Making predictions

INTRODUCTION TO REGRESSION IN R

Richie Cotton
Learning Solutions Architect at DataCamp

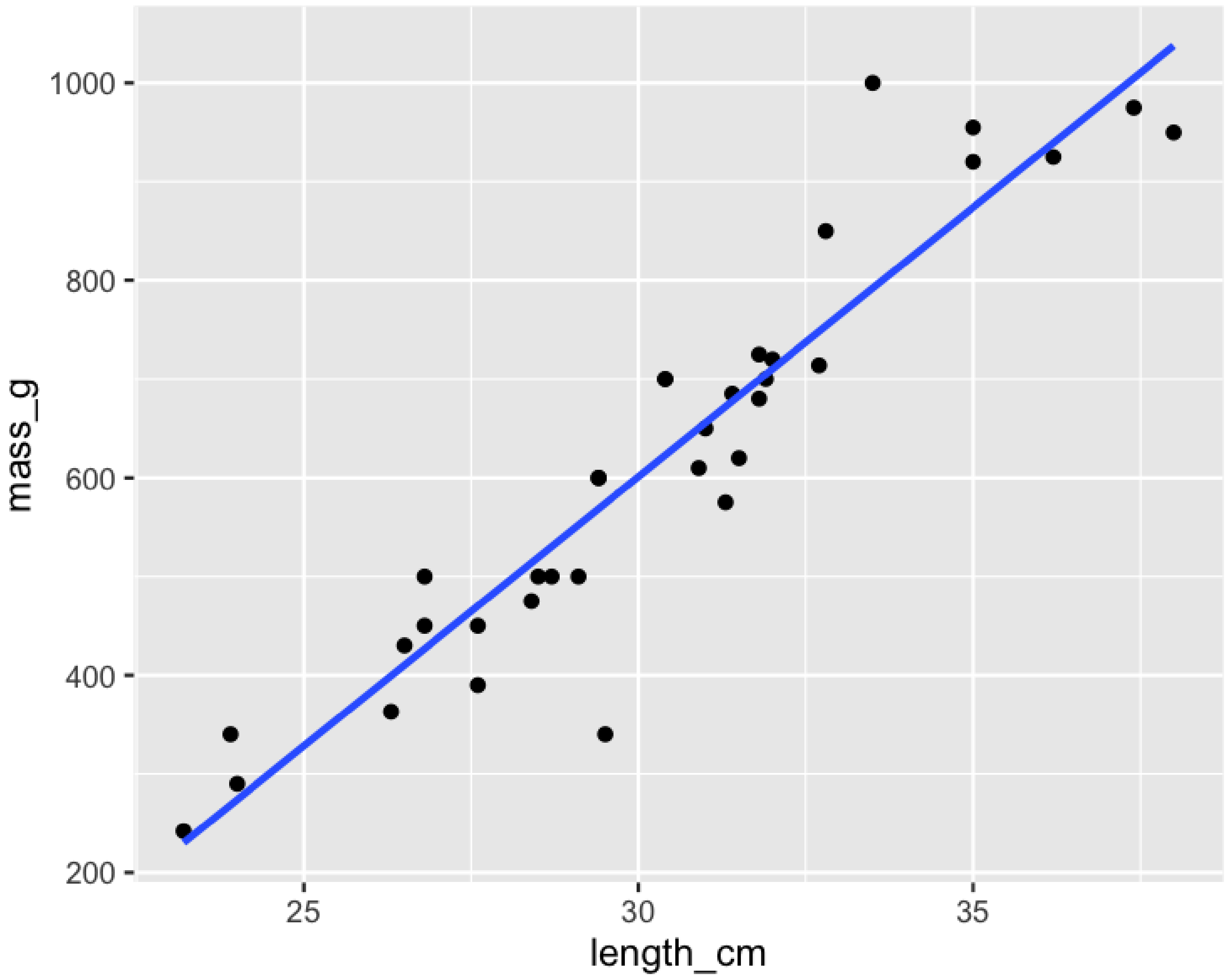
The fish dataset: bream

```
bream <- fish %>%
  filter(species == "Bream")
```

species	length_cm	mass_g
Bream	23.2	242
Bream	24.0	290
Bream	23.9	340
Bream	26.3	363
Bream	26.5	430
...	...	...

