Advanced Topics in Regression

W. Evan Johnson, Ph.D.
Professor, Division of Infectious Disease
Director, Center for Data Science
Rutgers University – New Jersey Medical School

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Introduction to regression

In data science applications, it is very common to be interested in the relationship between two or more variables. For example, we we might want to use a data-driven approach that examines the relationship between baseball player statistics and success to guide the building of a baseball team with a limited budget. Before delving into this more complex example, we introduce necessary concepts needed to understand regression.

Introduction to regression

In statistical modeling, regression analysis is a set of statistical processes for estimating the relationships between a dependent variable (often called the 'outcome' or 'response' variable, or a 'label' in machine learning parlance) and one or more independent variables (often called 'predictors', 'covariates', 'explanatory variables' or 'features'). The most common form of regression analysis is **linear regression**, in which one finds the line (or a more complex linear combination) that most closely fits the data according to a specific mathematical criterion.

Introduction to regression

Consider the model function

$$y_i = \alpha + \beta x_i,$$

which describes a line with slope β and y-intercept α.

Introduction to regression

In general such a relationship may not hold exactly for the largely unobserved population of values of the independent and dependent variables; we call the unobserved deviations from the above equation the errors. Suppose we observe n data pairs and call them

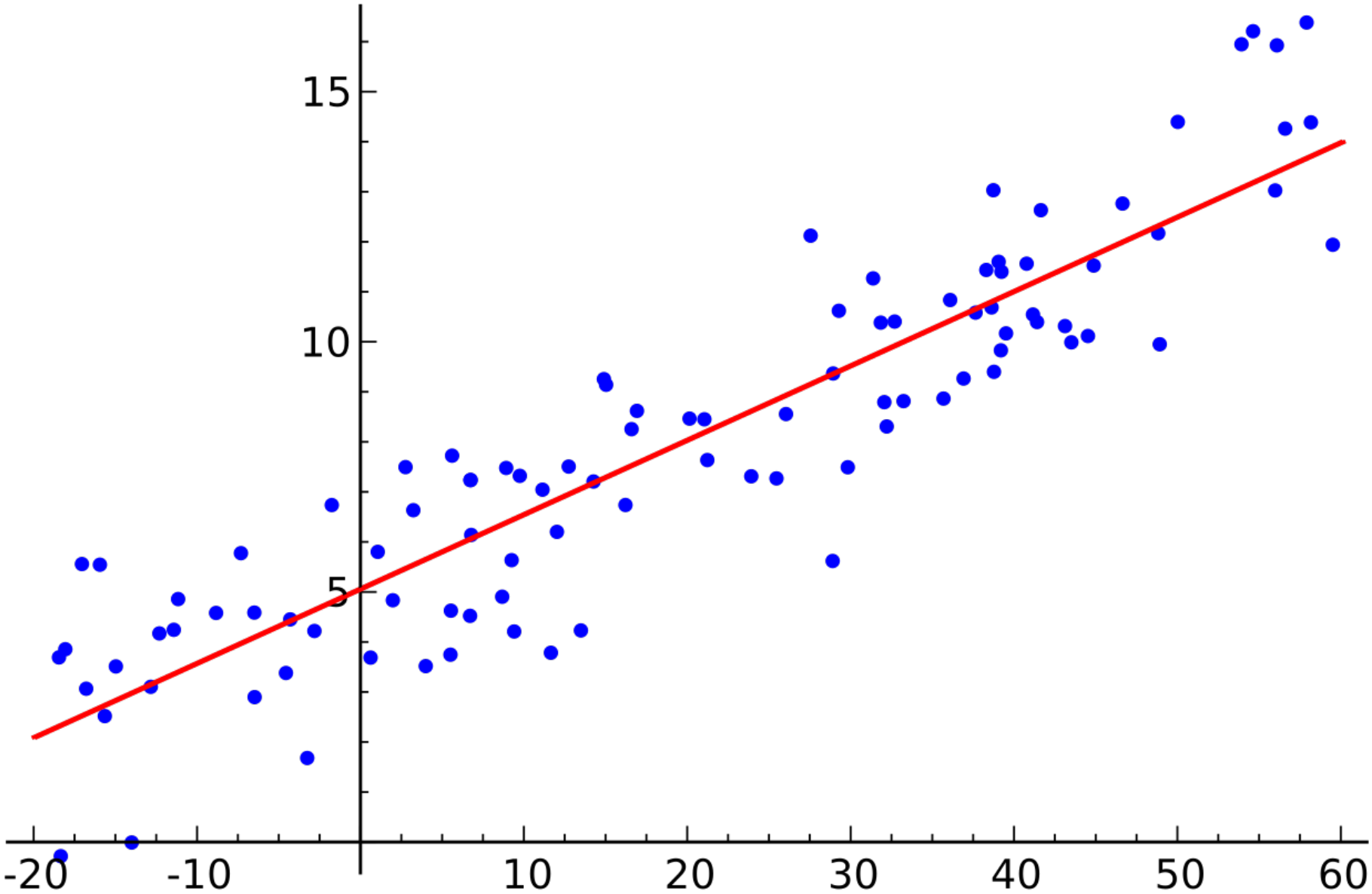
$$(x_i, y_i), i = 1, ..., n.$$

We can describe the underlying relationship between y_i and x_i involving this error term ϵ_i by

$$y_i = \alpha + \beta x_i + \epsilon_i.$$

This relationship between the true (but unobserved) underlying parameters α and β and the data points is called a **linear regression model**.

