1]), expression(D[0])))
) +
## Labels and Title
labs(
  title = "Relationship between Deviance and Model Complexity",
  x = "Number of Parameters",
  y = "Model Deviance"
) +
## Clean theme
theme_minimal(base_size = 14) +
theme(
  plot.title = element_text(hjust = 0.5),
  legend.position = "none" # Remove legend, as points are labeled
) +
scale_color_manual(values = c("M_0 (Null)" = "blue", "M_1 (Full)" = "blue", "M_Sat (Saturated)" = "red"))
```

Relationship between Deviance and Model Complexity



As the diagram illustrates, the null model (M_0) has fewer parameters (p_0) and a higher deviance (D_0 , or worse fit), while the full model (M_1) has more parameters (p_1) and a lower deviance (D_1). The Likelihood Ratio Test statistic D is the magnitude of this drop in deviance.

For assessing the overall significance of a regression model (`fit1_chd`), this involves comparing it to its corresponding intercept-only (null) model. The degrees of freedom for the χ^2 test is the difference in the number of parameters, $df = p_1 - p_0$, which equals the number of predictors in the full model.

Here is an R code chunk demonstrating how to compute this p-value directly from a `glm` fit object, assuming it is named `fit1_chd`.

```
## Calculate the Likelihood Ratio Test statistic (D) and degrees of freedom (df)
## by comparing the model's deviance to the null (intercept-only) deviance,
## both of which are stored in the 'fit1_chd' object.
summary(fit1_chd)
```

Call:

```
glm(formula = chd ~ smk + cat + sbp + age + chl + ecg + hpt,
family = binomial(link = "logit"), data = CHD.data)
```

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Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-6.048892	1.345165	-4.497	6.9e-06 ***
smk	0.855951	0.306505	2.793	0.00523 **
cat	0.732763	0.376129	1.948	0.05139 .
sbp	-0.006995	0.006976	-1.003	0.31600
age	0.033956	0.015344	2.213	0.02690 *
chl	0.008970	0.003274	2.740	0.00615 **
ecg	0.417776	0.295553	1.414	0.15750
hpt	0.655498	0.359976	1.821	0.06861 .

Signif. codes:	0 '***'	0.001 '**'	0.01 '*'	0.05 '.'
	0.1 ' '	1		

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 438.56 on 608 degrees of freedom
Residual deviance: 399.35 on 601 degrees of freedom
AIC: 415.35

Number of Fisher Scoring iterations: 5

```
lrt_statistic <- fit1_chd>null.deviance - fit1_chd$deviance
lrt_df <- fit1_chd$df.null - fit1_chd$df.residual

## Compute the p-value from the chi-squared distribution
## We use lower.tail = FALSE to get P(ChiSq > D)
p_value <- pchisq(lrt_statistic, lrt_df, lower.tail = FALSE)

## Create and print the result in an ANOVA-like table
## Row 1: Null model
## Row 2: Full model (fit1_chd), showing the test against the null
lrt_table <- data.frame(
  "Resid. Df" = c(fit1_chd$df.null, fit1_chd$df.residual),
  "Resid. Dev" = c(round(fit1_chd>null.deviance, 4), round(fit1_chd$deviance, 4)),
  "Test Df" = c(NA, lrt_df),
  "Test Statistic (D)" = c(NA, round(lrt_statistic, 4)),
  "p-value" = c(NA, format.pval(p_value, digits = 4)),
  row.names = c("Null Model", "Full Model (fit1_chd)"),
  check.names = FALSE # Prevent R from changing 'p-value' to 'p.value'
)

cat("Likelihood Ratio Test for Model Significance:\n")
```

Likelihood Ratio Test for Model Significance:

6.6 Assessing Statistical Significance with Wilks' Theorem (Analogue of F-test for OLS)

```
lrt_table
```

	Resid.	Df	Resid.	Dev	Test Df	Test Statistic (D)	p-value
Null Model		608		438.5583		NA	NA <NA>
Full Model (fit1_chd)		601		399.3539	7	39.2044	1.787e-06

Using built-in anova() function

```
fit0_chd <- glm (chd~1, data = CHD.data, family = binomial())
anova(fit0_chd, fit1_chd)
```

Analysis of Deviance Table

```
Model 1: chd ~ 1
Model 2: chd ~ smk + cat + sbp + age + chl + ecg + hpt
Resid. Df Resid. Dev Df Deviance Pr(>Chi)
1       608     438.56
2       601     399.35  7    39.204 1.787e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova(fit1_chd, test="LRT")
```

Analysis of Deviance Table

Model: binomial, link: logit

Response: chd

Terms added sequentially (first to last)

```
Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
NULL              608     438.56
smk   1    5.7453    607     432.81 0.0165324 *
cat   1   14.3716    606     418.44 0.0001501 ***
sbp   1    0.7574    605     417.68 0.3841353
age   1    5.2821    604     412.40 0.0215455 *
chl   1    7.8619    603     404.54 0.0050489 **
ecg   1    1.8701    602     402.67 0.1714609
hpt   1    3.3159    601     399.35 0.0686113 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

6.7 Assessing Predictive Effect-Size (Analogue to R^2_{adj})

While the LRT assesses overall model significance (in-sample fit), it's also crucial to evaluate how well the model predicts new, unseen data (out-of-sample performance). A common method is to split the data into a training set (e.g., 2/3 of the data) and a test set (e.g., 1/3). The model is fit using only the training data and then used to make predictions for the test data. We can then compare these predictions to the actual outcomes in the test set.

6.7.1 Understanding the Confusion Matrix and Metrics

To evaluate a model's predictive performance, we classify its probabilistic predictions using a threshold (typically 0.5) and compare them to the true outcomes in a **Confusion Matrix**:

	Predicted: 0	Predicted: 1
Actual: 0	True Negative (TN)	False Positive (FP)
Actual: 1	False Negative (FN)	True Positive (TP)

From this matrix, we derive several key performance metrics:

- **Misclassification Error Rate (ER):** The proportion of all predictions that were incorrect.

$$\text{Error Rate} = \frac{FP + FN}{TP + TN + FP + FN}$$

- **Precision (Positive Predictive Value):** Answers: “Of all the times the model predicted positive, how often was it correct?” This is crucial when the cost of a **False Positive** is high.

$$\text{Precision} = \frac{TP}{TP + FP}$$

- **Recall (Sensitivity or True Positive Rate):** Answers: “Of all the actual positive cases, how many did the model find?” This is crucial when the cost of a **False Negative** is high.

$$\text{Recall (TPR)} = \frac{TP}{TP + FN}$$

- **ROC Curve and AUC:** An **ROC (Receiver Operating Characteristic) Curve** is a graph that shows a model's diagnostic ability across *all possible classification thresholds*. It plots the **True Positive Rate (Recall)** on the y-axis against the **False Positive Rate (FPR)** ($FPR = \frac{FP}{FP+TN}$) on the x-axis.

- **Interpretation:** The curve shows the trade-off between sensitivity (finding all the positives) and specificity (not mislabeling negatives). A random “no-skill” classifier is represented by a diagonal line from (0,0) to (1,1). A perfect classifier would hug the **top-left corner** ($TPR = 1, FPR = 0$).

- **AUC (Area Under the Curve):** The AUC summarizes the entire curve into a single number from 0 to 1. An AUC of 0.5 corresponds to a random guess, while an AUC of 1.0 represents a perfect model.
- **Precision-Recall (PR) Curve:** A PR Curve plots **Precision** (y-axis) against **Recall** (x-axis) at all possible thresholds.
 - **Interpretation:** This curve shows the trade-off between how *reliable* a positive prediction is (Precision) and how *complete* the model is at finding all positives (Recall).
 - **When to Use:** The PR curve is particularly informative when the dataset is **imbalanced** (i.e., one class, like “fraud” or “disease,” is much rarer than the other). Unlike the ROC curve, the PR curve’s baseline (the “no-skill” line) is a horizontal line at the proportion of positive cases, which makes it easier to see if the model is performing significantly better than chance in a low-positive-rate scenario. A perfect classifier would hug the **top-right corner** (Precision = 1, Recall = 1).

6.7.2 Illustration with the Simulated Dataset

This section applies the train/test split and model evaluation workflow to the `sim.data` created in the previous step.

```
## Load the pROC library for AUC calculation
## install.packages("pROC") # Uncomment to install if needed
library(pROC)

## --- 1. Split the data ---
## We use 'sim.data' which has 200 rows
set.seed(123) # for reproducibility
n_sim <- nrow(sim.data)
train_size_sim <- floor(2/3 * n_sim)
train_indices_sim <- sample(1:n_sim, size = train_size_sim)
train_data_sim <- sim.data[train_indices_sim, ]
test_data_sim <- sim.data[-train_indices_sim, ]

## --- 2. Refit the model on the training data ---
## We fit the model  $y \sim x$  on the training data
fit_train_sim <- glm(
  y ~ x,
  data = train_data_sim,
  family = binomial(link = "logit")
)

## --- 3. Make predictions on the test data ---
## Note: The true probabilities 'p' are also in test_data_sim
## We predict from the *fitted* model
pred_probs_sim <- predict(fit_train_sim, newdata = test_data_sim, type = "response")
```

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Plotting the Predictive Probabilities with True Labels

```
## --- 5. Plot sorted predicted probabilities ---

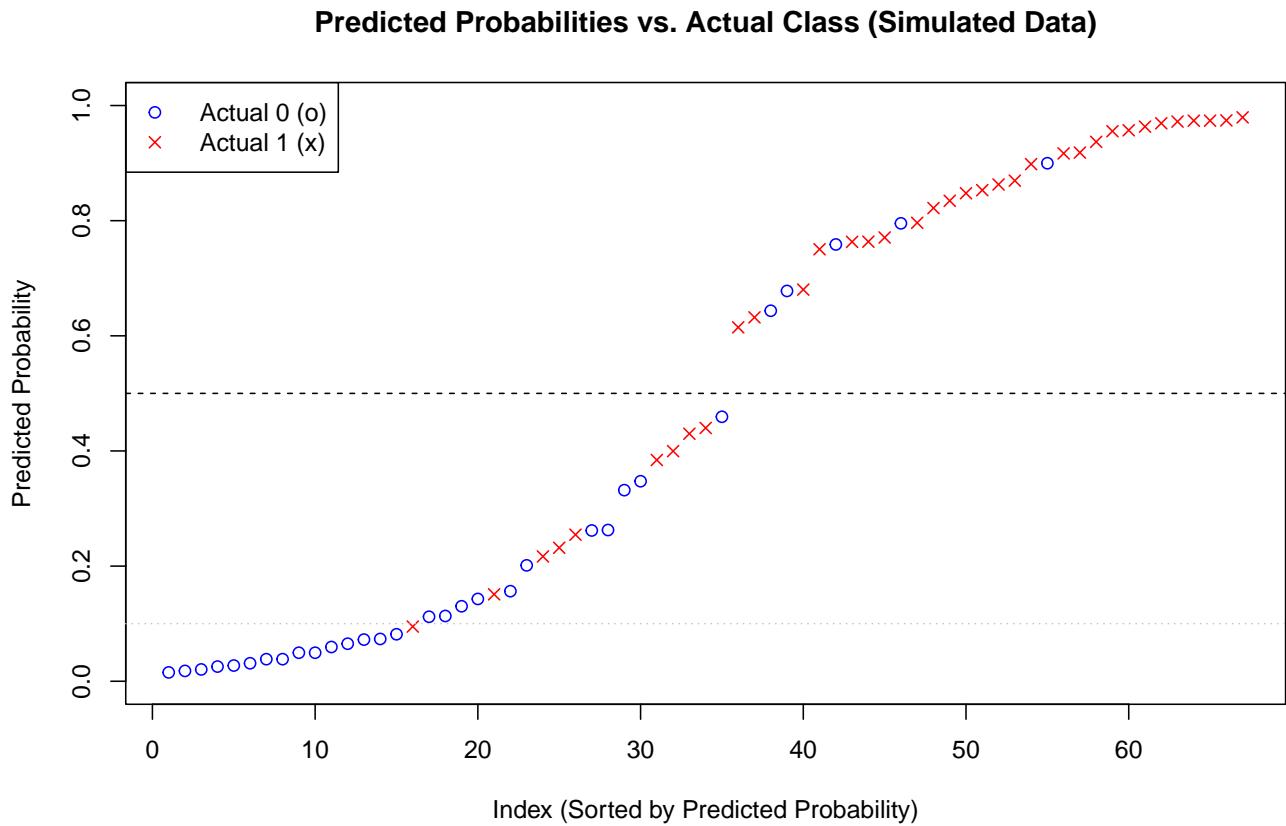
## Create a data frame for plotting
plot_data_sim <- data.frame(
  Prob = pred_probs_sim,
  Actual = as.factor(test_data_sim$y),
  TrueProb = test_data_sim$p # Include true probs for comparison
)

## Sort by predicted probability
plot_data_sim <- plot_data_sim[order(plot_data_sim$Prob), ]
plot_data_sim$Rank <- 1:nrow(plot_data_sim)

## Create the plot
plot(
  plot_data_sim$Rank,
  plot_data_sim$Prob,
  pch = ifelse(plot_data_sim$Actual == 0, 1, 4),
  col = ifelse(plot_data_sim$Actual == 0, "blue", "red"),
  xlab = "Index (Sorted by Predicted Probability)",
  ylab = "Predicted Probability",
  main = "Predicted Probabilities vs. Actual Class (Simulated Data)",
  ylim = c(0, 1)
)
abline(h = 0.5, lty = 2, col = "black")
abline(h = 0.1, lty = 3, col = "grey")

## Add the true probability curve (sorted by predicted prob)
## This shows how well the fitted model's predictions align with the true probs
#lines(plot_data_sim$Rank, plot_data_sim$TrueProb[order(plot_data_sim$Prob)], col = "darkgreen")

## Add a legend
legend(
  "topleft",
  legend = c("Actual 0 (o)", "Actual 1 (x)"),
  pch = c(1, 4),
  lty = c(NA, NA),
  lwd = c(NA, NA),
  col = c("blue", "red")
)
```