Plotting mass vs. length

```
ggplot(bream, aes(length_cm, mass_g)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE)
```



Running the model

```
mdl_mass_vs_length <- lm(mass_g ~ length_cm, data = bream)
```

```
Call:
lm(formula = mass_g ~ length_cm, data = bream)


Coefficients:
(Intercept)    length_cm
   -1035.35        54.55
```

Data on explanatory values to predict

> If I set the explanatory variables to these values,
> what value would the response variable have?

```
library(dplyr)
explanatory_data <- tibble(length_cm = 20:40)
```

Call predict()

```r
library(tibble)
explanatory_data <- tibble(length_cm = 20:40)
```

```r
predict(mdl_mass_vs_length, explanatory_data)
```

```
        1         2         3         4         5         6 
 55.65205 110.20203 164.75202 219.30200 273.85198 328.40196 
        7         8         9        10        11        12 
382.95194 437.50192 492.05190 546.60188 601.15186 655.70184 
       13        14        15        16        17        18 
710.25182 764.80181 819.35179 873.90177 928.45175 983.00173 
       19        20        21 
1037.55171 1092.10169 1146.65167 
```

Predicting inside a data frame

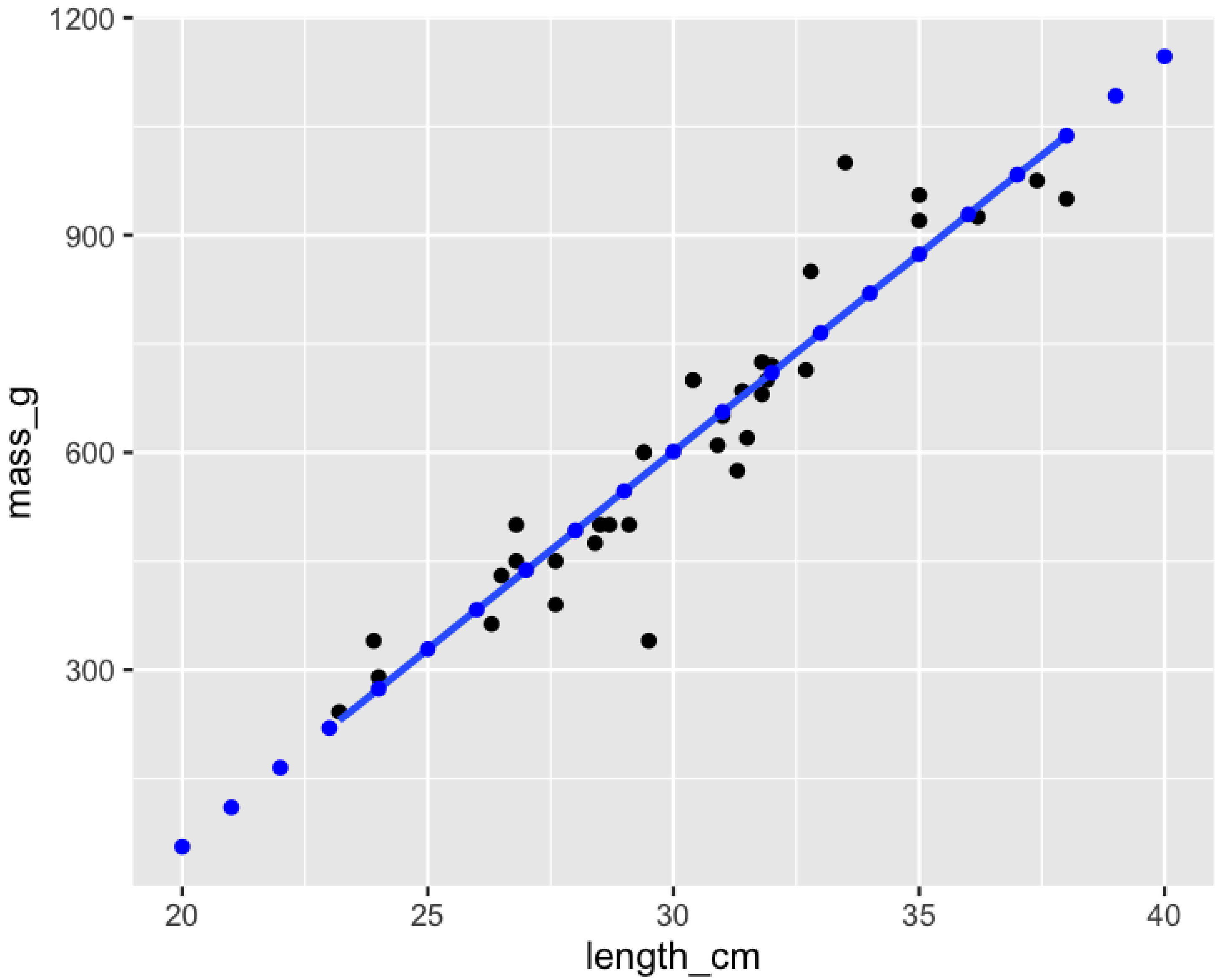
```
library(dplyr)
explanatory_data <- tibble(length_cm = 20:40)
```

```
prediction_data <- explanatory_data %>%
  mutate(
    mass_g = predict(
      mdl_mass_vs_length, explanatory_data
    )
  )
```

```
# A tibble: 21 x 2
   length_cm mass_g
       <int>  <dbl>
 1        20   55.7
 2        21  110.
 3        22  165.
 4        23  219.
 5        24  274.
 6        25  328.
 7        26  383.
 8        27  438.
 9        28  492.
10        29  547.
# ... with 11 more rows
```