Introduction to regression

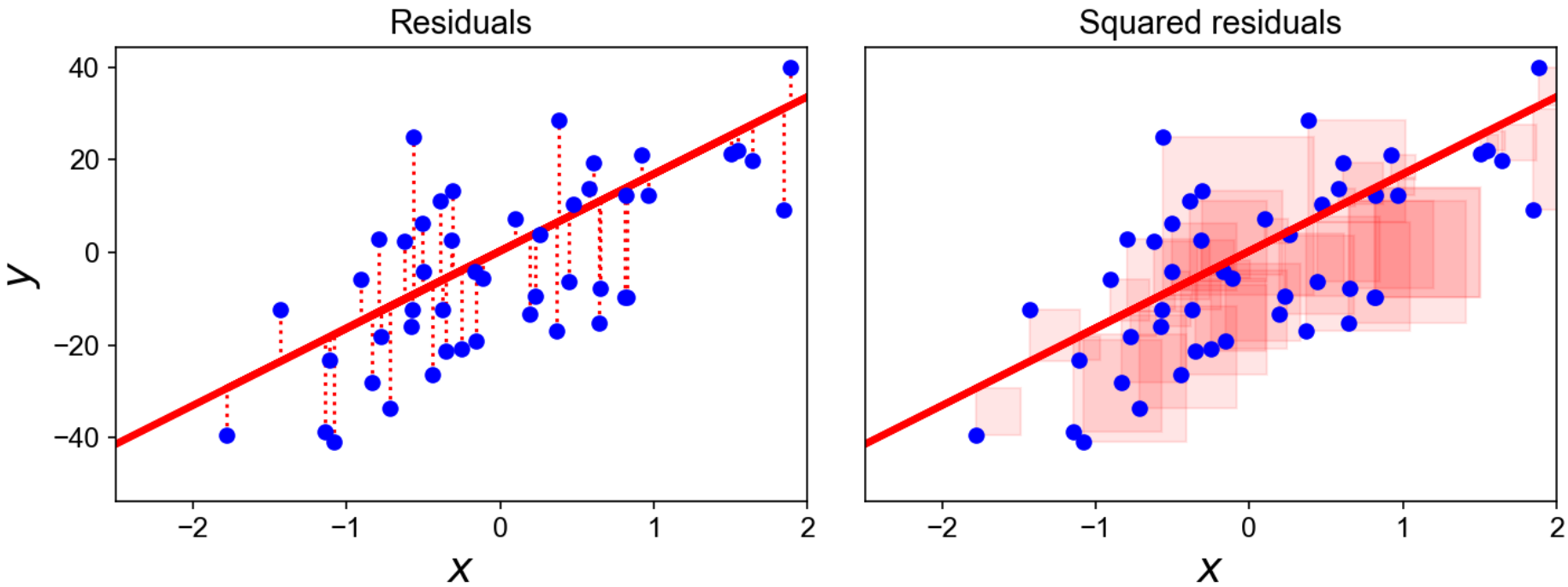


Introduction to regression

The goal is to find estimated values $\hat{\alpha}$ and $\hat{\beta}$ for the parameters α and β which would provide the "best" fit in some sense for the data points. Here, the "best" fit will be understood as in the least-squares approach: a line that minimizes the sum of squared residuals

$$\min_{\alpha,\beta} Q(\alpha, \beta) = \sum_{i=1}^{n} \epsilon_i^2 = \inf_{\alpha,\beta} \left\{ \sum_{i=1}^{n} (y_i - \alpha - \beta)^2 \right\}.$$

Introduction to regression



Introduction to regression

Now, we can extend this to include multiple (p) predictors:

$$y_i = x_{i1}\beta_1 + \ldots + x_{ip}\beta_p + \epsilon_i = \sum_{j=1}^{p} x_{ij}\beta_j + \epsilon_i.$$

Introduction to regression

In addition we can use matrices to represent our model. Assume $\mathbf{y} = (y_1, y_2, \ldots, y_n)$ with a matrix of predictors $\mathbf{X}$ and coefficient vector β ($n \times 1$ vector). Then we can define our regression equation as:

$$\mathbf{y} = X\beta + \epsilon,$$

where $\epsilon \sim N(\mathbf{0}, \sigma^2 I_n)$ and I_n is an identity matrix with dimension n.

Introduction to regression

Minimizing the least squared error is can be represented by

$$\hat{\beta} = \inf_{\beta} \left\{ \sum_{i=1}^{n} (y_i - \sum_{j=1}^{p} x_{ij}\beta_j)^2 \right\} = \inf_{\beta} \left\{ (\mathbf{y} - \mathbf{X}\beta)'(\mathbf{y} - \mathbf{X}\beta) \right\}$$

The regression fallacy

Wikipedia defines the *sophomore slump* as:

> *A sophomore slump or sophomore jinx or sophomore jitters refers to an instance in which a second, or sophomore, effort fails to live up to the standards of the first effort. It is commonly used to refer to the apathy of students (second year of high school, college or university), the performance of athletes (second season of play), singers/bands (second album), television shows (second seasons) and movies (sequels/prequels).*

The regression fallacy

In Major League Baseball, the rookie of the year (ROY) award is given to the first-year player who is judged to have performed the best. The *sophmore slump* phrase is used to describe the observation that ROY award winners don't do as well during their second year. For example, this Fox Sports article[1] asks "Will MLB's tremendous rookie class of 2015 suffer a sophomore slump?".