Confusion Matrix with threshold=0.5

```
## --- 4. Assess accuracy ---

## 4a. Misclassification Error Rate (using 0.5 threshold)
threshold <- 0.5
pred_class_sim <- ifelse(pred_probs_sim > threshold, 1, 0)
conf_matrix_sim <- table(Actual = test_data_sim$y, Predicted = pred_class_sim)

## --- MODIFIED LINES START ---
cat("Confusion Matrix (Counts, threshold = 0.5):\n")
```

Confusion Matrix (Counts, threshold = 0.5):

```
print(conf_matrix_sim)
```

		Predicted
Actual	0	1
	0 26 5	
1 9 27		

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```
cat("\nRow Proportions (Given Actual, % Predicted -- Relates to TPR/FPR):\n")
```

Row Proportions (Given Actual, % Predicted -- Relates to TPR/FPR):

```
## margin = 1 calculates proportions across rows
print(round(prop.table(conf_matrix_sim, margin = 1), 3))
```

		Predicted
Actual	0	1
0	0.839	0.161
1	0.250	0.750

```
cat("\nColumn Proportions (Given Predicted, % Actual -- Relates to Precision):\n")
```

Column Proportions (Given Predicted, % Actual -- Relates to Precision):

```
## margin = 2 calculates proportions across columns
print(round(prop.table(conf_matrix_sim, margin = 2), 3))
```

		Predicted
Actual	0	1
0	0.743	0.156
1	0.257	0.844

```
## --- MODIFIED LINES END ---
```

```
## Check if matrix has 2x2 dimensions, otherwise metrics will fail
if (all(dim(conf_matrix_sim) == c(2, 2))) {
  TN <- conf_matrix_sim[1, 1]
  FP <- conf_matrix_sim[1, 2]
  FN <- conf_matrix_sim[2, 1]
  TP <- conf_matrix_sim[2, 2]

  ## Calculate metrics
  error_rate <- (FP + FN) / (TP + TN + FP + FN)
  TPR_Recall <- TP / (TP + FN) # True Positive Rate (Recall / Sensitivity)
  FPR <- FP / (FP + TN)       # False Positive Rate (1 - Specificity)
  Precision <- TP / (TP + FP) # Positive Predictive Value
```

```

cat(paste("\nMisclassification Error Rate:", round(error_rate, 4), "\n"))
cat(paste("True Positive Rate (Recall):", round(TPR_Recall, 4), "\n"))
cat(paste("False Positive Rate:", round(FPR, 4), "\n"))
cat(paste("Precision:", round(Precision, 4), "\n"))
} else {
  cat("\nCannot calculate full metrics: model predicted only one class.\n")
}

```

Misclassification Error Rate: 0.209
 True Positive Rate (Recall): 0.75
 False Positive Rate: 0.1613
 Precision: 0.8438

Confusion Matrix with threshold=0.1

```

threshold <- 0.1
pred_class_sim <- ifelse(pred_probs_sim > threshold, 1, 0)
conf_matrix_sim <- table(Actual = test_data_sim$y, Predicted = pred_class_sim)

## --- MODIFIED LINES START ---
cat("Confusion Matrix (Counts, threshold = 0.1):\n")

```

Confusion Matrix (Counts, threshold = 0.1):

```
print(conf_matrix_sim)
```

		Predicted
Actual	0	1
	0	15
1	1	35

```
cat("\nRow Proportions (Given Actual, % Predicted -- Relates to TPR/FPR):\n")
```

Row Proportions (Given Actual, % Predicted -- Relates to TPR/FPR):

```
## margin = 1 calculates proportions across rows
print(round(prop.table(conf_matrix_sim, margin = 1), 3))
```

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```
Predicted  
Actual      0      1  
0 0.484 0.516  
1 0.028 0.972
```

```
cat("\nColumn Proportions (Given Predicted, % Actual -- Relates to Precision):\n")
```

```
Column Proportions (Given Predicted, % Actual -- Relates to Precision):
```

```
## margin = 2 calculates proportions across columns  
print(round(prop.table(conf_matrix_sim, margin = 2), 3))
```

```
Predicted  
Actual      0      1  
0 0.938 0.314  
1 0.062 0.686
```

```
## --- MODIFIED LINES END ---
```

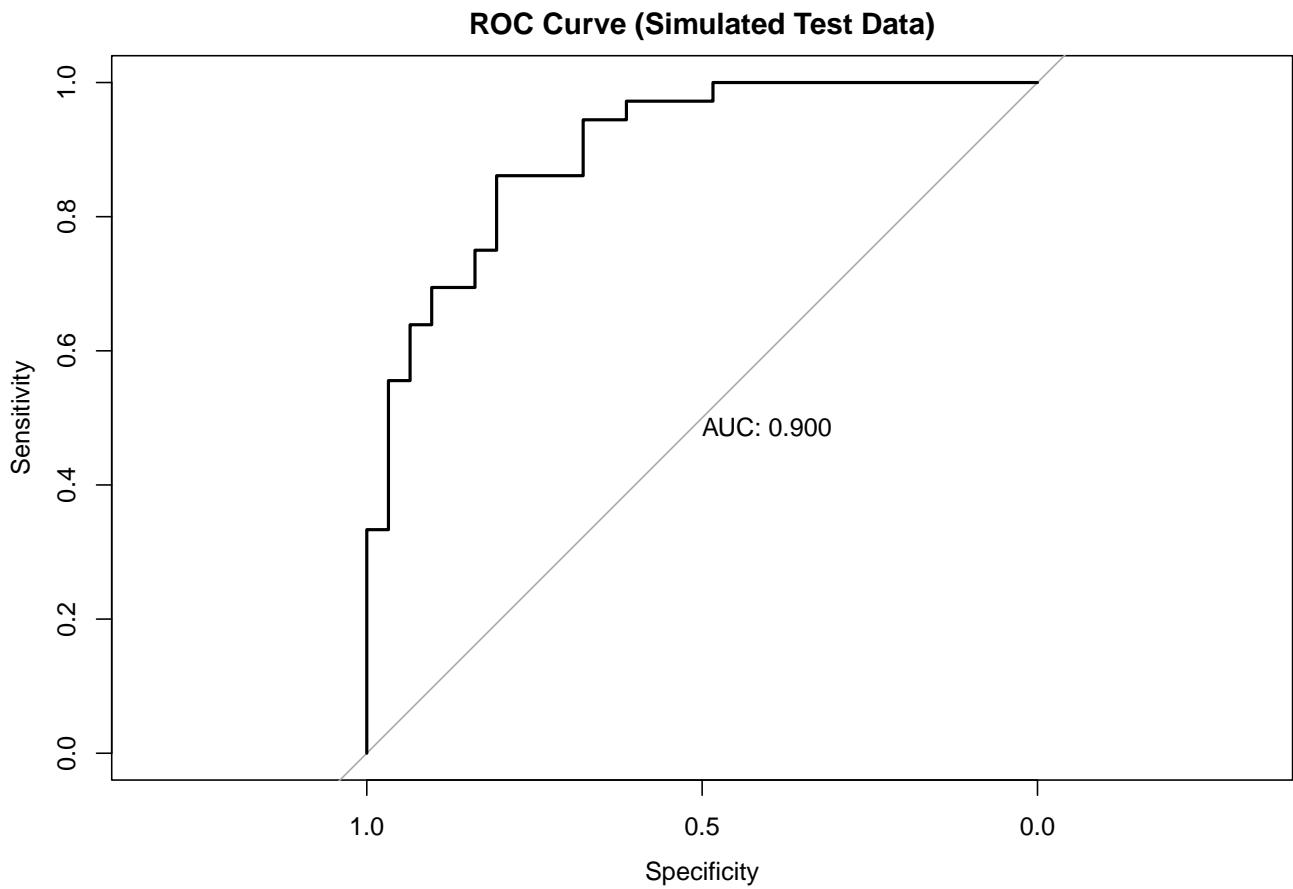
```
## Check if matrix has 2x2 dimensions  
if (all(dim(conf_matrix_sim) == c(2, 2))) {  
  TN <- conf_matrix_sim[1, 1]  
  FP <- conf_matrix_sim[1, 2]  
  FN <- conf_matrix_sim[2, 1]  
  TP <- conf_matrix_sim[2, 2]  
  
  ## Calculate metrics  
  error_rate <- (FP + FN) / (TP + TN + FP + FN)  
  TPR_Recall <- TP / (TP + FN) # True Positive Rate (Recall / Sensitivity)  
  FPR <- FP / (FP + TN)       # False Positive Rate (1 - Specificity)  
  Precision <- TP / (TP + FP) # Positive Predictive Value  
  
  cat(paste("\nMisclassification Error Rate:", round(error_rate, 4), "\n"))  
  cat(paste("True Positive Rate (Recall):", round(TPR_Recall, 4), "\n"))  
  cat(paste("False Positive Rate:", round(FPR, 4), "\n"))  
  cat(paste("Precision:", round(Precision, 4), "\n"))  
} else {  
  cat("\nCannot calculate full metrics: model predicted only one class.\n")  
}
```

Misclassification Error Rate: 0.2537
 True Positive Rate (Recall): 0.9722
 False Positive Rate: 0.5161
 Precision: 0.6863

ROC curve and Area Under the ROC (AUC)

```
## 4b. Area Under the Curve (AUC)
roc_curve_sim <- roc(test_data_sim$y, pred_probs_sim, quiet = TRUE)

## Plot the ROC curve
plot(roc_curve_sim, main = "ROC Curve (Simulated Test Data)", print.auc = TRUE)
```



```
auc_value_sim <- auc(roc_curve_sim)
cat(paste("Area Under the Curve (AUC):", round(auc_value_sim, 4), "\n\n"))
```

Area Under the Curve (AUC): 0.8996

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PR curve and Area Under PR Curve (AUPR)

```
## Load the ROCR library
## install.packages("ROCR") # Uncomment to install if needed
library(ROCR)

## --- 1. Create a 'prediction' object ---
## 'prediction' takes all predictions and all true labels
pred_obj <- prediction(pred_probs_sim, test_data_sim$y)

## --- 2. Create a 'performance' object for PR ---
## "prec" is for precision, "rec" is for recall
perf_pr <- performance(pred_obj, measure = "prec", x.measure = "rec")

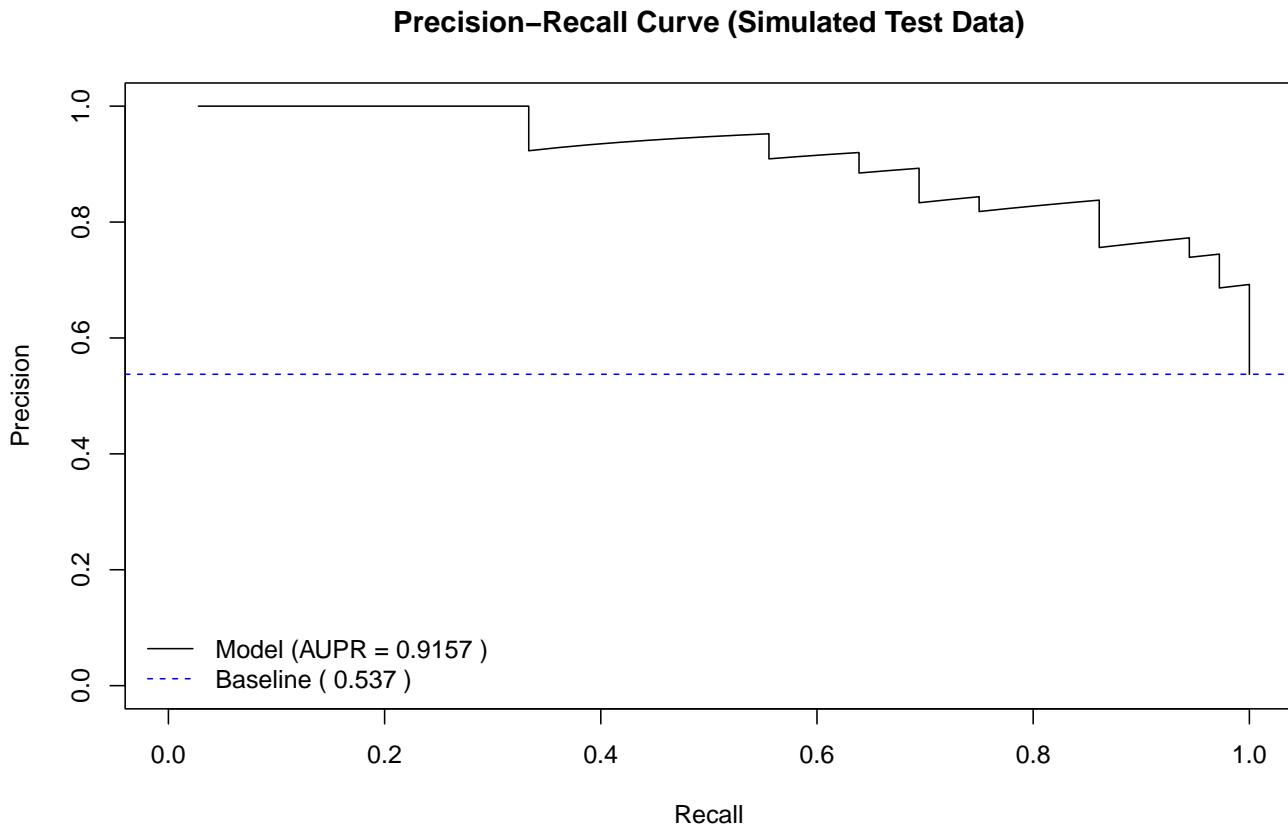
## --- 3. Calculate Area Under the PR Curve (AUPR) ---
perf_auc <- performance(pred_obj, measure = "aucpr") # "aucpr" = Area Under PR Curve
aupr_value <- perf_auc@y.values[[1]]
cat(paste("Area Under PR Curve (AUPR):", round(aupr_value, 4), "\n"))
```