Showing predictions

```
ggplot(bream, aes(length_cm, mass_g)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE) +
  geom_point(
    data = prediction_data,
    color = "blue"
  )
```

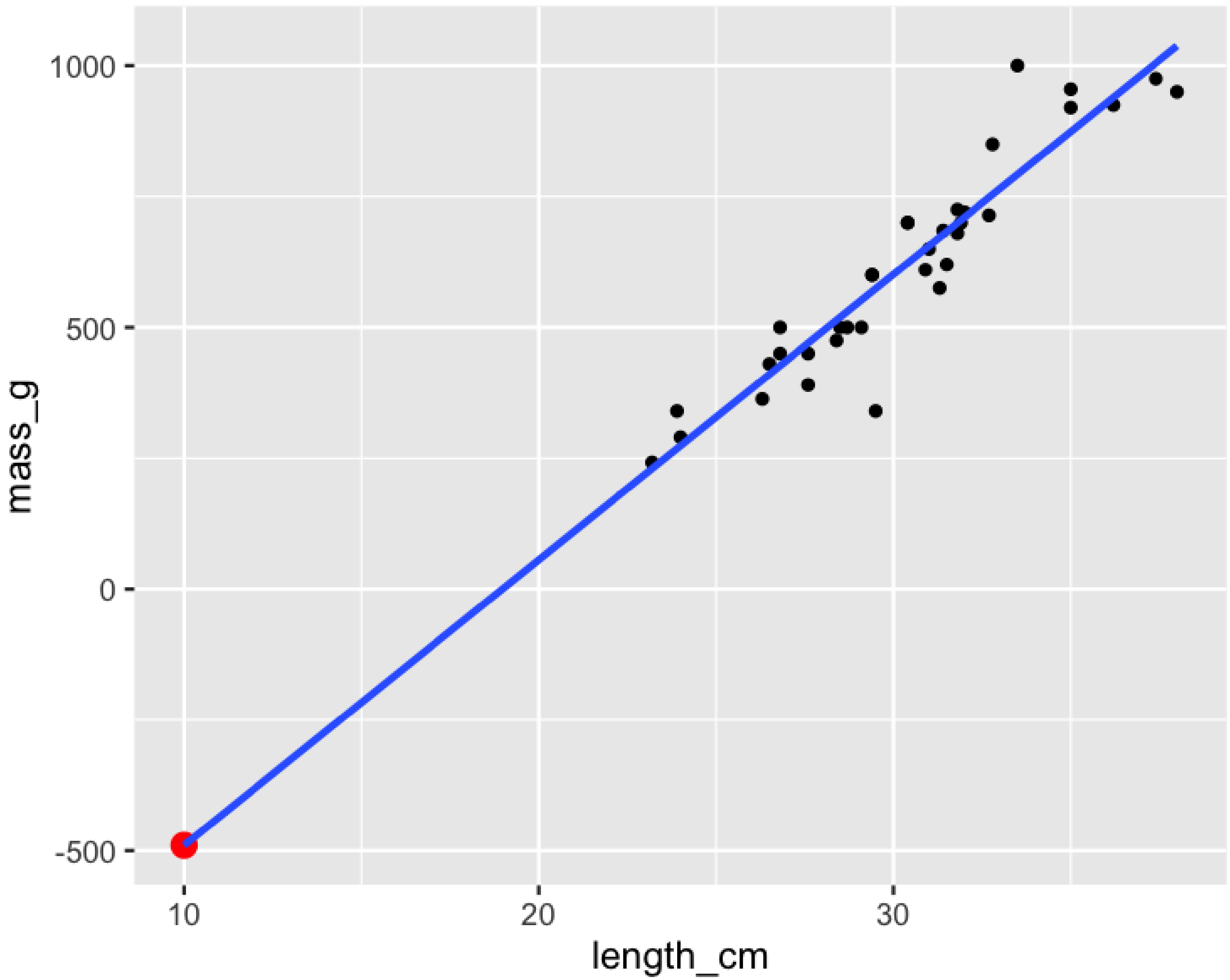


Extrapolating

Extrapolating means making predictions outside the range of observed data.

```
explanatory_little_bream <- tibble(length_cm = 10)
explanatory_little_bream %>%
  mutate(
    mass_g = predict(
      mdl_mass_vs_length, explanatory_little_bream
    )
  )
```

```
# A tibble: 1 x 2
  length_cm mass_g
      <dbl>  <dbl>
1        10  -490.
```



Let's practice!

INTRODUCTION TO REGRESSION IN R

Working with model objects

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Richie Cotton
Learning Solutions Architect at DataCamp

coefficients()

```
mdl_mass_vs_length <- lm(mass_g ~ length_cm, data = bream)
```

```
Call:
lm(formula = mass_g ~ length_cm, data = bream)

Coefficients:
(Intercept)    length_cm
   -1035.35        54.55
```

```
coefficients(mdl_mass_vs_length)
```

```
(Intercept)   length_cm
-1035.34757    54.54998
```

fitted()

fitted values: predictions on the original dataset

```
fitted(mdl_mass_vs_length)
```

or equivalently

```
explanatory_data <- bream %>%
  select(length_cm)

predict(mdl_mass_vs_length, explanatory_data)
```

```
       1        2        3        4        5
230.2120 273.8520 268.3970 399.3169 410.2269
       6        7        8        9       10
426.5919 426.5919 470.2319 470.2319 519.3269
      11       12       13       14       15
513.8719 530.2369 552.0569 573.8769 568.4219
      16       17       18       19       20
568.4219 622.9719 622.9719 650.2468 655.7018
      21       22       23       24       25
672.0668 677.5218 682.9768 699.3418 704.7968
      26       27       28       29       30
699.3418 710.2518 748.4368 753.8918 792.0768
      31       32       33       34       35
873.9018 873.9018 939.3617 1004.8217 1037.5517
```

residuals()