[1] http://www.foxsports.com/mlb/story/kris-bryant-carlos-correa-rookies-of-year-award-matt-duffy-francisco-lindor-kang-sano-120715

The regression fallacy

Does the data confirm the existence of a sophomore slump? Let's take a look. Examining the data for batting average, we see that this observation holds true for the top performing ROYs:

nameFirst	nameLast	rookie_year	rookie	sophomore
Willie	McCovey	1959	0.3541667	0.2384615
Ichiro	Suzuki	2001	0.3497110	0.3214838
Al	Bumbry	1973	0.3370787	0.2333333
Fred	Lynn	1975	0.3314394	0.3136095
Albert	Pujols	2001	0.3288136	0.3135593

In fact, the proportion of players that have a lower batting average their sophomore year is 0.7037037.

The regression fallacy

So is it "jitters" or "jinx"? To answer this question, let's turn our attention to all players that played the 2013 and 2014 seasons and batted more than 130 times (minimum to win Rookie of the Year).

The same pattern arises when we look at the top performers: batting averages go down for most of the top performers.

nameFirst	nameLast	2013	2014
Miguel	Cabrera	0.3477477	0.3126023
Hanley	Ramirez	0.3453947	0.2828508
Michael	Cuddyer	0.3312883	0.3315789
Scooter	Gennett	0.3239437	0.2886364
Joe	Mauer	0.3235955	0.2769231

But these are not rookies!

The regression fallacy

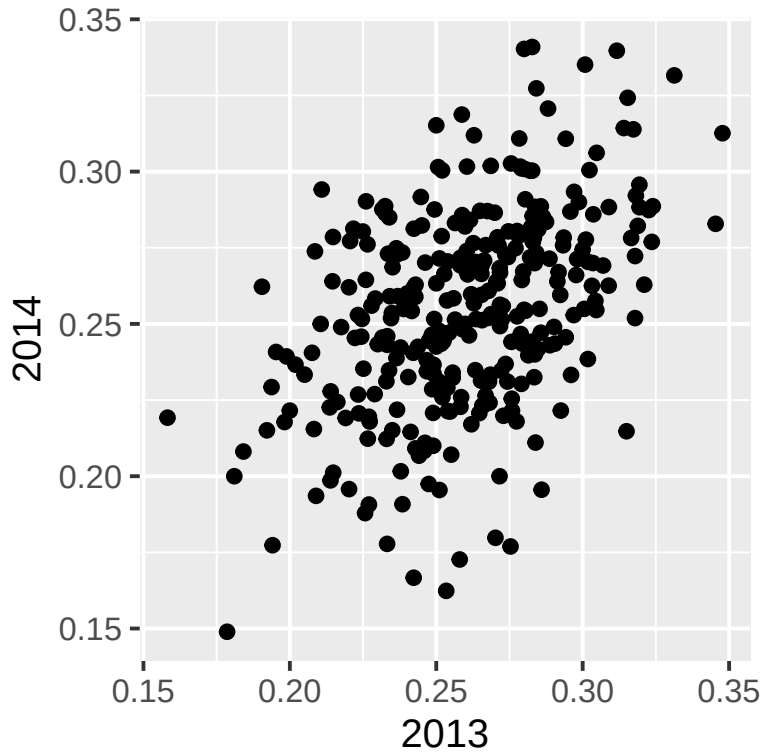
Also, look at what happens to the worst performers of 2013:

nameFirst	nameLast	2013	2014
Danny	Espinosa	0.1582278	0.2192192
Dan	Uggla	0.1785714	0.1489362
Jeff	Mathis	0.1810345	0.2000000
B. J.	Upton	0.1841432	0.2080925
Adam	Rosales	0.1904762	0.2621951

Their batting averages mostly go up!

The regression fallacy

Is this some sort of reverse sophomore slump? It is not. There is no such thing as the sophomore slump. This is all explained with a simple statistical fact: the correlation for performance in two separate years is high, but not perfect:



The regression fallacy

The correlation is 0.460254 and the data look very much like a bivariate normal distribution, which means we predict a 2014 batting average Y for any given player that had a 2013 batting average X with:

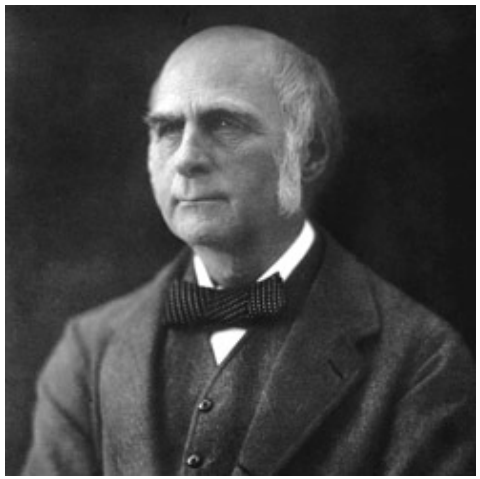
$$\frac{Y - .255}{.032} = 0.46\left(\frac{X - .261}{.023}\right)$$

Because the correlation is not perfect, regression tells us that, on average, expect high performers from 2013 to do a bit worse in 2014. It's not a jinx; it's just due to chance. The ROY are selected from the top values of X so it is expected that Y will **regress to the mean**.

Case study: is height hereditary?

Lets take a look that the datasetfrom which regression was born:

Francis Galton[2] studied the variation and heredity of human traits. Among many other traits, Galton collected and studied height data from families to try to understand heredity. While doing this, he developed the concepts of correlation and regression, as well as a connection to pairs of data that follow a normal distribution.



[2] https://en.wikipedia.org/wiki/Francis_Galton

Case study: is height hereditary?

A very specific question Galton tried to answer was: how well can we predict a child's height based on the parents' height? The technique he developed to answer this question was called **regression**!