Area Under PR Curve (AUPR): 0.9157

```
## --- 4. Plot the performance object ---
plot(perf_pr,
      main = "Precision-Recall Curve (Simulated Test Data)",
      xlim = c(0, 1),
      ylim = c(0, 1),
      col = "black")

## --- 5. Calculate and add the 'no-skill' baseline ---
baseline_precision_sim <- sum(test_data_sim$y == 1) / length(test_data_sim$y)
abline(h = baseline_precision_sim, col = "blue", lty = 2)

## --- 6. Add a legend with AUPR ---
legend("bottomleft",
       legend = c(
           paste("Model (AUPR =", round(aupr_value, 4), ")"), # <-- MODIFIED LINE
           paste("Baseline (", round(baseline_precision_sim, 3), ")")
       ),
       col = c("black", "blue"),
       lty = c(1, 2),
       bty = "n") # bty="n" removes the box
```



6.7.3 Application to the CHD Dataset

```

## Load the pROC library for AUC calculation
## install.packages("pROC") # Uncomment to install if needed
library(pROC)

## --- 1. Split the data ---
set.seed(123) # for reproducibility
n <- nrow(CHD.data)
train_size <- floor(2/3 * n)
train_indices <- sample(1:n, size = train_size)
train_data <- CHD.data[train_indices, ]
test_data <- CHD.data[-train_indices, ]

## --- 2. Refit the model on the training data ---
fit_train <- glm(
  chd ~ smk + cat + sbp + age + chl + ecg + hpt,
  data = train_data,
  family = binomial(link = "logit")
)

```

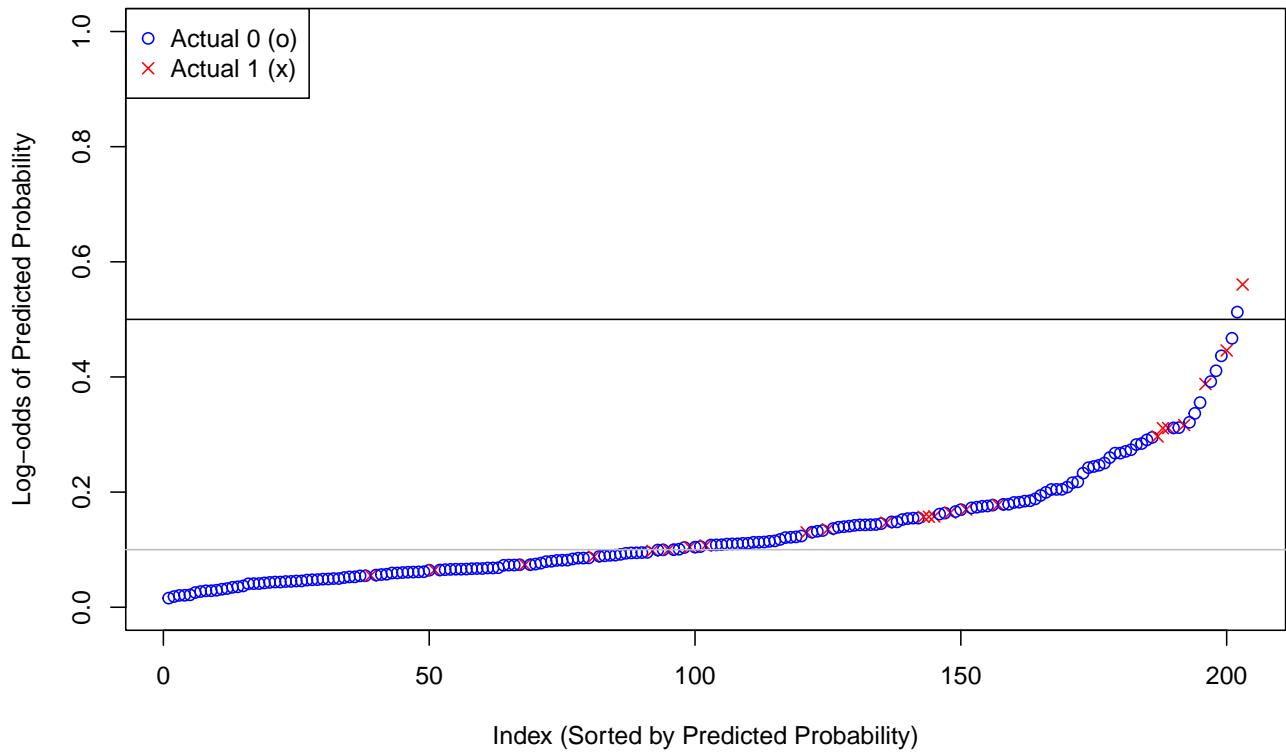
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```
)  
  
## --- 3. Make predictions on the test data ---  
pred_probs <- predict(fit_train, newdata = test_data, type = "response")
```

Plot Predictive Probabilities

```
## --- 5. Plot sorted predicted probabilities ---  
  
## Create a data frame for plotting  
plot_data <- data.frame(  
  Prob = pred_probs,  
  Actual = as.factor(test_data$chd)  
)  
  
## Sort by predicted probability  
plot_data <- plot_data[order(plot_data$Prob), ]  
plot_data$Rank <- 1:nrow(plot_data)  
  
## Create the plot  
## We use 'pch' (plot character) to set different symbols  
## 'pch = 1' is 'o' (default)  
## 'pch = 4' is 'x'  
plot(  
  plot_data$Rank,  
  plot_data$Prob,  
  pch = ifelse(plot_data$Actual == 0, 1, 4),  
  col = ifelse(plot_data$Actual == 0, "blue", "red"),  
  xlab = "Index (Sorted by Predicted Probability)",  
  ylab = "Log-odds of Predicted Probability",  
  main = "Predicted Probabilities vs. Actual Class",  
  ylim = c(0,1)  
)  
abline(h=0.5)  
abline(h=0.1, col="grey")  
  
## Add a legend  
legend(  
  "topleft",  
  legend = c("Actual 0 (o)", "Actual 1 (x)"),  
  pch = c(1, 4),  
  col = c("blue", "red")  
)
```

Predicted Probabilities vs. Actual Class

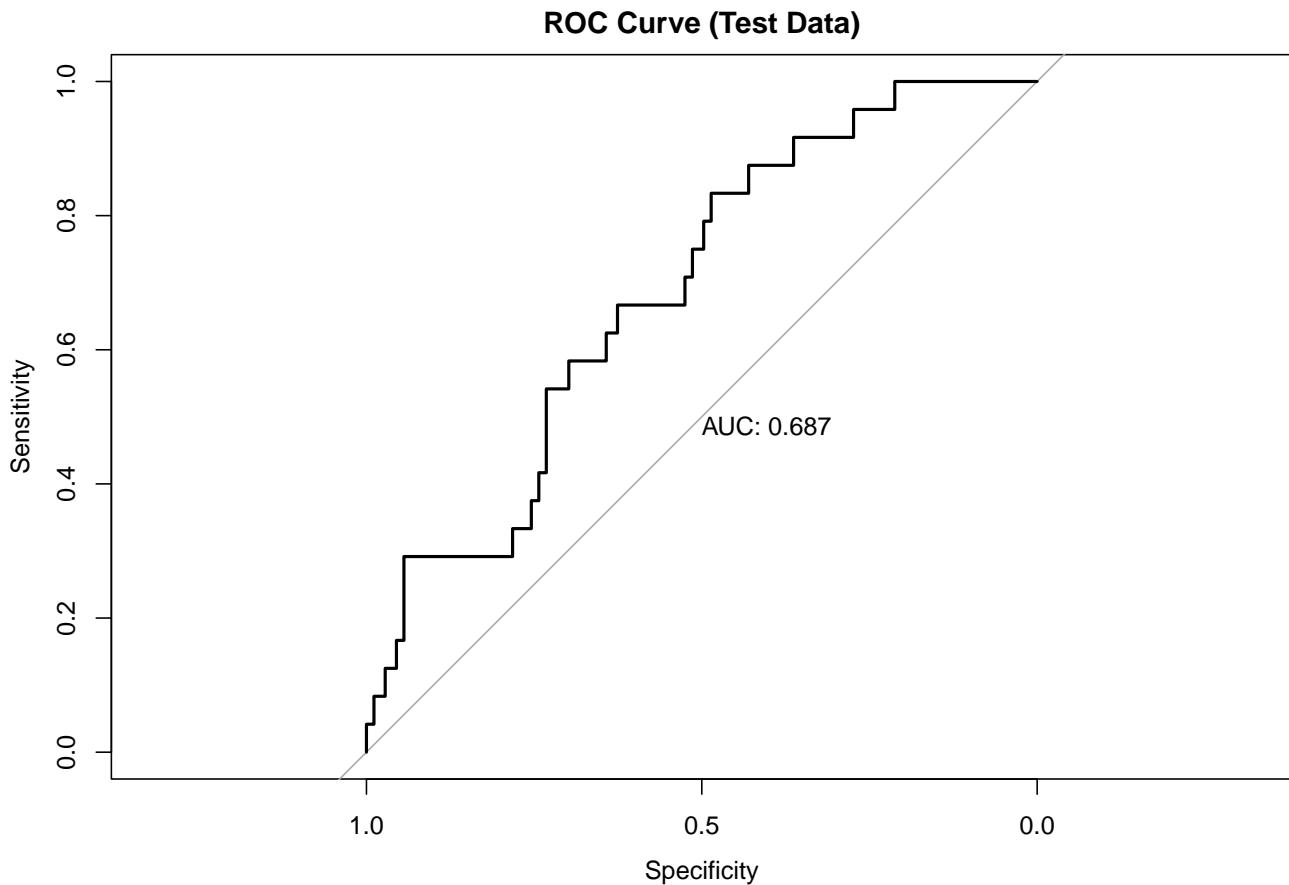


ROC curve and Area Under the ROC (AUC)

```
## 4b. Area Under the Curve (AUC)
roc_curve <- roc(test_data$chd, pred_probs, quiet = TRUE)

## Plot the ROC curve
plot(roc_curve, main = "ROC Curve (Test Data)", print.auc = TRUE)
```

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```
auc_value <- auc(roc_curve)
cat(paste("Area Under the Curve (AUC):", round(auc_value, 4), "\n\n"))
```

Area Under the Curve (AUC): 0.6872

PR curve and Area Under PR Curve (AUPR)

```
## Load the ROCR library
## install.packages("ROCR") # Uncomment to install if needed
library(ROCR)

## --- 1. Create a 'prediction' object ---
## 'prediction' takes all predictions and all true labels
## We use 'pred_probs' and 'test_data$chd' from the CHD data split
pred_obj <- prediction(pred_probs, test_data$chd)

## --- 2. Create a 'performance' object for PR ---
## "prec" is for precision, "rec" is for recall
```

```

perf_pr <- performance(pred_obj, measure = "prec", x.measure = "rec")

## --- 3. Calculate Area Under the PR Curve (AUPR) ---
perf_auc <- performance(pred_obj, measure = "aucpr") # "aucpr" = Area Under PR Curve
aupr_value <- perf_auc@y.values[[1]]
cat(paste("Area Under PR Curve (AUPR):", round(aupr_value, 4), "\n"))

```

Area Under PR Curve (AUPR): 0.2826

```

## --- 4. Plot the performance object ---
plot(perf_pr,
      main = "Precision-Recall Curve (Test Data)",
      xlim = c(0, 1),
      ylim = c(0, 1),
      col = "black")

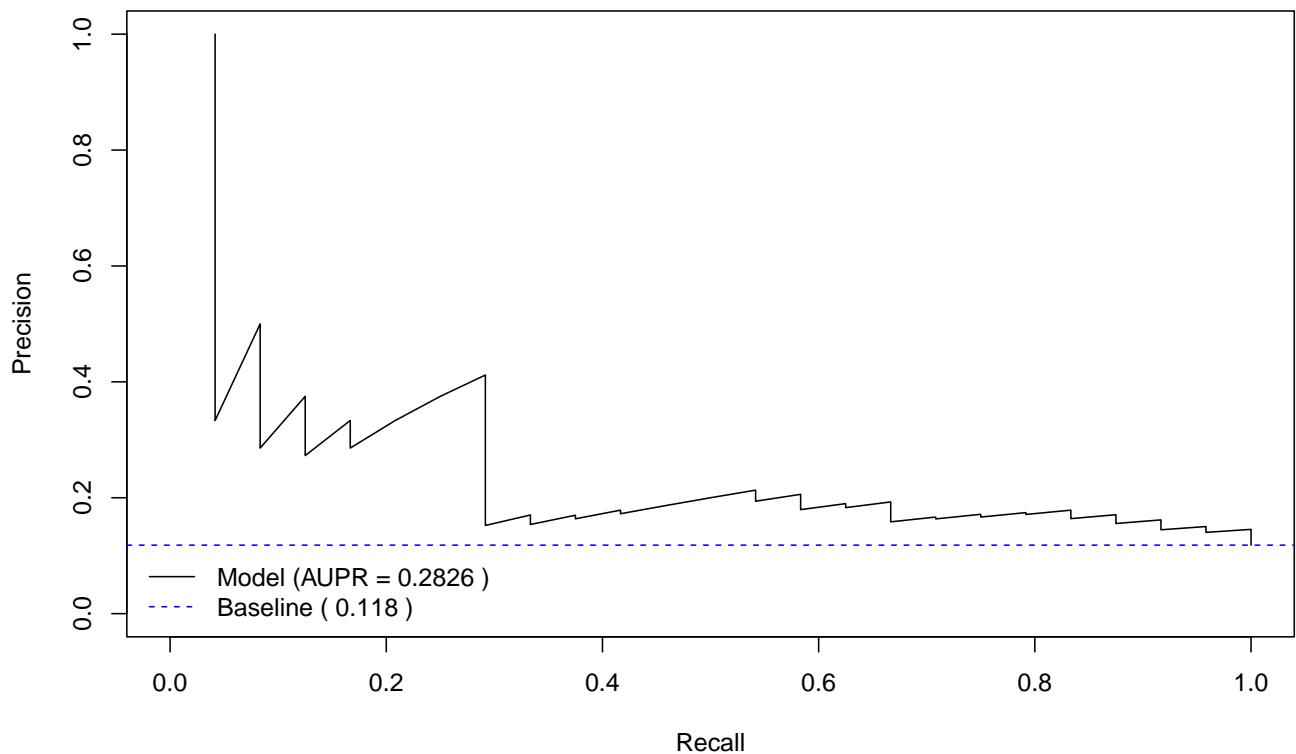
## --- 5. Calculate and add the 'no-skill' baseline ---
baseline_precision <- sum(test_data$chd == 1) / length(test_data$chd)
abline(h = baseline_precision, col = "blue", lty = 2)

## --- 6. Add a legend with AUPR ---
legend("bottomleft",
       legend = c(
         paste("Model (AUPR =", round(aupr_value, 4), ")"), # <-- MODIFIED LINE
         paste("Baseline (", round(baseline_precision, 3), ")"),
         ),
       col = c("black", "blue"),
       lty = c(1, 2),
       bty = "n") # bty="n" removes the box

```

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Precision–Recall Curve (Test Data)



7 One-factor Design

7.1 Completely Randomized Design

7.1.1 Plasma Etching Experiment

This section analyzes data from a **Completely Randomized Design (CRD)**. In a CRD, experimental units (in this case, the silicon wafers being etched) are assigned to treatments (the RF Power levels) completely at random. The primary goal is to determine if changing the RF Power level has a statistically significant effect on the mean etch rate.