Residuals: actual response values minus predicted response values

```
residuals(mdl_mass_vs_length)
```

or equivalently

```
bream$mass_g - fitted(mdl_mass_vs_length)
```

```
      1        2        3        4        5
 11.788   16.148   71.603  -36.317   19.773
      6        7        8        9       10
 23.408   73.408  -80.232  -20.232  -19.327
     11       12       13       14       15
-38.872  -30.237  -52.057 -233.877   31.578
     16       17       18       19       20
 31.578   77.028   77.028  -40.247   -5.702
     21       22       23       24       25
-97.067    7.478  -62.977  -19.342   -4.797
     26       27       28       29       30
 25.658    9.748  -34.437   96.108  207.923
     31       32       33       34       35
 46.098   81.098  -14.362  -29.822  -87.552
```

summary()

```r
summary(mdl_mass_vs_length)
```

```
Call:
lm(formula = mass_g ~ length_cm, data = bream)

Residuals:
   Min     1Q Median     3Q    Max 
-233.9  -35.4   -4.8   31.6  207.9 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) -1035.35     107.97   -9.59  4.6e-11 ***
length_cm      54.55       3.54   15.42  < 2e-16 ***

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

Residual standard error: 74.2 on 33 degrees of freedom
Multiple R-squared:  0.878,    Adjusted R-squared:  0.874 
F-statistic:  238 on 1 and 33 DF,  p-value: <2e-16
```

summary(): call

```
Call:
lm(formula = mass_g ~ length_cm, data = bream)
```

summary(): residuals

```
Residuals:
   Min     1Q Median     3Q    Max 
-233.9  -35.4   -4.8   31.6  207.9 
```

summary(): coefficients

```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -1035.35     107.97   -9.59  4.6e-11 ***
length_cm      54.55       3.54   15.42  < 2e-16 ***

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

summary(): model metrics

```
Residual standard error: 74.2 on 33 degrees of freedom
Multiple R-squared:  0.878,    Adjusted R-squared:  0.874
F-statistic:  238 on 1 and 33 DF,  p-value: <2e-16
```

tidy()

```
library(broom)

tidy(mdl_mass_vs_length)
```

```
# A tibble: 2 x 5
  term        estimate std.error statistic  p.value
  <chr>          <dbl>     <dbl>     <dbl>    <dbl>
1 (Intercept)  -1035.     108.       -9.59 4.58e-11
2 length_cm       54.5      3.54     15.4  1.22e-16
```

augment()

```r
augment(mdl_mass_vs_length)
```

```
# A tibble: 35 × 8
   mass_g length_cm .fitted .resid   .hat .sigma .cooksd .std.resid
    <dbl>     <dbl>   <dbl>  <dbl>  <dbl>  <dbl>   <dbl>      <dbl>
 1    242      23.2    230.   11.8 0.144    75.3 0.00247      0.172
 2    290      24      274.   16.1 0.119    75.2 0.00364      0.232
 3    340      23.9    268.   71.6 0.122    74.1 0.0738       1.03
 4    363      26.3    399.  -36.3 0.0651   75.0 0.00894     -0.507
 5    430      26.5    410.   19.8 0.0616   75.2 0.00248      0.275
 6    450      26.8    427.   23.4 0.0566   75.2 0.00317      0.325
 7    500      26.8    427.   73.4 0.0566   74.1 0.0311       1.02
 8    390      27.6    470.  -80.2 0.0452   73.9 0.0291      -1.11
 9    450      27.6    470.  -20.2 0.0452   75.2 0.00185     -0.279
10    500      28.5    519.  -19.3 0.0360   75.2 0.00132     -0.265
# ... with 25 more rows
```

glance()