Historical note: Galton made important contributions to statistics and genetics, but he was also one of the first proponents of eugenics, a scientifically flawed philosophical movement favored by many biologists of Galton's time but with horrific historical consequences. You can read more about it here: https://pged.org/history-eugenics-and-genetics/.

Case study: is height hereditary?

We have access to Galton's family height data through the **HistData** package. To imitate Galton's analysis, we will create a dataset with the heights of fathers and a randomly selected son of each family:

```
library(tidyverse)
library(HistData)
data("GaltonFamilies")

set.seed(1983)
galton_heights <- GaltonFamilies %>%
  filter(gender == "male") %>%
  group_by(family) %>%
  sample_n(1) %>%
  ungroup() %>%
  select(father, childHeight) %>%
  rename(son = childHeight)
```

Case study: is height hereditary?

Suppose we were asked to summarize the father and son data. Since both distributions are well approximated by the normal distribution, we could use the two averages and two standard deviations as summaries:

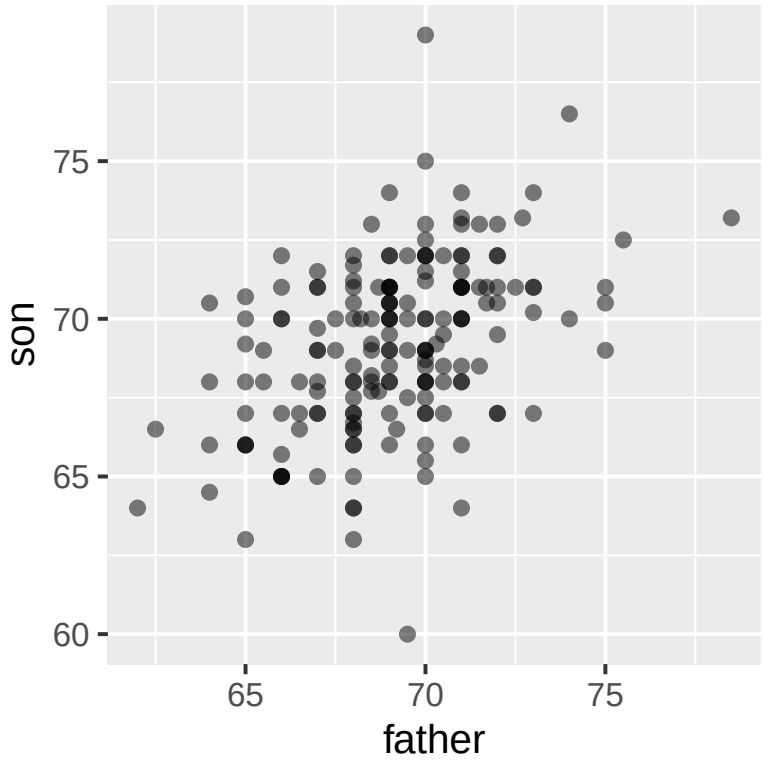
```
galton_heights %>%
  summarize(mean(father), sd(father), mean(son), sd(son))
```

```
## # A tibble: 1 x 4
##   `mean(father)` `sd(father)` `mean(son)` `sd(son)`
##            <dbl>        <dbl>       <dbl>     <dbl>
## 1           69.1         2.55        69.2      2.71
```

However, this summary fails to describe an important characteristic of the data: the trend that the taller the father, the taller the son.

Case study: is height hereditary?

```
galton_heights %>% ggplot(aes(father, son)) +
  geom_point(alpha = 0.5)
```



Case study: is height hereditary?

The correlation between father and son's heights is:

```
galton_heights %>%
    summarize(r = cor(father, son)) %>%
    pull(r)
```

```
## [1] 0.4334102
```

Diversion: Maximum Likelihood for a Normal mean

Assume $\mathbf{x} = (x_1, x_2, \ldots, x_N)$, where x_is are independent from a Normal(μ, σ^2) distribution, where $\mathbf{x}$ is observed and σ^2 is known. Then

$$L(\mu|\mathbf{x}) = \left\{ \frac{1}{2\pi\sigma^2} \right\}^{N/2} exp \left\{ -\frac{1}{2\sigma^2} \sum_{i=1}^{N} (x_i - \mu)^2 \right\}$$

Diversion: Maximum Likelihood for a Normal mean

Assume $\mathbf{x} = (x_1, x_2, \ldots, x_N)$, where x_is are independent from a Normal(μ, σ^2) distribution, where $\mathbf{x}$ is observed and σ^2 is known. Then

$$L(\mu|\mathbf{x}) = \left\{ \frac{1}{2\pi\sigma^2} \right\}^{N/2} exp \left\{ -\frac{1}{2\sigma^2} \sum_{i=1}^{N} (x_i - \mu)^2 \right\}$$

Notice we can maximize $L(\mu|\mathbf{x})$ by minimizing $\sum_{i=1}^{N}(x_i - \mu)^2$ for μ.