7.1.1.1 Data and Visualization

We begin by loading the data into a single, tidy `data.frame`. The response variable, `rate`, contains all the etch rate observations. The predictor variable, `power`, is a **factor**, which is R's way of representing a categorical variable. This tells R to treat the different power levels as distinct groups.

```
## Define the data vectors
rate <- c(575, 542, 530, 539, 570, 565, 593, 590, 579, 610,
       600, 651, 610, 637, 629, 725, 700, 715, 685, 710)
power_levels <- c(160, 180, 200, 220)

## Create the data frame
etching_df <- data.frame(
  rate = rate,
  power = factor(rep(power_levels, each = 5))
)

## Display the first few rows
etching_df
```

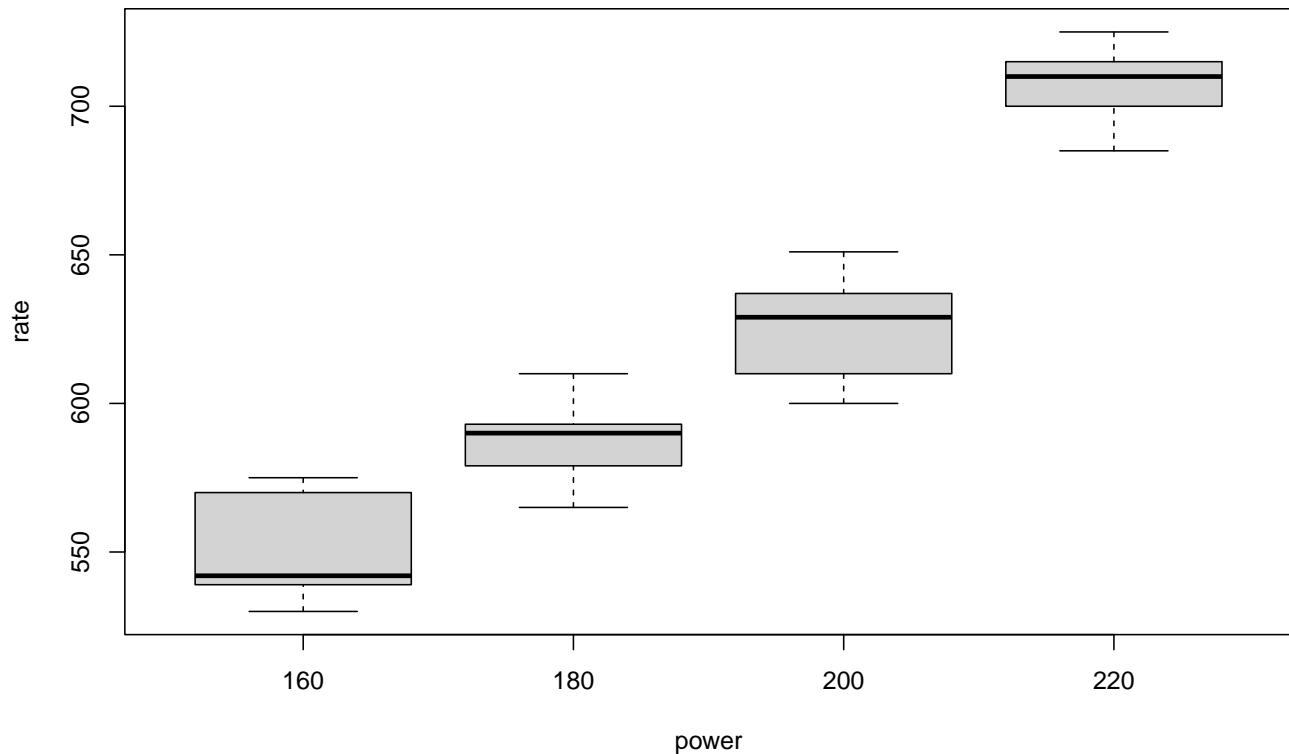
	rate	power
1	575	160
2	542	160
3	530	160
4	539	160
5	570	160

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6	565	180
7	593	180
8	590	180
9	579	180
10	610	180
11	600	200
12	651	200
13	610	200
14	637	200
15	629	200
16	725	220
17	700	220
18	715	220
19	685	220
20	710	220

Grouped Boxplots

```
boxplot(rate~power, data=etching_df)
```



Using ggplot to visualize grouped data

```

library(ggplot2)
library(dplyr) # Using dplyr for easier data manipulation

## Calculate group means and their start/end indices
mean_rates <- etching_df %>%
  mutate(obs_index = row_number()) %>%
  group_by(power) %>%
  summarise(
    mean_rate = mean(rate),
    x_start = min(obs_index) - 0.5,
    x_end = max(obs_index) + 0.5
  )

ggplot(etching_df, aes(x = 1:nrow(etching_df), y = rate, color = power)) +
  geom_point(size = 3, alpha = 0.7) + # Plot individual data points
  geom_segment(
    data = mean_rates,
    aes(x = x_start, xend = x_end, y = mean_rate, yend = mean_rate),
    linetype = "dashed",
    size = 1.2
  ) + # Add line segments for group means
  labs(
    title = "Etch Rate Observations by RF Power Level",
    x = "Observation Index",
    y = "Etch Rate",
    color = "RF Power (W)"
  ) +
  scale_color_brewer(palette = "Set1") +
  theme_minimal() +
  theme(plot.title = element_text(hjust = 0.5))

```

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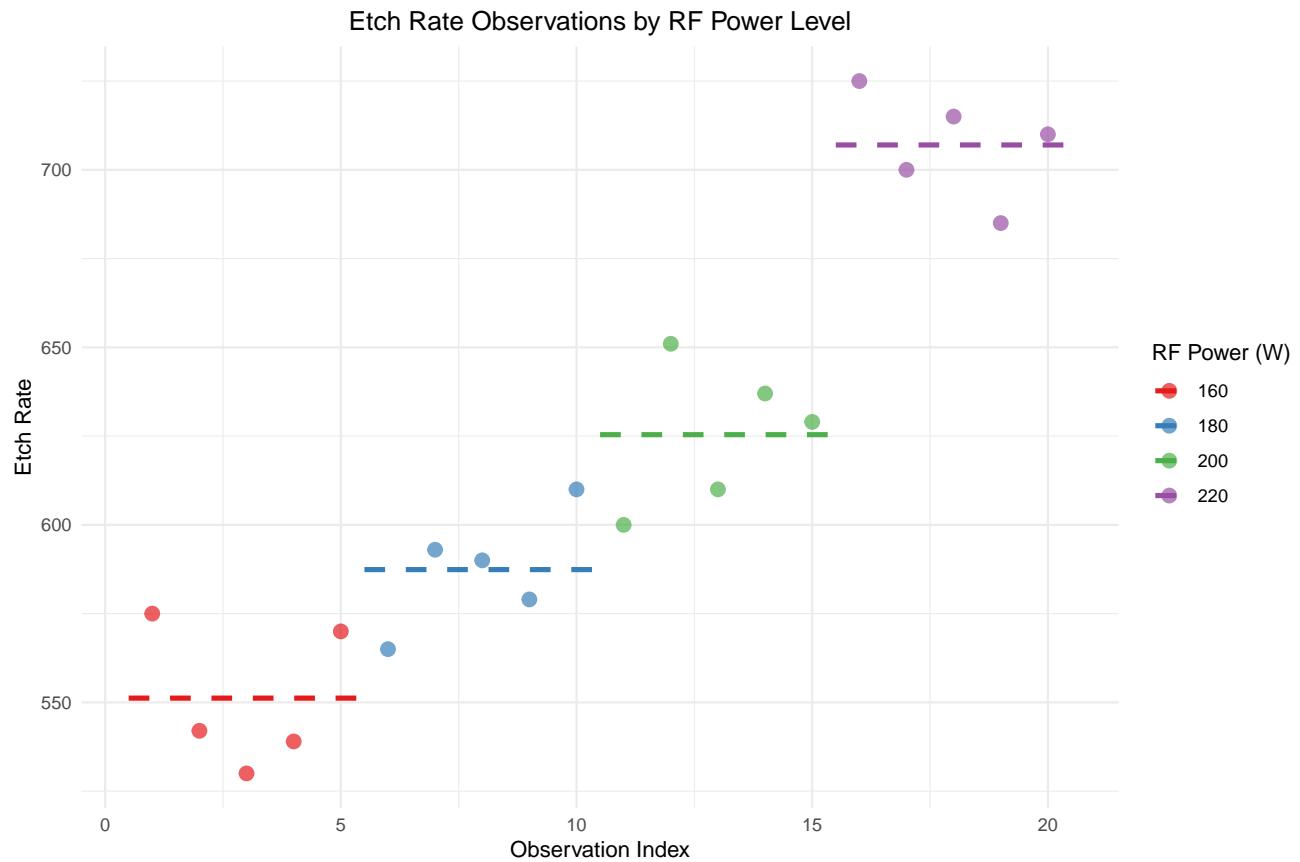


Figure 7.1: Index Plot of Etch Rate with Group-Specific Mean Lines

7.1.1.2 Model Fitting with Sum-to-Zero Constraint

We fit a linear model using the `lm()` function to perform an **Analysis of Variance (ANOVA)**. The model is specified as `rate ~ power`, and we now include the `data = etching_df` argument.

To get interpretable estimates for the treatment effects (τ_i), we use a **sum-to-zero constraint** (`contr.sum`), which forces the sum of the treatment effects to be zero ($\sum \tau_i = 0$).

```
fit <- lm(rate ~ power, data = etching_df, contrasts = list(power = contr.sum))
cat ("Model Matrix:\n")
```

Model Matrix:

```
model.matrix(fit)
```

	(Intercept)	power1	power2	power3
1	1	1	0	0

```

2      1      1      0      0
3      1      1      0      0
4      1      1      0      0
5      1      1      0      0
6      1      0      1      0
7      1      0      1      0
8      1      0      1      0
9      1      0      1      0
10     1      0      1      0
11     1      0      0      1
12     1      0      0      1
13     1      0      0      1
14     1      0      0      1
15     1      0      0      1
16     1     -1     -1     -1
17     1     -1     -1     -1
18     1     -1     -1     -1
19     1     -1     -1     -1
20     1     -1     -1     -1

attr(,"assign")
[1] 0 1 1 1
attr(,"contrasts")
attr(,"contrasts")$power
 [,1] [,2] [,3]
160    1    0    0
180    0    1    0
200    0    0    1
220   -1   -1   -1

summary.fit <- summary(fit)
cat ("Summary of lm fitting results:\n")

```

Summary of lm fitting results:

```
summary.fit
```

Call:

```
lm(formula = rate ~ power, data = etching_df, contrasts = list(power = contr.sum))
```

Residuals:

Min	1Q	Median	3Q	Max
-25.4	-13.0	2.8	13.2	25.6

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```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) 617.750     4.085 151.234 < 2e-16 ***
power1      -66.550    7.075 -9.406 6.39e-08 ***
power2      -30.350    7.075 -4.290 0.000563 ***
power3       7.650     7.075  1.081 0.295602  
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 18.27 on 16 degrees of freedom
Multiple R-squared:  0.9261, Adjusted R-squared:  0.9122 
F-statistic: 66.8 on 3 and 16 DF,  p-value: 2.883e-09
```

7.1.1.3 Point Estimation of Parameters

The output of the model provides estimates for the overall mean ($\hat{\mu}$) and the treatment effects for the first k-1 levels ($\hat{\tau}_1, \hat{\tau}_2, \hat{\tau}_3$).

- $\hat{\mu}$ (the Intercept) is the estimate of the grand mean etch rate across all power levels.
- $\hat{\tau}_i$ is the estimated effect of the i-th power level, representing how much that level's mean deviates from the grand mean.

Using the sum-to-zero constraint, we can manually calculate the effect for the final level, $\hat{\tau}_4$.

```
## Extract coefficients
est <- coef(fit)
tau4.hat <- -sum(est[-1])
taui.hat <- c(est[-1], tau4.hat)
print("Estimated Treatment Effects (tau_i):")
```

```
[1] "Estimated Treatment Effects (tau_i):"
```

```
print(taui.hat)
```

```
power1 power2 power3
-66.55 -30.35    7.65  89.25
```

```
## Estimates of treatment means (mu_i)
mu.hat <- est[1]
mui.hat <- mu.hat + taui.hat
print("Estimated Treatment Means (mu_i):")
```

```
[1] "Estimated Treatment Means (mu_i):"
```

```
print(mui.hat)
```

```
power1 power2 power3
 551.2  587.4  625.4  707.0
```

7.1.1.4 ANOVA Table

The ANOVA table partitions the total variation into variation **between** treatment groups (power) and variation **within** treatment groups (random error). The **p-value** ($\text{Pr}(>F)$) indicates if the treatment has a significant effect.

```
anova(fit)
```

Analysis of Variance Table

```
Response: rate
          Df Sum Sq Mean Sq F value    Pr(>F)
power      3 66871 22290.2 66.797 2.883e-09 ***
Residuals 16 5339   333.7
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

7.1.1.5 95% Confidence Intervals for Treatment Means

A **confidence interval** provides a range of plausible values for the true mean etch rate at each power level.

```
## Number of replicates
n <- 5
## Extract sqrt(MSE) and error df
sqrt.MSE <- summary.fit$sigma
DF <- fit$df.residual
## Find t-value
t.value <- qt(0.975, DF)
## Calculate CIs
CI.lower <- mui.hat - t.value * sqrt.MSE / sqrt(n)
CI.upper <- mui.hat + t.value * sqrt.MSE / sqrt(n)

## Display CIs
data.frame(Power_Level = power_levels, Mean = mui.hat, Lower_CI = CI.lower, Upper_CI = CI.upper)
```

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	Power_Level	Mean	Lower_CI	Upper_CI
power1	160	551.2	533.8815	568.5185
power2	180	587.4	570.0815	604.7185
power3	200	625.4	608.0815	642.7185
	220	707.0	689.6815	724.3185

Alternatively, one can use a model without intercept

```
fit_nointercpt <- lm(rate ~ 0+power, data = etching_df)
summary(fit_nointercpt)
```

Call:

```
lm(formula = rate ~ 0 + power, data = etching_df)
```

Residuals:

Min	1Q	Median	3Q	Max
-25.4	-13.0	2.8	13.2	25.6

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
power160	551.200	8.169	67.47	<2e-16 ***
power180	587.400	8.169	71.90	<2e-16 ***
power200	625.400	8.169	76.55	<2e-16 ***
power220	707.000	8.169	86.54	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 18.27 on 16 degrees of freedom

Multiple R-squared: 0.9993, Adjusted R-squared: 0.9991

F-statistic: 5768 on 4 and 16 DF, p-value: < 2.2e-16

```
confint(fit_nointercpt)
```

	2.5 %	97.5 %
power160	533.8815	568.5185
power180	570.0815	604.7185
power200	608.0815	642.7185
power220	689.6815	724.3185

7.1.1.6 Comparison with Default “Treatment” Contrast

Fitting the model without specifying contrasts uses R’s default (“treatment” contrast), which sets $\tau_1 = 0$. The fundamental results (ANOVA, treatment means) remain unchanged.

```
fit1 <- lm(rate ~ power, data = etching_df)
summary(fit1)
```

```
Call:
lm(formula = rate ~ power, data = etching_df)

Residuals:
    Min      1Q  Median      3Q     Max 
 -25.4   -13.0    2.8   13.2   25.6 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) 551.200    8.169   67.471 < 2e-16 ***
power180     36.200   11.553   3.133  0.00642 ** 
power200     74.200   11.553   6.422 8.44e-06 ***
power220    155.800   11.553  13.485 3.73e-10 *** 
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 18.27 on 16 degrees of freedom
Multiple R-squared:  0.9261,    Adjusted R-squared:  0.9122 
F-statistic:  66.8 on 3 and 16 DF,  p-value: 2.883e-09
```

7.1.1.7 Pairwise Comparisons

Since our ANOVA result was significant, we perform **post-hoc tests** to determine exactly which pairs of power levels have different means.

7.1.1.7.1 Tukey’s HSD Test

Tukey’s Honest Significant Difference (HSD) controls the **family-wise error rate**, adjusting p-values to account for multiple comparisons.

```
fit.aov <- aov(rate ~ power, data = etching_df)
TukeyHSD(fit.aov)
```

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```
Tukey multiple comparisons of means
  95% family-wise confidence level

Fit: aov(formula = rate ~ power, data = etching_df)

$power
    diff      lwr      upr     p adj
180-160 36.2  3.145624 69.25438 0.0294279
200-160 74.2 41.145624 107.25438 0.0000455
220-160 155.8 122.745624 188.85438 0.0000000
200-180 38.0  4.945624 71.05438 0.0215995
220-180 119.6 86.545624 152.65438 0.0000001
220-200 81.6  48.545624 114.65438 0.0000146
```

7.1.1.7.2 Fisher's LSD Test

The **Fisher's Least Significant Difference (LSD)** test does not control the family-wise error rate but is more powerful.

```
with(etching_df, pairwise.t.test(rate, power, p.adj = "none"))
```

```
Pairwise comparisons using t tests with pooled SD

data: rate and power

  160     180     200
180 0.0064  -
200 8.4e-06 0.0046  -
220 3.7e-10 1.7e-08 2.7e-06

P value adjustment method: none
```

7.1.1.8 Checking Model Assumptions

The validity of our ANOVA results depends on three key assumptions about the model's residuals. We use diagnostic plots to check them.

```
r <- rstudent(fit)
fitted <- fitted.values(fit)
```

7.1.1.8.1 Normality of Residuals

A **Normal Q-Q plot** is used to check if the residuals are normally distributed. The points should fall closely along the straight diagonal line.

```
qqnorm(r)
qqline(r)
```

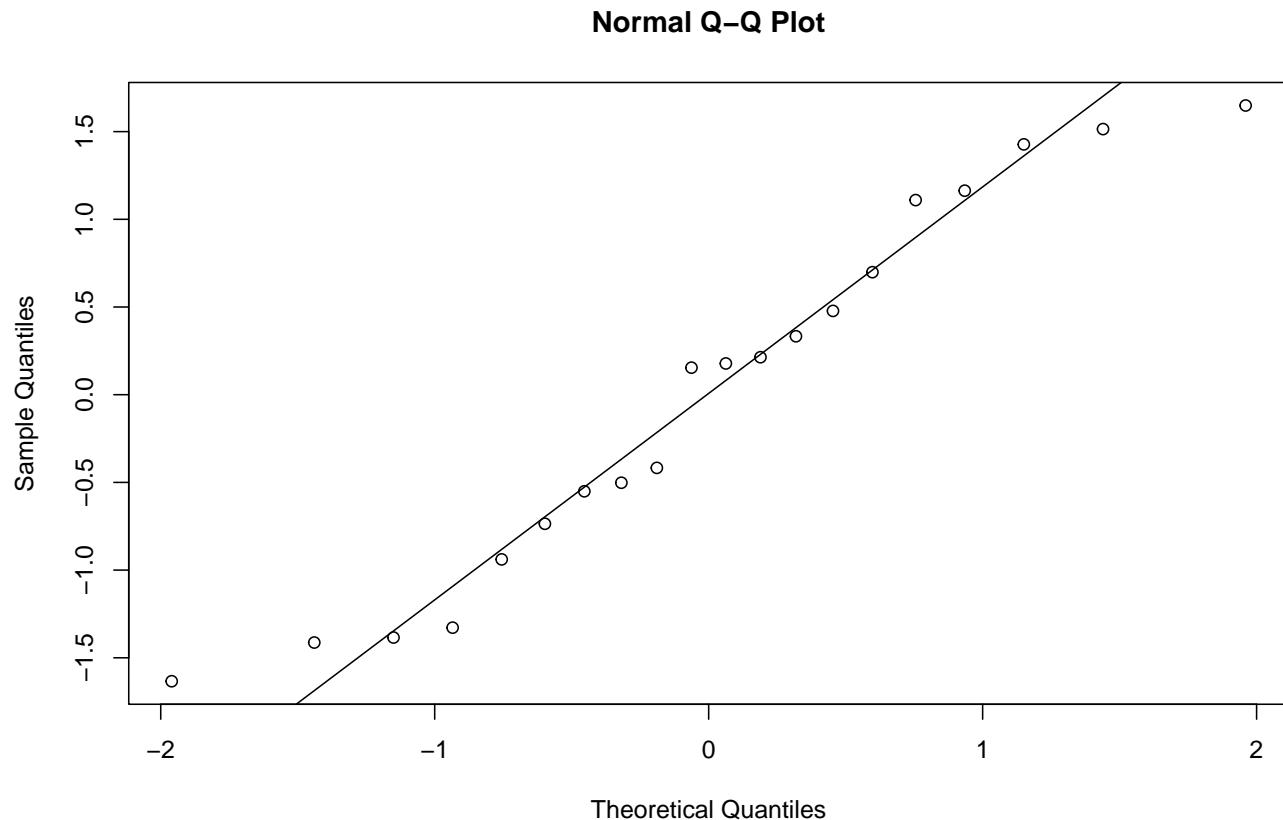


Figure 7.2: Normal Q-Q plot of standardized residuals.

7.1.1.8.2 Independence of Residuals

A plot of **residuals versus run order** helps check for independence. We look for random scatter around the zero line.

```
plot(r, ylab = "Standardized residuals", xlab = "Run order",
      main = "Plot of residuals vs. run order")
abline(h = 0)
```

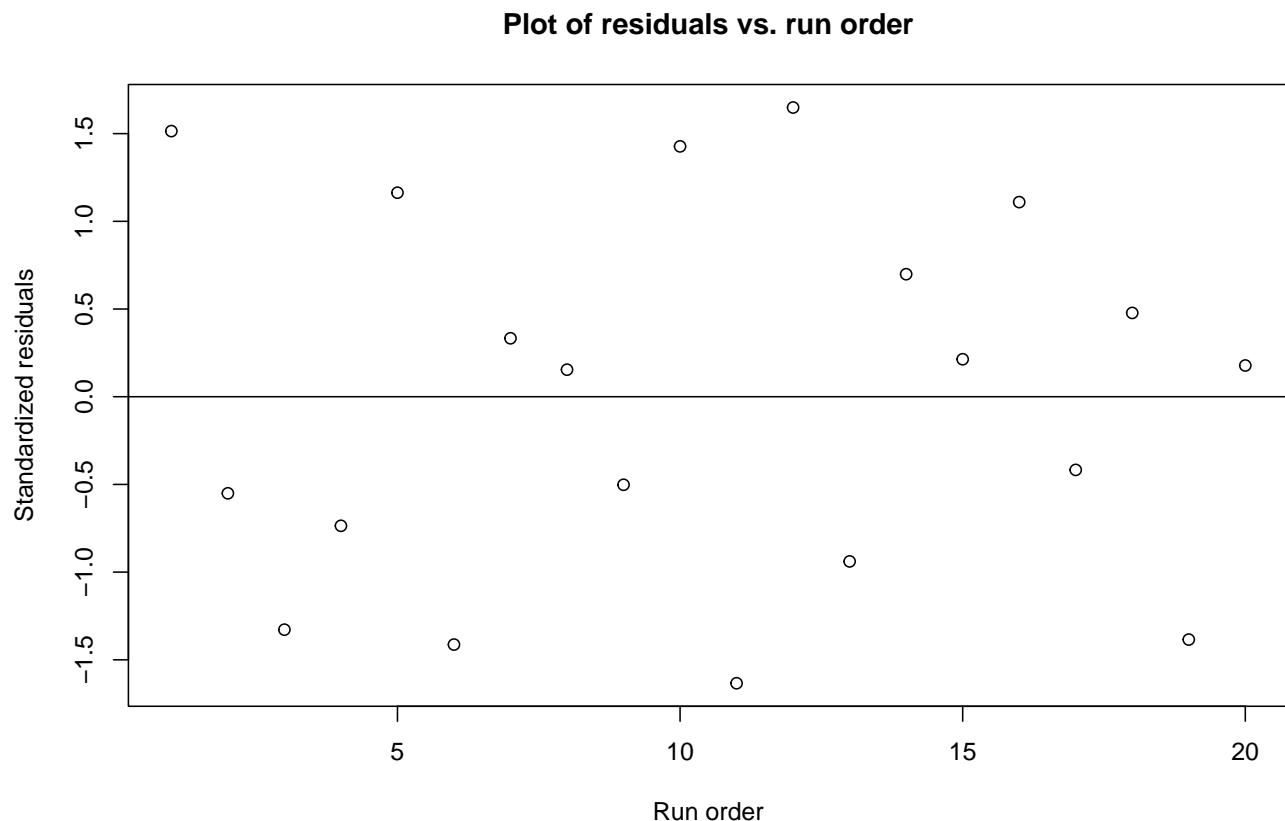


Figure 7.3: Standardized residuals vs. run order.

7.1.1.8.3 Constant Variance (Homoscedasticity)

A plot of **residuals versus fitted values** helps check for constant variance. The spread of residuals should be roughly constant across all fitted values.

```
plot(fitted, r, ylab = "Standardized residuals",
      xlab = "Fitted values", main = "Plot of residuals vs. fitted values")
abline(h = 0)
```

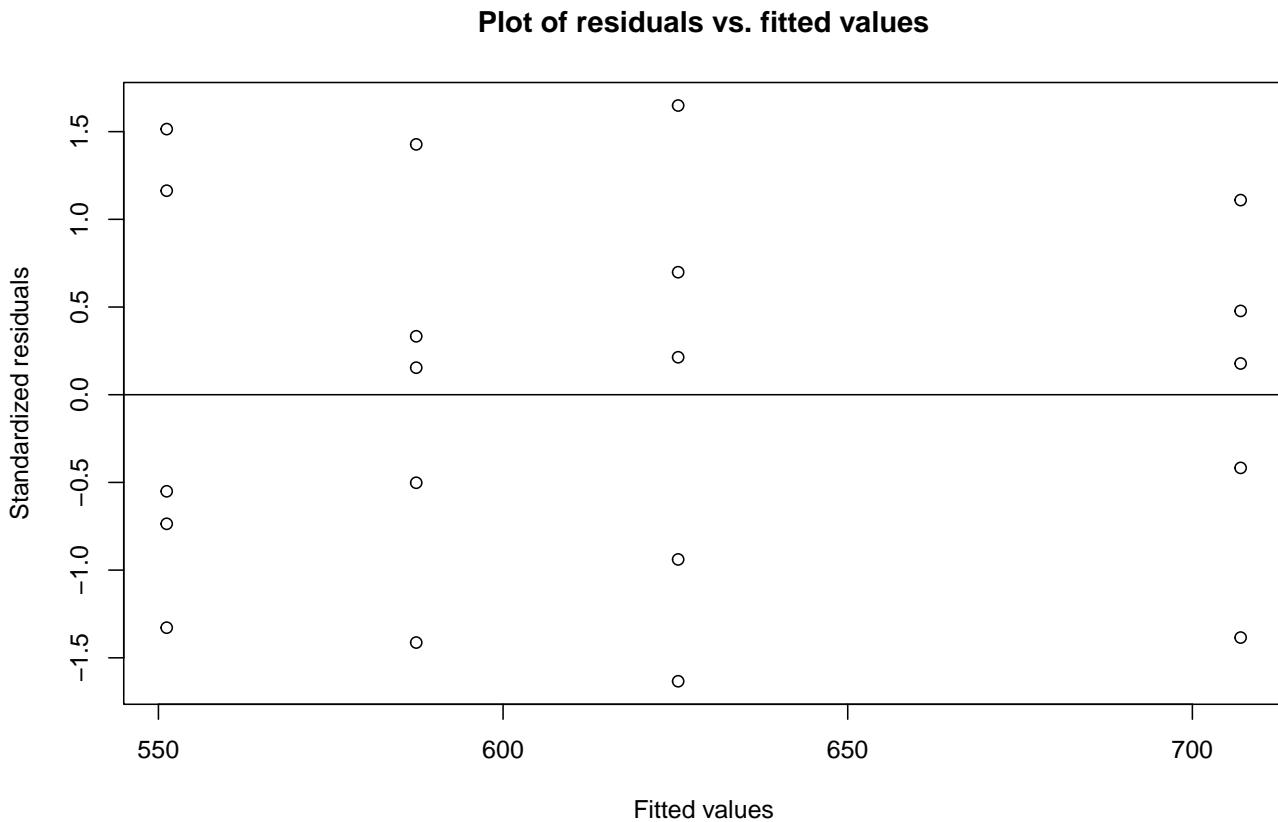


Figure 7.4: Standardized residuals vs. fitted values.

7.2 Unbalanced Designs with Unequal Sample Sizes

The ANOVA framework also handles **unbalanced designs**. We again start by creating a data frame.