Diversion: Maximum Likelihood for a Normal mean

Note the following:

$$\sum_{i=1}^{N}(x_i - \mu)^2 = \sum_{i=1}^{N}(x_i^2 - 2\mu x_i + \mu^2)$$

Diversion: Maximum Likelihood for a Normal mean

Note the following:

$$\sum_{i=1}^{N}(x_i - \mu)^2 = \sum_{i=1}^{N}(x_i^2 - 2\mu x_i + \mu^2)$$

$$= \sum_{i=1}^{N} x_i^2 - 2\mu \sum_{i=1}^{N} x_i + N\mu^2$$

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Diversion: Maximum Likelihood for a Normal mean

therefore:

$$\frac{\partial}{\partial \mu} = -2 \sum x_i + 2N\hat{\mu} \stackrel{set}{=} 0$$

Diversion: Maximum Likelihood for a Normal mean

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$$\frac{\partial}{\partial \mu} = -2\sum x_i + 2N\hat{\mu} \stackrel{set}{=} 0$$

$$\Rightarrow N\hat{\mu} = \sum x_i$$

Diversion: Maximum Likelihood for a Normal mean

therefore:

$$\begin{aligned}\frac{\partial}{\partial \mu} &= -2\sum x_i + 2N\hat{\mu} \stackrel{set}{=} 0 \\ &\Rightarrow N\hat{\mu} = \sum x_i \\ &\Rightarrow \hat{\mu} = \frac{\sum x_i}{N}\end{aligned}$$

Diversion: Maximum Likelihood for Regression

Assume $\mathbf{y} = (y_1, y_2, \ldots, y_N)$ with a matrix of predictors $\mathbf{X}$ and coefficient vector β ($n \times 1$ vector). Then we can define our regression equation as:

$$\mathbf{y} = X\beta + \epsilon,$$

where $\epsilon \sim N(\mathbf{0}, \sigma^2 I_N)$ and I_N is an identity matrix with dimension N.

Diversion: Maximum Likelihood for Regression

Now, extending the Normal mean MLE to regression, we note that

$$\sum_{i=1}^{N}(y_i - x_1\beta_1 - \ldots - x_N\beta_N)^2 = (\mathbf{y} - \mathbf{X}\beta)'(\mathbf{y} - \mathbf{X}\beta),$$

Diversion: Maximum Likelihood for Regression

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$$\sum_{i=1}^{N}(y_i - x_1\beta_1 - \ldots - x_N\beta_N)^2 = (\mathbf{y} - \mathbf{X}\beta)'(\mathbf{y} - \mathbf{X}\beta),$$

so

$$L(\beta|\mathbf{X}, \mathbf{y}) = \left\{\frac{1}{2\pi\sigma^2}\right\}^{N/2} exp\left\{-\frac{1}{2\sigma^2}(\mathbf{y} - \mathbf{X}\beta)'(\mathbf{y} - \mathbf{X}\beta)\right\}.$$

Thus maximizing the Likelihood is equivalent to minimizing $(\mathbf{y} - \mathbf{X}\beta)'(\mathbf{y} - \mathbf{X}\beta)$, or in other words, minimizing the sum of the squared error!

Diversion: Maximum Likelihood for Regression

Note

$$(\mathbf{y} - \mathbf{X}\beta)'(\mathbf{y} - \mathbf{X}\beta) = \mathbf{y}'\mathbf{y} - 2\beta'\mathbf{X}'\mathbf{y} + \beta'\mathbf{X}'\mathbf{X}\beta,$$

Diversion: Maximum Likelihood for Regression

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and therefore

$$\frac{\partial}{\partial \beta} = -2\mathbf{X}'\mathbf{y} + 2\mathbf{X}'\mathbf{X}\hat{\beta} \stackrel{set}{=} 0$$

Diversion: Maximum Likelihood for Regression

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$$\Rightarrow \mathbf{X}'\mathbf{X}\hat{\beta} = \mathbf{X}'\mathbf{y}$$

Diversion: Maximum Likelihood for Regression

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and therefore

$$\begin{aligned}
\frac{\partial}{\partial \beta} &= -2\mathbf{X}'\mathbf{y} + 2\mathbf{X}'\mathbf{X}\hat{\beta} \overset{set}{=} 0 \\
&\Rightarrow \mathbf{X}'\mathbf{X}\hat{\beta} = \mathbf{X}'\mathbf{y} \\
&\Rightarrow (\mathbf{X}'\mathbf{X})^{-1}\mathbf{X}'\mathbf{X}\hat{\beta} = (\mathbf{X}'\mathbf{X})^{-1}\mathbf{X}'\mathbf{y}
\end{aligned}$$

Diversion: Maximum Likelihood for Regression

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$$(\mathbf{y} - \mathbf{X}\beta)'(\mathbf{y} - \mathbf{X}\beta) = \mathbf{y}'\mathbf{y} - 2\beta'\mathbf{X}'\mathbf{y} + \beta'\mathbf{X}'\mathbf{X}\beta,$$

and therefore

$$\begin{aligned}
\frac{\partial}{\partial \beta} &= -2\mathbf{X}'\mathbf{y} + 2\mathbf{X}'\mathbf{X}\hat{\beta} \overset{set}{=} 0 \\
&\Rightarrow \mathbf{X}'\mathbf{X}\hat{\beta} = \mathbf{X}'\mathbf{y} \\
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&\Rightarrow \hat{\beta} = (\mathbf{X}'\mathbf{X})^{-1}\mathbf{X}'\mathbf{y}
\end{aligned}$$

Diversion: Maximum Likelihood for Regression

Now note:

$$E[\hat{\beta}] = E[(\mathbf{X}'\mathbf{X})^{-1}\mathbf{X}'\mathbf{y}]$$

Diversion: Maximum Likelihood for Regression

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$$\begin{aligned} E[\hat{\beta}] &= E[(\mathbf{X}'\mathbf{X})^{-1}\mathbf{X}'\mathbf{y}] \\ &= (\mathbf{X}'\mathbf{X})^{-1}\mathbf{X}'E[\mathbf{y}] \end{aligned}$$

Diversion: Maximum Likelihood for Regression

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Diversion: Maximum Likelihood for Regression