```
## Create the data frame
bricks_df <- data.frame(
  density = c(21.8, 21.9, 21.7, 21.6, 21.7,
             21.7, 21.4, 21.5, 21.4,
             21.9, 21.8, 21.8, 21.6, 21.5,
             21.9, 21.7, 21.8, 21.4),
  temperature = factor(c(rep(100, 5), rep(125, 4), rep(150, 5), rep(175, 4)))
)

bricks_df
```

	density	temperature
1	21.8	100
2	21.9	100

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```
3    21.7      100
4    21.6      100
5    21.7      100
6    21.7      125
7    21.4      125
8    21.5      125
9    21.4      125
10   21.9      150
11   21.8      150
12   21.8      150
13   21.6      150
14   21.5      150
15   21.9      175
16   21.7      175
17   21.8      175
18   21.4      175
```

```
## Fit the model and get the ANOVA table
fit2 <- lm(density ~ temperature, data = bricks_df)
summary(fit2)
```

Call:

```
lm(formula = density ~ temperature, data = bricks_df)
```

Residuals:

Min	1Q	Median	3Q	Max
-0.300	-0.100	0.000	0.095	0.200

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	21.74000	0.07171	303.150	<2e-16 ***
temperature125	-0.24000	0.10757	-2.231	0.0425 *
temperature150	-0.02000	0.10142	-0.197	0.8465
temperature175	-0.04000	0.10757	-0.372	0.7156

Signif. codes:	0 ***	0.001 **	0.01 *	0.05 .
	'	'	'	'

Residual standard error: 0.1604 on 14 degrees of freedom

Multiple R-squared: 0.3025, Adjusted R-squared: 0.153

F-statistic: 2.024 on 3 and 14 DF, p-value: 0.1569

```
anova(fit2)
```

Analysis of Variance Table

```
Response: density
  Df  Sum Sq  Mean Sq F value Pr(>F)
temperature   3 0.15611 0.052037  2.0237 0.1569
Residuals   14 0.36000 0.025714
```

In this case, the large p-value (0.133) indicates that there is no statistically significant evidence that firing temperature affects brick density.

7.3 Randomized Complete Block Design

7.3.1 Vascular Graft Experiment

This section analyzes a **Randomized Complete Block Design (RCBD)**, used to control for a known source of variability (here, “batches of resin,” treated as **blocks**).

7.3.1.1 Data and Visualization

We structure the data in a `data.frame` to identify the response, treatment (`pressure`), and block (`batch`) for each observation.

```
## Define data vectors
strength <- c(90.3, 89.2, 98.2, 93.9, 87.4, 97.9,
             92.5, 89.5, 90.6, 94.7, 87.0, 95.8,
             85.5, 90.8, 89.6, 86.2, 88.0, 93.4,
             82.5, 89.5, 85.6, 87.4, 78.9, 90.7)
pressure_levels <- rep(c(8500, 8700, 8900, 9100), each = 6)
batch_levels <- rep(1:6, 4)

## Create the data frame
graft_df <- data.frame(
  strength = strength,
  pressure = factor(pressure_levels),
  batch = factor(batch_levels)
)

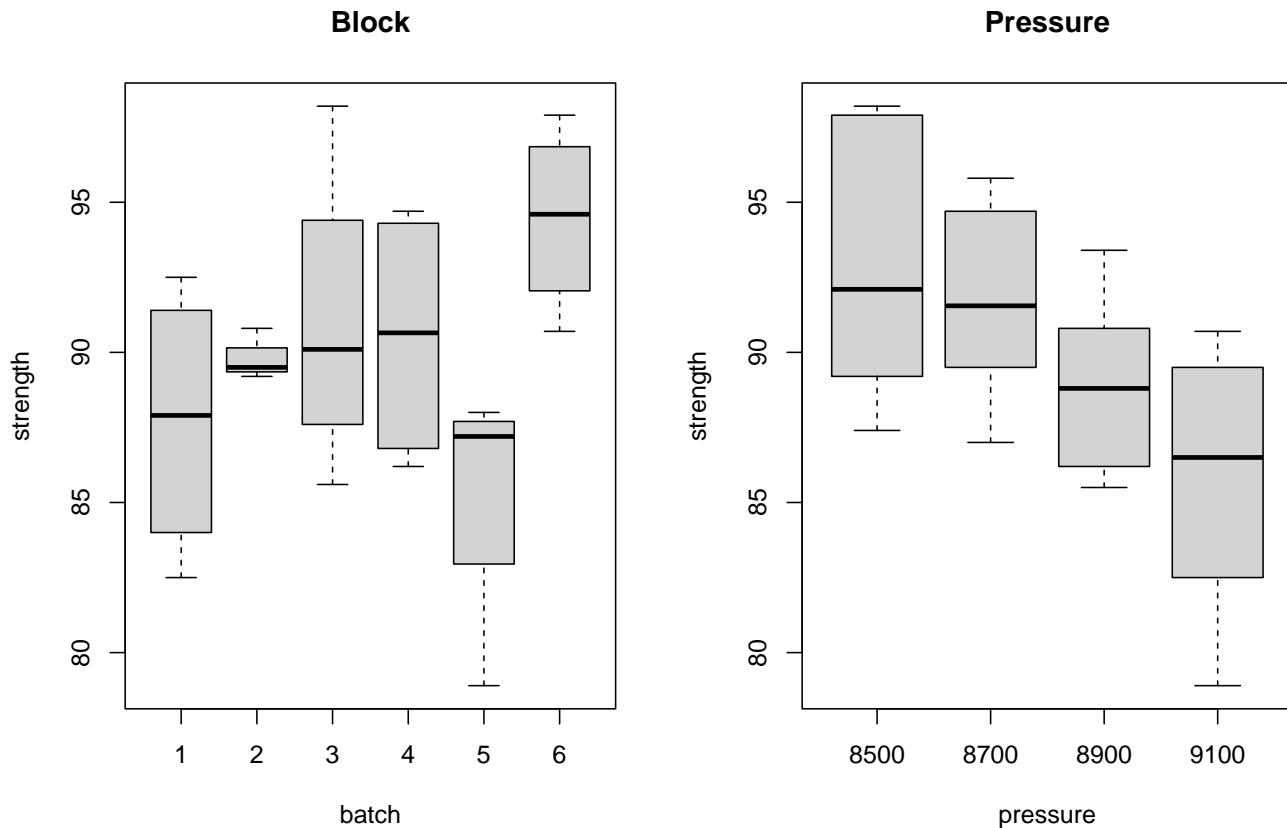
graft_df
```

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	strength	pressure	batch
1	90.3	8500	1
2	89.2	8500	2
3	98.2	8500	3
4	93.9	8500	4
5	87.4	8500	5
6	97.9	8500	6
7	92.5	8700	1
8	89.5	8700	2
9	90.6	8700	3
10	94.7	8700	4
11	87.0	8700	5
12	95.8	8700	6
13	85.5	8900	1
14	90.8	8900	2
15	89.6	8900	3
16	86.2	8900	4
17	88.0	8900	5
18	93.4	8900	6
19	82.5	9100	1
20	89.5	9100	2
21	85.6	9100	3
22	87.4	9100	4
23	78.9	9100	5
24	90.7	9100	6

Visualize the Block and Treatment Effects

```
par (mfrow = c(1,2))
#boxplot
plot(strength ~ batch, data=graft_df , main = "Block")
plot(strength ~ pressure, data=graft_df , main = "Pressure")
```



Interaction Plots

```
ggplot(graft_df, aes(x = pressure, y = strength, group = batch, color = batch)) +
  stat_summary(fun = mean, geom = "line", size = 1) +
  stat_summary(fun = mean, geom = "point", size = 3) +
  labs(
    title = "Interaction Plot: Batch and Pressure",
    x = "Pressure",
    y = "Strength",
    color = "Batch"
  ) +
  theme_minimal() +
  theme(plot.title = element_text(hjust = 0.5))
```

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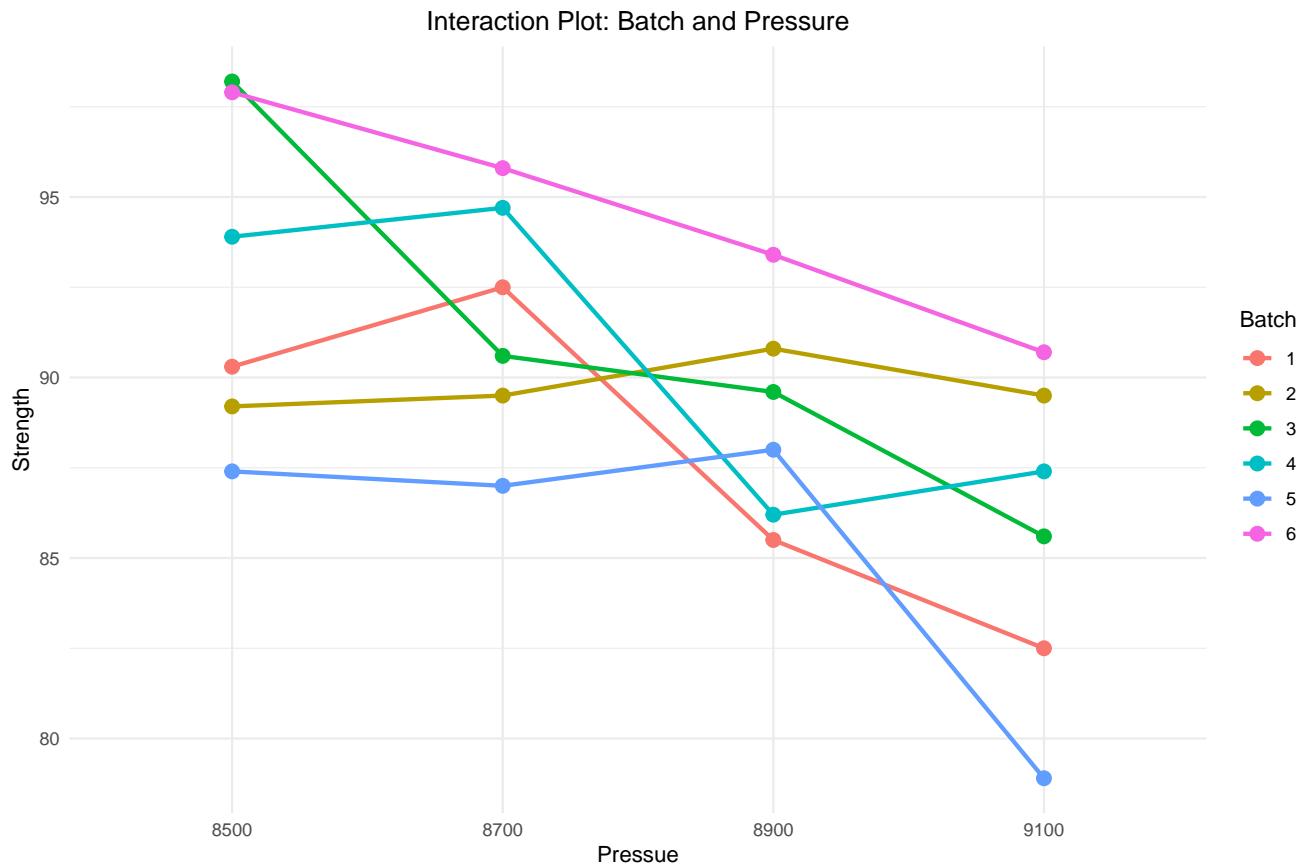


Figure 7.5: Interaction between Material Type and Temperature.

7.3.1.2 Model Fitting and ANOVA

The model `strength ~ pressure + batch` partitions the total variance into treatment, block, and error components. Our primary interest is in the significance of the `pressure` factor.

```
rcbd.fit1 <- aov(strength ~ pressure + batch, data = graft_df)
anova(rcbd.fit1)
```

Analysis of Variance Table

```
Response: strength
          Df Sum Sq Mean Sq F value    Pr(>F)
pressure     3 178.17  59.390  8.1071 0.001916 ***
batch       5 192.25  38.450  5.2487 0.005532 ***
Residuals  15 109.89    7.326
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The small p-value for pressure (0.0019) provides strong evidence that extrusion pressure significantly affects graft strength after accounting for batch differences.

7.3.1.3 Model Adequacy Checks

The assumptions for an RCBD are the same as for a CRD. We perform the same diagnostic checks.

```
rcbd.r1 <- rstudent(rcbd.fit1)
rcbd.fitted1 <- fitted.values(rcbd.fit1)

qqnorm(rcbd.r1, main = "Normal Q-Q Plot")
qqline(rcbd.r1)
plot(rcbd.fitted1, rcbd.r1, ylab = "Standardized residuals",
      xlab = "Fitted values", main = "Residuals vs. Fitted")
abline(h = 0)
plot(graft_df$pressure, rcbd.r1, ylab = "Standardized residuals",
      xlab = "Extrusion pressure", main = "Residuals vs. Treatment")
abline(h = 0)
plot(graft_df$batch, rcbd.r1, ylab = "Standardized residuals",
      xlab = "Batches of raw material", main = "Residuals vs. Block")
abline(h = 0)
```

7.3.1.4 Pairwise Comparisons

Again, since the treatment factor (pressure) is significant, we perform post-hoc tests.

7.3.1.4.1 Tukey's HSD Test

Tukey's HSD compares all pairs of treatment levels while controlling the family-wise error rate.

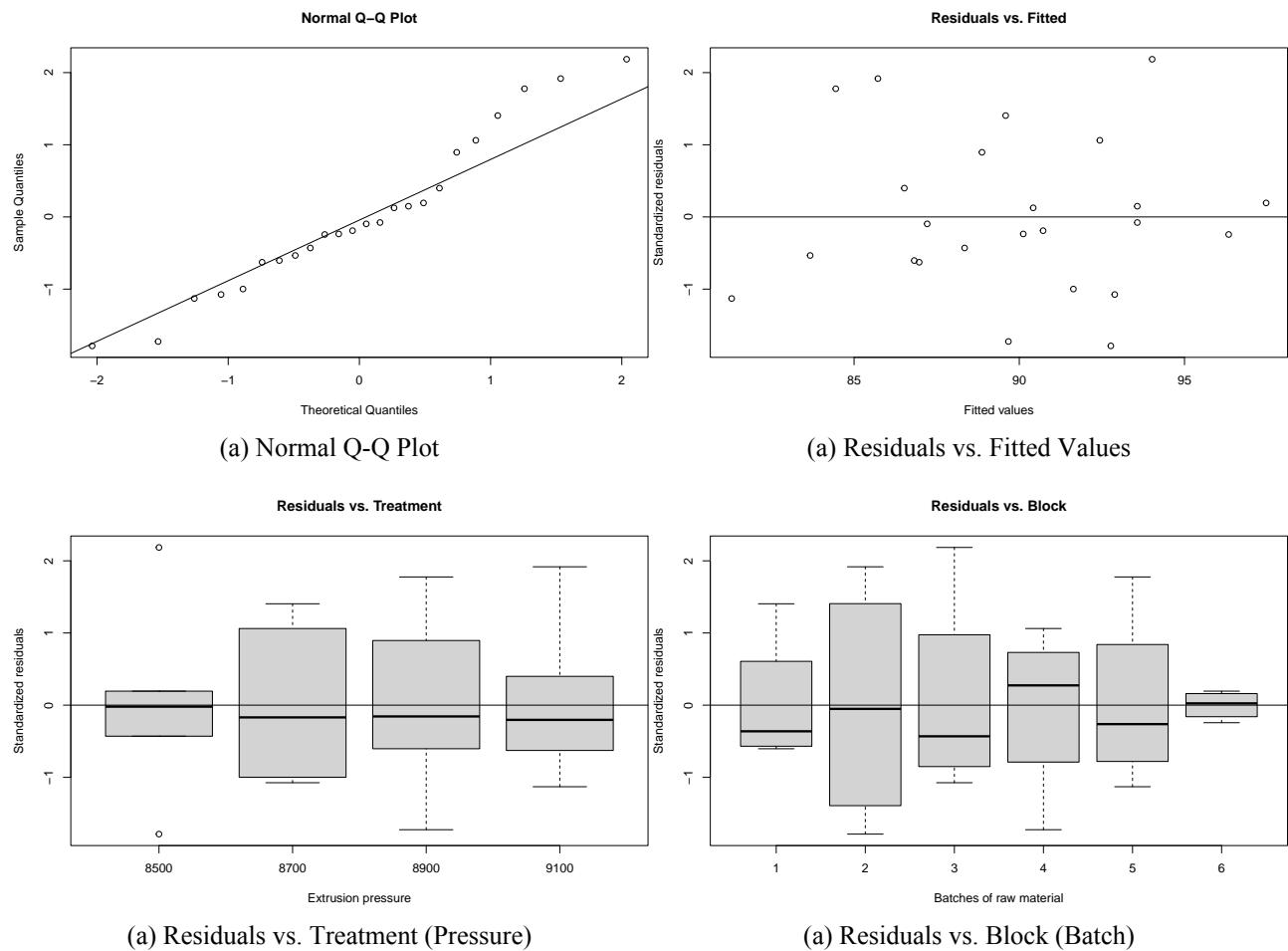
```
TukeyHSD(rcbd.fit1, which = "pressure")
```

```
Tukey multiple comparisons of means
95% family-wise confidence level

Fit: aov(formula = strength ~ pressure + batch, data = graft_df)

$pressure
    diff      lwr      upr      p adj
8700-8500 -1.133333 -5.637161 3.370495 0.8854831
8900-8500 -3.900000 -8.403828 0.603828 0.1013084
9100-8500 -7.050000 -11.553828 -2.546172 0.0020883
```

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```
8900-8700 -2.766667 -7.270495 1.737161 0.3245644
9100-8700 -5.916667 -10.420495 -1.412839 0.0086667
9100-8900 -3.150000 -7.653828 1.353828 0.2257674
```

7.3.1.4.2 Fisher's LSD Test

The `LSD.test()` function from the `agricolae` package correctly handles the error structure of an RCBD.

```
## install.packages("agricolae")
library(agricolae)

out <- LSD.test(rcbd.fit1, trt = "pressure", p.adj = "none", group = FALSE)
print(out$comparison)
```

	difference	pvalue	signif.	LCL	UCL
8500 - 8700	1.133333	0.4795		-2.1974047	4.464071
8500 - 8900	3.900000	0.0247	*	0.5692620	7.230738
8500 - 9100	7.050000	0.0004	***	3.7192620	10.380738
8700 - 8900	2.766667	0.0970	.	-0.5640714	6.097405
8700 - 9100	5.916667	0.0018	**	2.5859286	9.247405
8900 - 9100	3.150000	0.0621	.	-0.1807380	6.480738

8 Two-Factor Factorial Design

8.1 Battery Design Experiment

This analysis explores data from a **two-factor factorial experiment** designed to assess the lifespan of a battery. The experiment investigates two factors: **material type** (with 3 levels) and **operating temperature** (with 3 levels: 15°C, 70°C, and 125°C). The primary goal is to understand not only how each factor individually affects battery life but, more importantly, whether the effect of temperature depends on the material type used. This combined effect is known as an **interaction**.

8.2 Data Setup and Preparation

First, we organize the raw data into a structured `data.frame`. This is a best practice in R that makes the data easier to manage and the code more readable. We create columns for the response variable `life` and the two factors, `material` and `temperature`, ensuring they are treated as categorical variables (factors) for the analysis.

```
## Response variable: battery life
life <- c(130,155,74,180, 34,40,80,75, 20,70,82,58,
         150,188,159,126, 136,122,106,115, 25,70,58,45,
         138,110,168,160, 174,120,150,139, 96,104,82,60)

## Create the data frame
battery_df <- data.frame(
  life = life,
  material = factor(rep(1:3, each = 12)),
  temperature = factor(rep(rep(c(15, 70, 125), each = 4), 3))
)

## Preview the data
battery_df
```

	life	material	temperature
1	130	1	15
2	155	1	15
3	74	1	15

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4	180	1	15
5	34	1	70
6	40	1	70
7	80	1	70
8	75	1	70
9	20	1	125
10	70	1	125
11	82	1	125
12	58	1	125
13	150	2	15
14	188	2	15
15	159	2	15
16	126	2	15
17	136	2	70
18	122	2	70
19	106	2	70
20	115	2	70
21	25	2	125
22	70	2	125
23	58	2	125
24	45	2	125
25	138	3	15
26	110	3	15
27	168	3	15
28	160	3	15
29	174	3	70
30	120	3	70
31	150	3	70
32	139	3	70
33	96	3	125
34	104	3	125
35	82	3	125
36	60	3	125

8.3 Exploratory Data Analysis and Visualization

Before fitting a formal model, we visualize the data to get an intuition for the relationships between the factors and the response.

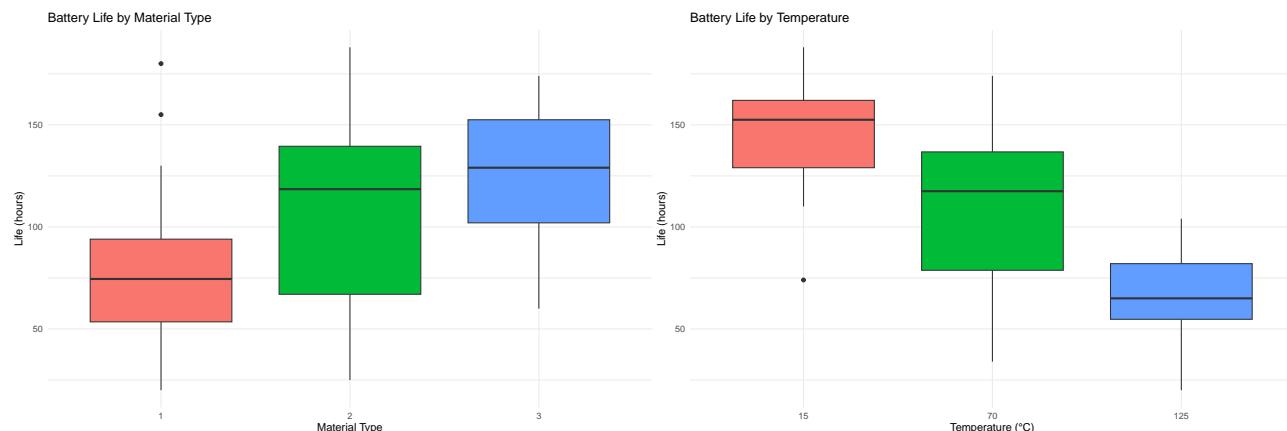
8.4 Boxplots of Main Effects

Boxplots are excellent for examining the distribution of battery life for each level of our factors independently. This gives us a preliminary look at the **main effects**—the individual impact of material type and temperature.

```
library(ggplot2)

## Boxplot for Material Type
ggplot(battery_df, aes(x = material, y = life, fill = material)) +
  geom_boxplot() +
  labs(title = "Battery Life by Material Type", x = "Material Type", y = "Life (hours)") +
  theme_minimal() +
  theme(legend.position = "none")

## Boxplot for Temperature
ggplot(battery_df, aes(x = temperature, y = life, fill = temperature)) +
  geom_boxplot() +
  labs(title = "Battery Life by Temperature", x = "Temperature (°C)", y = "Life (hours)") +
  theme_minimal() +
  theme(legend.position = "none")
```



(a) Distribution of Battery Life by Material and Temperature.(a) Distribution of Battery Life by Material and Temperature.

8.5 Interaction Plot

The most crucial plot for a factorial experiment is the **interaction plot**. It displays the mean battery life for each combination of material and temperature. If the lines are parallel, it suggests there is no interaction. If the lines are not parallel (i.e., they cross or diverge), it indicates that the effect of temperature on battery life is different for each material type, signaling a likely interaction.

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```
ggplot(battery_df, aes(x = temperature, y = life, group = material, color = material)) +  
  stat_summary(fun = mean, geom = "line", size = 1) +  
  stat_summary(fun = mean, geom = "point", size = 3) +  
  labs(  
    title = "Interaction Plot: Material Type and Temperature",  
    x = "Temperature (°C)",  
    y = "Average Battery Life (hours)",  
    color = "Material Type"  
) +  
  theme_minimal() +  
  theme(plot.title = element_text(hjust = 0.5))
```

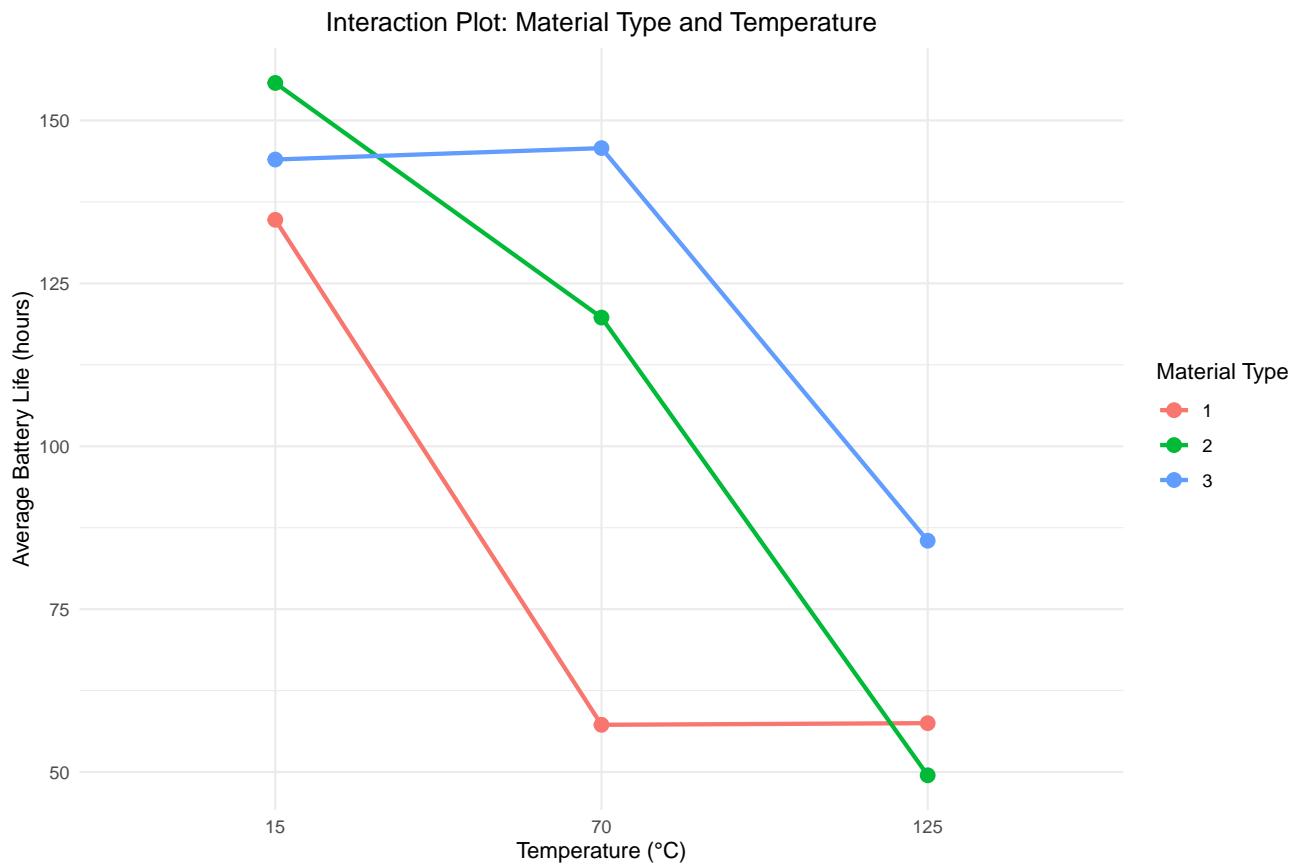


Figure 8.3: Interaction between Material Type and Temperature.

The non-parallel lines in the plot strongly suggest that a significant interaction effect is present. Specifically, the performance of Material 3 drops less dramatically with increasing temperature compared to Materials 1 and 2.

8.6 Model Fitting and Analysis of Variance (ANOVA)

We now fit a linear model to formally test the significance of the main effects and the interaction term. The model `life ~ material * temperature` is shorthand for `life ~ material + temperature + material:temperature`. We use a sum-to-zero contrast (`contr.sum`) for balanced interpretation of the effects. The **ANOVA table** will tell us if the variation caused by our factors is statistically significant compared to the random variation in the data.