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Diversion: Maximum Likelihood for Regression

And, remembering that

$$Var[\mathbf{Ay}] = \mathbf{A}\{Var[\mathbf{y}]\}\mathbf{A}',$$

so therefore,

$$Var[\hat{\beta}] = Var[(\mathbf{X}'\mathbf{X})^{-1}\mathbf{X}'\mathbf{y}]$$

Diversion: Maximum Likelihood for Regression

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Diversion: Maximum Likelihood for Regression

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Diversion: Maximum Likelihood for Regression

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Diversion: Maximum Likelihood for Regression

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Typically, we use the following to estimate σ^2:

$$\hat{\sigma}^2 = \frac{1}{N-p-1}(\mathbf{y} - X\widehat{\beta})'(\mathbf{y} - X\widehat{\beta})$$

Diversion: Maximum Likelihood for Regression

So we can conduct a hypothesis test β, where $H_0 : \beta_j = 0$ versus $H_a : \beta_j \neq 0$ using the statistic:

$$t_{\beta_j} = \frac{\hat{\beta}_j}{\hat{\sigma}\sqrt{v_{jj}}},$$

where v_{jj} is the jth diagonal element of $\mathbf{V} = (\mathbf{X}'\mathbf{X})^{-1}$. Under H_0, t_{β_j} will follow a t distribution with $N - p - 1$ degrees of freedom.

Case study: is height hereditary?

Thus using our estimator for β:

$$\widehat{\beta} = (X'X)^{-1}X'\mathbf{y}$$

```
X <- cbind(1,galton_heights$father)
y <- galton_heights$son
beta_hat <- solve(t(X)%*%X)%*%t(X)%*%y
beta_hat
```

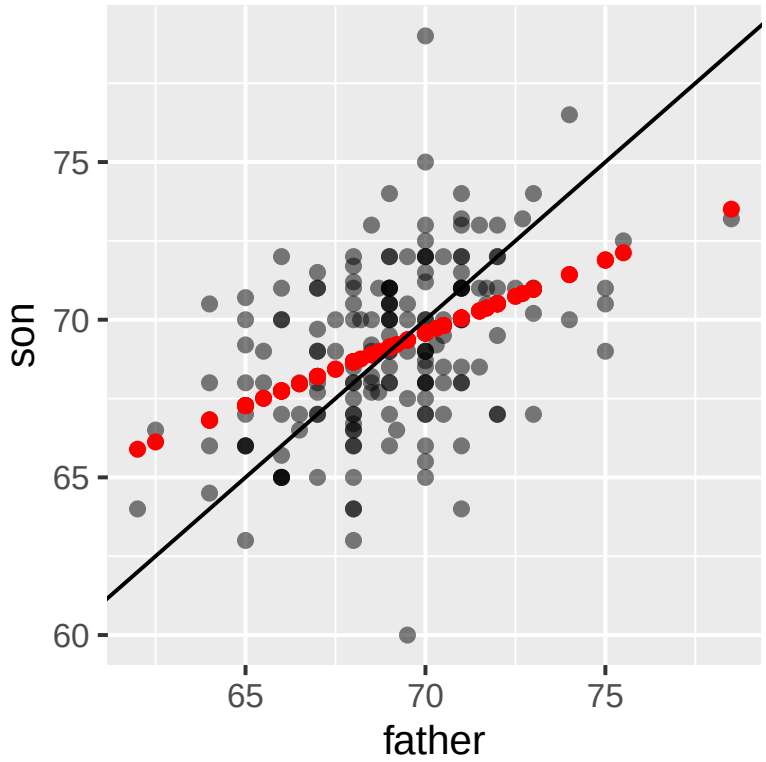
```
##             [,1]
## [1,] 37.287605
## [2,]  0.461392
```

Case study: is height hereditary?