```
## Fit the full factorial model
battery_fit <- lm(life ~ material * temperature,
                   data = battery_df,
                   contrasts = list(material = contr.sum, temperature = contr.sum))

summary(battery_fit)
```

Call:

```
lm(formula = life ~ material * temperature, data = battery_df,
   contrasts = list(material = contr.sum, temperature = contr.sum))
```

Residuals:

Min	1Q	Median	3Q	Max
-60.750	-14.625	1.375	17.938	45.250

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	105.528	4.331	24.367	< 2e-16 ***
material1	-22.361	6.125	-3.651	0.00111 **
material2	2.806	6.125	0.458	0.65057
temperature1	39.306	6.125	6.418	7.1e-07 ***
temperature2	2.056	6.125	0.336	0.73975
material1:temperature1	12.278	8.662	1.417	0.16778
material2:temperature1	8.111	8.662	0.936	0.35735
material1:temperature2	-27.972	8.662	-3.229	0.00325 **
material2:temperature2	9.361	8.662	1.081	0.28936

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 25.98 on 27 degrees of freedom

Multiple R-squared: 0.7652, Adjusted R-squared: 0.6956

F-statistic: 11 on 8 and 27 DF, p-value: 9.426e-07

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```
## Generate the ANOVA table  
anova(battery_fit)
```

Analysis of Variance Table

Response: life

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
material	2	10684	5341.9	7.9114	0.001976 **
temperature	2	39119	19559.4	28.9677	1.909e-07 ***
material:temperature	4	9614	2403.4	3.5595	0.018611 *
Residuals	27	18231	675.2		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1					

The ANOVA table shows very small p-values ($\text{Pr}(>F)$) for material, temperature, and, most importantly, the material:temperature interaction. This confirms our visual inspection: all effects are statistically significant. **Because the interaction is significant, our interpretation should focus on the interaction itself rather than the main effects in isolation.**

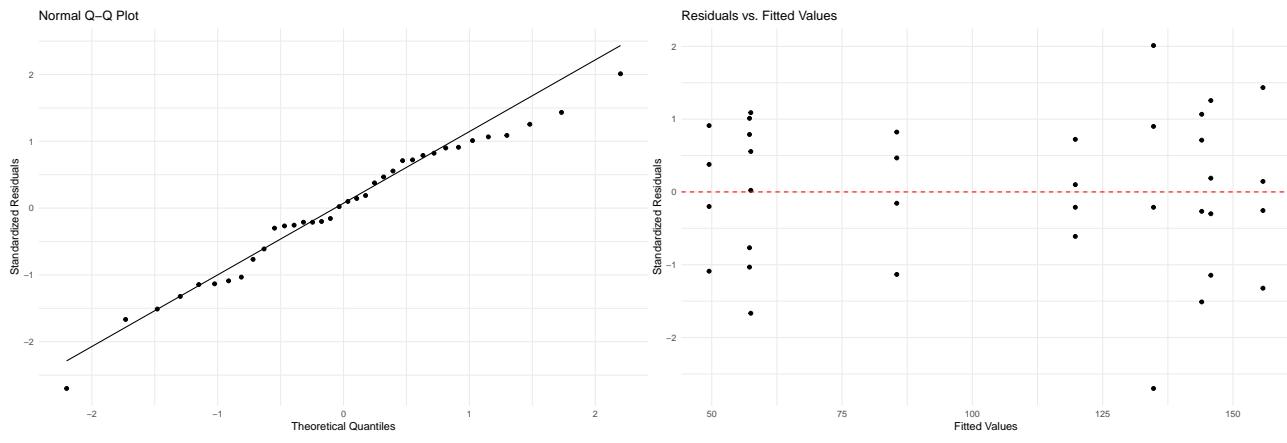
8.7 Model Adequacy Checks

The validity of our ANOVA results depends on the model's residuals meeting certain assumptions (normality, constant variance, independence). We check these with diagnostic plots.

```
## Extract standardized residuals and fitted values  
battery_fit_diag <- data.frame(  
  residuals = rstandard(battery_fit),  
  fitted = fitted.values(battery_fit)  
)  
  
## Normal Q-Q Plot  
p1 <- ggplot(battery_fit_diag, aes(sample = residuals)) +  
  stat_qq() +  
  stat_qq_line() +  
  labs(title = "Normal Q-Q Plot", x = "Theoretical Quantiles", y = "Standardized Residuals") +  
  theme_minimal()  
  
## Residuals vs. Fitted Plot  
p2 <- ggplot(battery_fit_diag, aes(x = fitted, y = residuals)) +  
  geom_point() +  
  geom_hline(yintercept = 0, linetype = "dashed", color = "red") +  
  labs(title = "Residuals vs. Fitted Values", x = "Fitted Values", y = "Standardized Residuals")
```

```
theme_minimal()

p1
p2
```



The Normal Q-Q plot shows the points falling roughly along the line, suggesting the normality assumption is met. The Residuals vs. Fitted plot shows a random scatter of points around the zero line, indicating that the variance is reasonably constant. The model assumptions appear to be satisfied.

8.8 Post-Hoc Analysis: Pairwise Comparisons

Since the interaction is significant, we must compare the means of the nine specific treatment combinations (3 materials \times 3 temperatures). Simply comparing the average effect of Material 1 vs. Material 2 would be misleading, as that difference depends on the temperature.

8.9 Tukey's HSD Test

Tukey's Honest Significant Difference (HSD) test is a post-hoc test that compares all possible pairs of means while controlling the family-wise error rate. We apply it to an `aov` model object. The output for the `material:temperature` interaction shows which specific combinations are significantly different from one another.

```
## Fit the model using aov() for Tukey's test
battery_aov <- aov(life ~ material * temperature, data = battery_df)
```

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```
## Perform Tukey's HSD test
TukeyHSD(battery_aov)
```

Tukey multiple comparisons of means
95% family-wise confidence level

Fit: aov(formula = life ~ material * temperature, data = battery_df)

\$material

	diff	lwr	upr	p adj
2-1	25.16667	-1.135677	51.46901	0.0627571
3-1	41.91667	15.614323	68.21901	0.0014162
3-2	16.75000	-9.552344	43.05234	0.2717815

\$temperature

	diff	lwr	upr	p adj
70-15	-37.25000	-63.55234	-10.94766	0.0043788
125-15	-80.66667	-106.96901	-54.36432	0.0000001
125-70	-43.41667	-69.71901	-17.11432	0.0009787

\$`material:temperature`

	diff	lwr	upr	p adj
2:15-1:15	21.00	-40.823184	82.823184	0.9616404
3:15-1:15	9.25	-52.573184	71.073184	0.9998527
1:70-1:15	-77.50	-139.323184	-15.676816	0.0065212
2:70-1:15	-15.00	-76.823184	46.823184	0.9953182
3:70-1:15	11.00	-50.823184	72.823184	0.9994703
1:125-1:15	-77.25	-139.073184	-15.426816	0.0067471
2:125-1:15	-85.25	-147.073184	-23.426816	0.0022351
3:125-1:15	-49.25	-111.073184	12.573184	0.2016535
3:15-2:15	-11.75	-73.573184	50.073184	0.9991463
1:70-2:15	-98.50	-160.323184	-36.676816	0.0003449
2:70-2:15	-36.00	-97.823184	25.823184	0.5819453
3:70-2:15	-10.00	-71.823184	51.823184	0.9997369
1:125-2:15	-98.25	-160.073184	-36.426816	0.0003574
2:125-2:15	-106.25	-168.073184	-44.426816	0.0001152
3:125-2:15	-70.25	-132.073184	-8.426816	0.0172076
1:70-3:15	-86.75	-148.573184	-24.926816	0.0018119
2:70-3:15	-24.25	-86.073184	37.573184	0.9165175
3:70-3:15	1.75	-60.073184	63.573184	1.0000000
1:125-3:15	-86.50	-148.323184	-24.676816	0.0018765
2:125-3:15	-94.50	-156.323184	-32.676816	0.0006078
3:125-3:15	-58.50	-120.323184	3.323184	0.0742711
2:70-1:70	62.50	0.676816	124.323184	0.0460388

```

3:70-1:70      88.50   26.676816 150.323184 0.0014173
1:125-1:70      0.25   -61.573184  62.073184 1.0000000
2:125-1:70     -7.75   -69.573184  54.073184 0.9999614
3:125-1:70     28.25   -33.573184  90.073184 0.8281938
3:70-2:70      26.00   -35.823184  87.823184 0.8822881
1:125-2:70     -62.25  -124.073184 -0.426816 0.0474675
2:125-2:70     -70.25  -132.073184 -8.426816 0.0172076
3:125-2:70     -34.25  -96.073184  27.573184 0.6420441
1:125-3:70     -88.25  -150.073184 -26.426816 0.0014679
2:125-3:70     -96.25  -158.073184 -34.426816 0.0004744
3:125-3:70     -60.25  -122.073184  1.573184 0.0604247
2:125-1:125    -8.00   -69.823184  53.823184 0.9999508
3:125-1:125    28.00   -33.823184  89.823184 0.8347331
3:125-2:125    36.00   -25.823184  97.823184 0.5819453

```

8.10 Fisher's LSD Method

The **Fisher's Least Significant Difference (LSD)** method is another option for pairwise comparisons. To test the interaction means, we must specify both factors in the `trt` argument.

```

library(agricolae)

## Perform LSD test on the interaction term
lsd_results <- LSD.test(battery_aov, trt = c("material", "temperature"),
                        p.adj = "none", group = FALSE)

## Print the comparison table
print(lsd_results$comparison)

```

	difference	pvalue	signif.	LCL	UCL
1:125 - 1:15	-77.25	0.0003	***	-114.950479	-39.549521
1:125 - 1:70	0.25	0.9892		-37.450479	37.950479
1:125 - 2:125	8.00	0.6667		-29.700479	45.700479
1:125 - 2:15	-98.25	0.0000	***	-135.950479	-60.549521
1:125 - 2:70	-62.25	0.0022	**	-99.950479	-24.549521
1:125 - 3:125	-28.00	0.1392		-65.700479	9.700479
1:125 - 3:15	-86.50	0.0001	***	-124.200479	-48.799521
1:125 - 3:70	-88.25	0.0001	***	-125.950479	-50.549521
1:15 - 1:70	77.50	0.0002	***	39.799521	115.200479
1:15 - 2:125	85.25	0.0001	***	47.549521	122.950479
1:15 - 2:15	-21.00	0.2631		-58.700479	16.700479
1:15 - 2:70	15.00	0.4214		-22.700479	52.700479
1:15 - 3:125	49.25	0.0124	*	11.549521	86.950479

8 Two-Factor Factorial Design

1:15 - 3:15	-9.25	0.6187	-46.950479	28.450479
1:15 - 3:70	-11.00	0.5544	-48.700479	26.700479
1:70 - 2:125	7.75	0.6765	-29.950479	45.450479
1:70 - 2:15	-98.50	0.0000	*** -136.200479	-60.799521
1:70 - 2:70	-62.50	0.0021	** -100.200479	-24.799521
1:70 - 3:125	-28.25	0.1358	-65.950479	9.450479
1:70 - 3:15	-86.75	0.0001	*** -124.450479	-49.049521
1:70 - 3:70	-88.50	0.0000	*** -126.200479	-50.799521
2:125 - 2:15	-106.25	0.0000	*** -143.950479	-68.549521
2:125 - 2:70	-70.25	0.0007	*** -107.950479	-32.549521
2:125 - 3:125	-36.00	0.0605	. -73.700479	1.700479
2:125 - 3:15	-94.50	0.0000	*** -132.200479	-56.799521
2:125 - 3:70	-96.25	0.0000	*** -133.950479	-58.549521
2:15 - 2:70	36.00	0.0605	. -1.700479	73.700479
2:15 - 3:125	70.25	0.0007	*** 32.549521	107.950479
2:15 - 3:15	11.75	0.5279	-25.950479	49.450479
2:15 - 3:70	10.00	0.5907	-27.700479	47.700479
2:70 - 3:125	34.25	0.0732	. -3.450479	71.950479
2:70 - 3:15	-24.25	0.1980	-61.950479	13.450479
2:70 - 3:70	-26.00	0.1685	-63.700479	11.700479
3:125 - 3:15	-58.50	0.0036	** -96.200479	-20.799521
3:125 - 3:70	-60.25	0.0029	** -97.950479	-22.549521
3:15 - 3:70	-1.75	0.9248	-39.450479	35.950479

The results from both Tukey's HSD and Fisher's LSD provide detailed p-values for comparing pairs of treatment combinations, allowing us to make specific conclusions, such as "at 125°C, Material 3 has a significantly longer life than Materials 1 and 2."