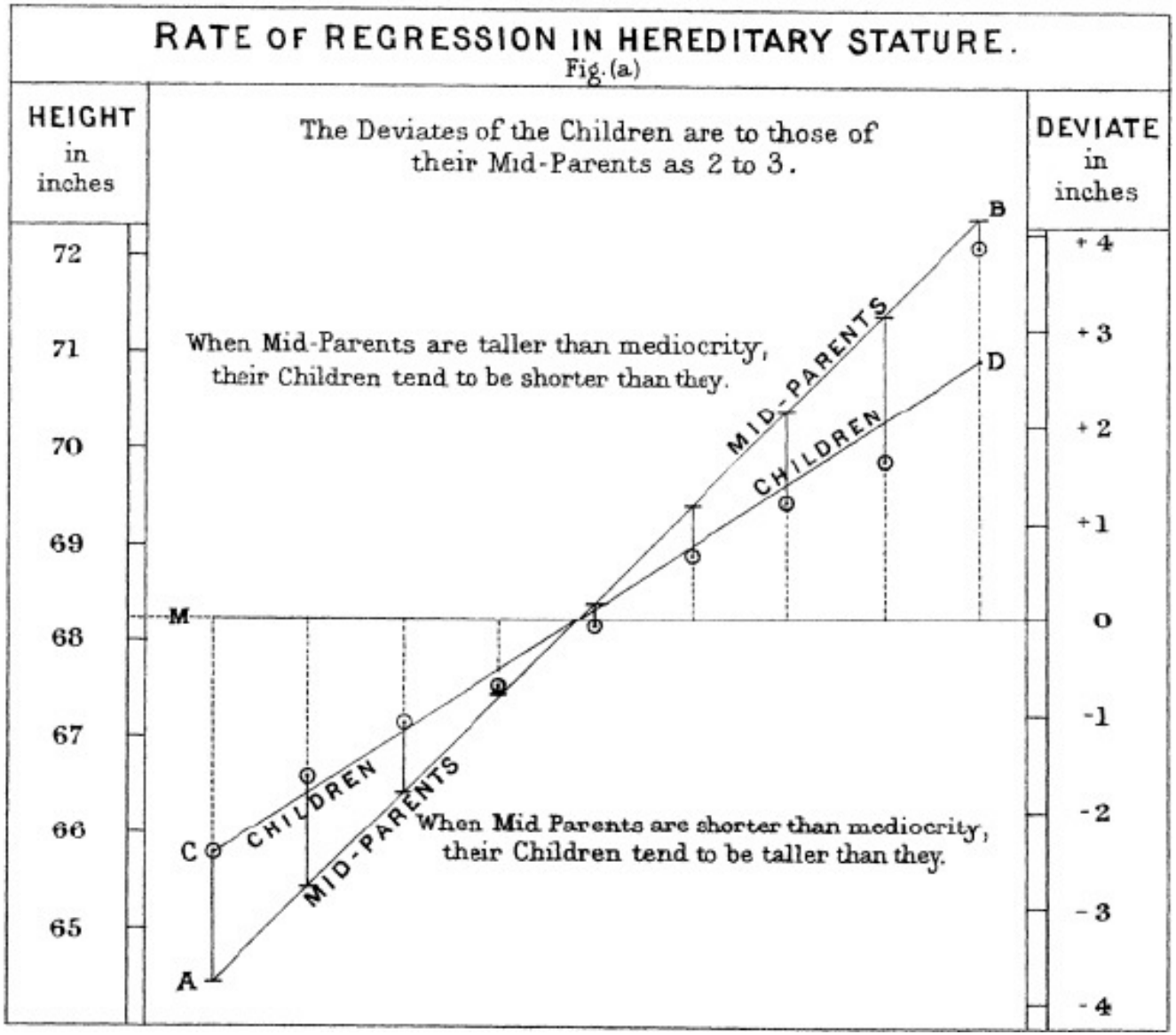
Predicted values can be obtained by: $\hat{y} = X\hat{\beta}$, In R:

```
y_hat <- X %*% beta_hat

galton_heights %>% ggplot(aes(father, son)) +
  geom_point(alpha = 0.5) +
  geom_point(aes(y = y_hat), col = "red") +
  geom_abline(slope = 1, intercept = 0)
```



Case study: is height hereditary?



Case study: is height hereditary?

For hypothesis testing we can optain a standard error:

$$SE(\hat{\beta}_i) = \hat{\sigma}\sqrt{v_{ii}},$$

where v_{ii} is the ith diagonal element of $(X'X)^{-1}$, and

$$\hat{\sigma}^2 = \frac{1}{N-p-1}(\mathbf{y} - X\widehat{\beta})'(\mathbf{y} - X\widehat{\beta})$$

```
N <- length(y)
p <- length(beta_hat)
sigma2_hat <- 1 / (N - p - 1) *
  t(y - X %*% beta_hat) %*% (y - X %*% beta_hat)
V <- solve(t(X) %*% X)
Z2 <- beta_hat[2] / sqrt(sigma2_hat * V[2, 2])
Z2
```

```
##          [,1]
## [1,] 6.380223
```

Case study: is height hereditary?

In R, we can obtain the least squares estimates using the `lm` function. To fit the model:

$$Y_i = \beta_0 + \beta_1 x_i + \varepsilon_i$$

with Y_i the son's height and x_i the father's height, we can use this code to obtain the least squares estimates:

```
fit <- lm(son ~ father, data = galton_heights)
fit$coef
```

```
## (Intercept)      father
##   37.287605    0.461392
```

Case study: is height hereditary?

The object `fit` includes more information about the fit. We can use the function `summary` to extract more of this information:

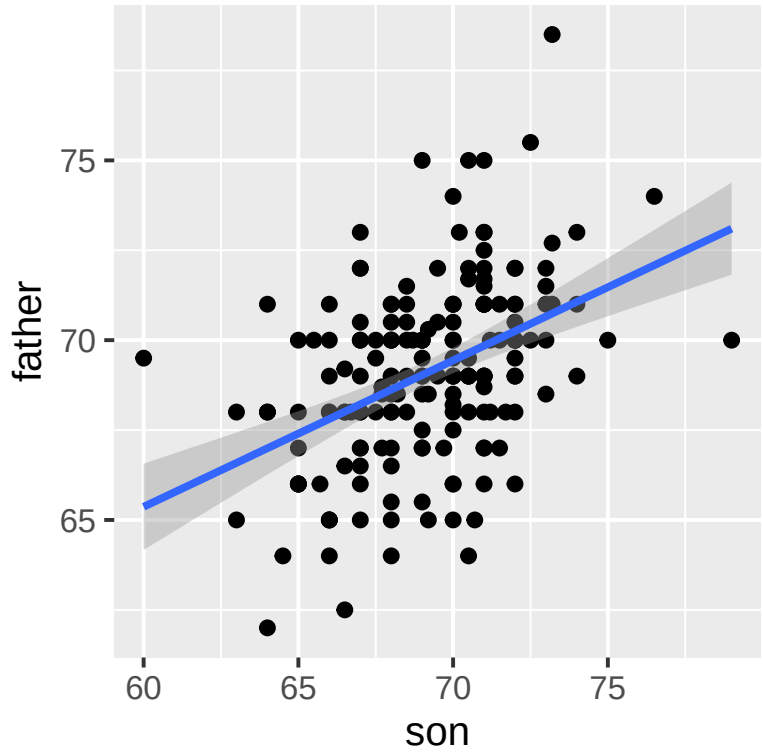
```
summary(fit)
```

```
##
## Call:
## lm(formula = son ~ father, data = galton_heights)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -9.3543 -1.5657 -0.0078  1.7263  9.4150
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 37.28761    4.98618   7.478 3.37e-12 ***
## father       0.46139    0.07211   6.398 1.36e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.45 on 177 degrees of freedom
## Multiple R-squared:  0.1878, Adjusted R-squared:  0.1833
## F-statistic: 40.94 on 1 and 177 DF,  p-value: 1.36e-09
```

Case study: is height hereditary?

We can use **ggplot2** layers to plot $\hat{Y}$ with its confidence intervals:

```
galton_heights %>% ggplot(aes(son, father)) +
  geom_point() +
  geom_smooth(method = "lm")
```



Case study: is height hereditary?

The R function `predict` takes an `lm` object as input and returns the prediction. If requested, the standard errors and other information from which we can construct confidence intervals is provided:

```
fit <- galton_heights %>% lm(son ~ father, data = .)

y_hat <- predict(fit, se.fit = TRUE)

names(y_hat)
```

```
## [1] "fit"            "se.fit"         "df"             "residual.scale"
```

Linear regression in the tidyverse (the broom package)

The **broom** package has three main functions, all of which extract information from the object returned by `lm` and return it in a **tidyverse** friendly data frame. These functions are `tidy`, `glance`, and `augment`. The `tidy` function returns estimates and related information as a data frame:

```
library(broom)
fit <- galton_heights %>% lm(son ~ father, data = .)
tidy(fit)
```

```
## # A tibble: 2 x 5
##   term        estimate std.error statistic  p.value
##   <chr>          <dbl>     <dbl>     <dbl>    <dbl>
## 1 (Intercept)   37.3      4.99       7.48 3.37e-12
## 2 father         0.461    0.0721     6.40 1.36e- 9
```

Linear regression in the tidyverse (the broom package)

We can add other important summaries, such as confidence intervals:

```
tidy(fit, conf.int = TRUE)
```

```
## # A tibble: 2 x 7
##   term        estimate std.error statistic  p.value conf.low conf.high
##   <chr>          <dbl>     <dbl>     <dbl>    <dbl>    <dbl>     <dbl>
## 1 (Intercept)   37.3      4.99        7.48 3.37e-12   27.4      47.1
## 2 father         0.461    0.0721      6.40 1.36e- 9    0.319     0.604
```

Linear regression in the tidyverse (the broom package)

Because the outcome is a data frame, we can immediately use it with `summarize` to string together the commands that produce the table we are after. Because a data frame is returned, we can filter and select the rows and columns we want, which facilitates working with **ggplot2**:

Linear regression in the tidyverse (the broom package)

```
galton_heights %>%
    lm(son ~ father, data = .) %>%
    tidy(conf.int = TRUE) %>%
    filter(term == "father") %>%
    select(estimate, conf.low, conf.high) # %>%
```

```
## # A tibble: 1 x 3
##   estimate conf.low conf.high
##      <dbl>    <dbl>     <dbl>
## 1    0.461    0.319     0.604
```

```
    #ggplot(aes(x = estimate, xmin = conf.low, xmax = conf.high, y=1)) +
    #geom_errorbar() +
    #geom_point()
```

Linear regression in the tidyverse (the broom package)

The other functions provided by **broom**, `glance`, and `augment`, relate to model-specific and observation-specific outcomes, respectively. Here, we can see the model fit summaries `glance` returns:

```
glance(fit)
```

```
## # A tibble: 1 x 12
##   r.squared adj.r.squared sigma statistic       p.value    df logLik   AIC   BIC
##       <dbl>         <dbl> <dbl>     <dbl>         <dbl> <dbl>  <dbl> <dbl> <dbl>
## 1     0.188         0.183  2.45      40.9 0.00000000136     1  -413.  833.  842.
## # i 3 more variables: deviance <dbl>, df.residual <int>, nobs <int>
```

Session Info

```
sessionInfo()
```

```
## R version 4.3.2 (2023-10-31)
## Platform: aarch64-apple-darwin20 (64-bit)
## Running under: macOS Ventura 13.5.1
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRlapack.dylib;  LAPACK version 3
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## time zone: America/Denver
## tzcode source: internal
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
##  [1] broom_1.0.5     HistData_0.9-1  Lahman_11.0-0   lubridate_1.9.3
##  [5] forcats_1.0.0   stringr_1.5.1   dplyr_1.1.3     purrr_1.0.2
##  [9] readr_2.1.4     tidyr_1.3.0     tibble_3.2.1    ggplot2_3.4.4
## [13] tidyverse_2.0.0
##
## loaded via a namespace (and not attached):
##  [1] utf8_1.2.4        generics_0.1.3    xml2_1.3.5        lattice_0.22-5
##  [5] stringi_1.8.1     hms_1.1.3         digest_0.6.33     magrittr_2.0.3
##  [9] evaluate_0.23     grid_4.3.2        timechange_0.2.0  fastmap_1.1.1
## [13] Matrix_1.6-3      backports_1.4.1   mgcv_1.9-0        httr_1.4.7
## [17] rvest_1.0.3       fansi_1.0.5       viridisLite_0.4.2 scales_1.2.1
## [21] cli_3.6.1         rlang_1.1.2       ellipsis_0.3.2    splines_4.3.2
```