```
glance(mdl_mass_vs_length)
```

```
# A tibble: 1 × 12
  r.squared adj.r.squared sigma statistic  p.value    df logLik   AIC   BIC
      <dbl>         <dbl> <dbl>     <dbl>    <dbl> <dbl>  <dbl> <dbl> <dbl>
1     0.878         0.874  74.2      238. 1.22e-16     1  -199.  405.  409.
# ... with 3 more variables: deviance <dbl>, df.residual <int>, nobs <int>
```

Let's practice!

Regression to the mean

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Richie Cotton
Learning Solutions Architect

The concept

- Response value = fitted value + residual
- "The stuff you explained" + "the stuff you couldn't explain"
- Residuals exist due to problems in the model *and* fundamental randomness
- Extreme cases are often due to randomness
- *Regression to the mean* means extreme cases don't persist over time

Pearson's father son dataset

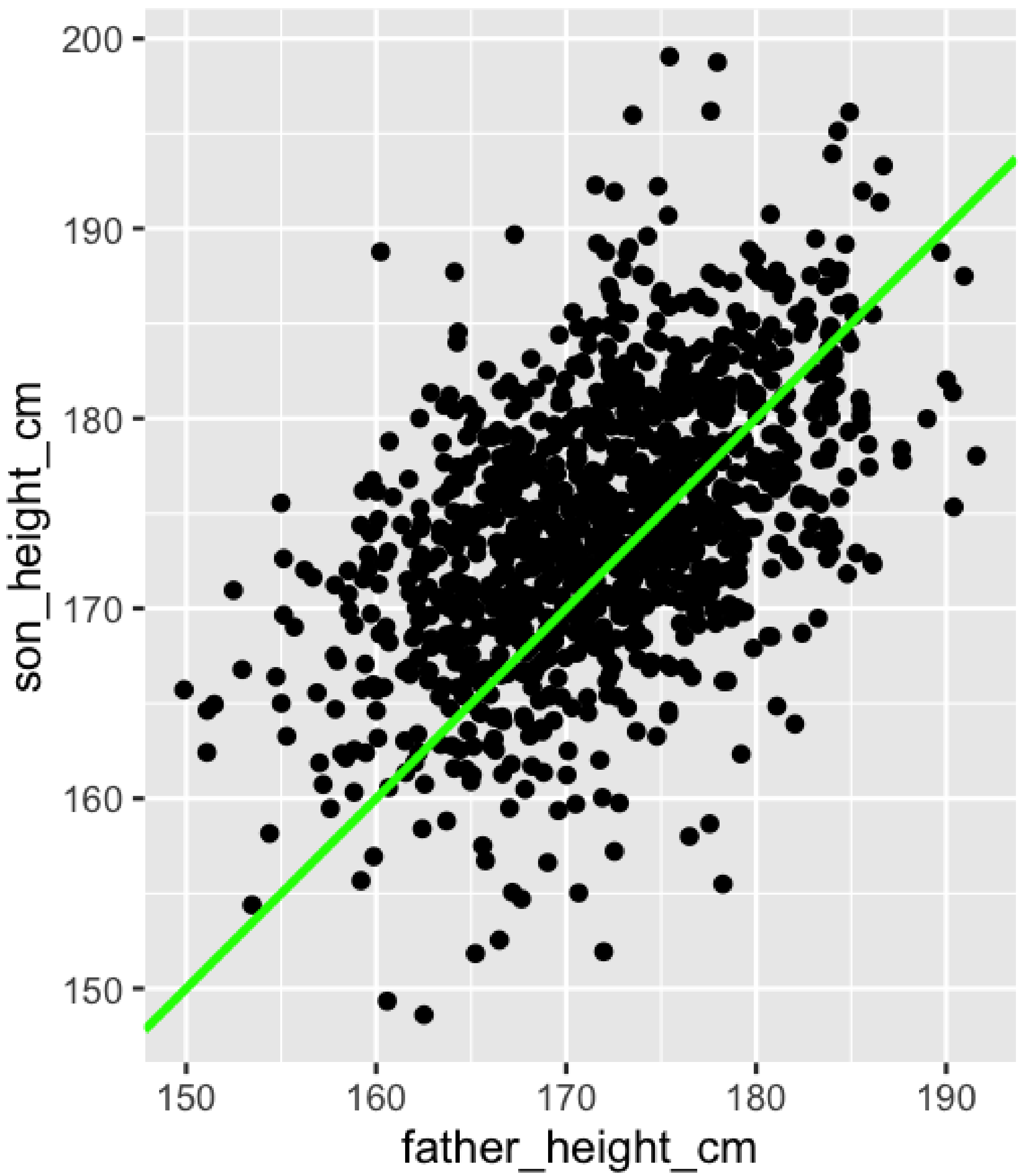
- 1078 father/son pairs
- Do tall fathers have tall sons?

father_height_cm	son_height_cm
165.2	151.8
160.7	160.6
165.0	160.9
167.0	159.5
155.3	163.3
...	...

[1] Adapted from https://www.rdocumentation.org/packages/UsingR/topics/father.son

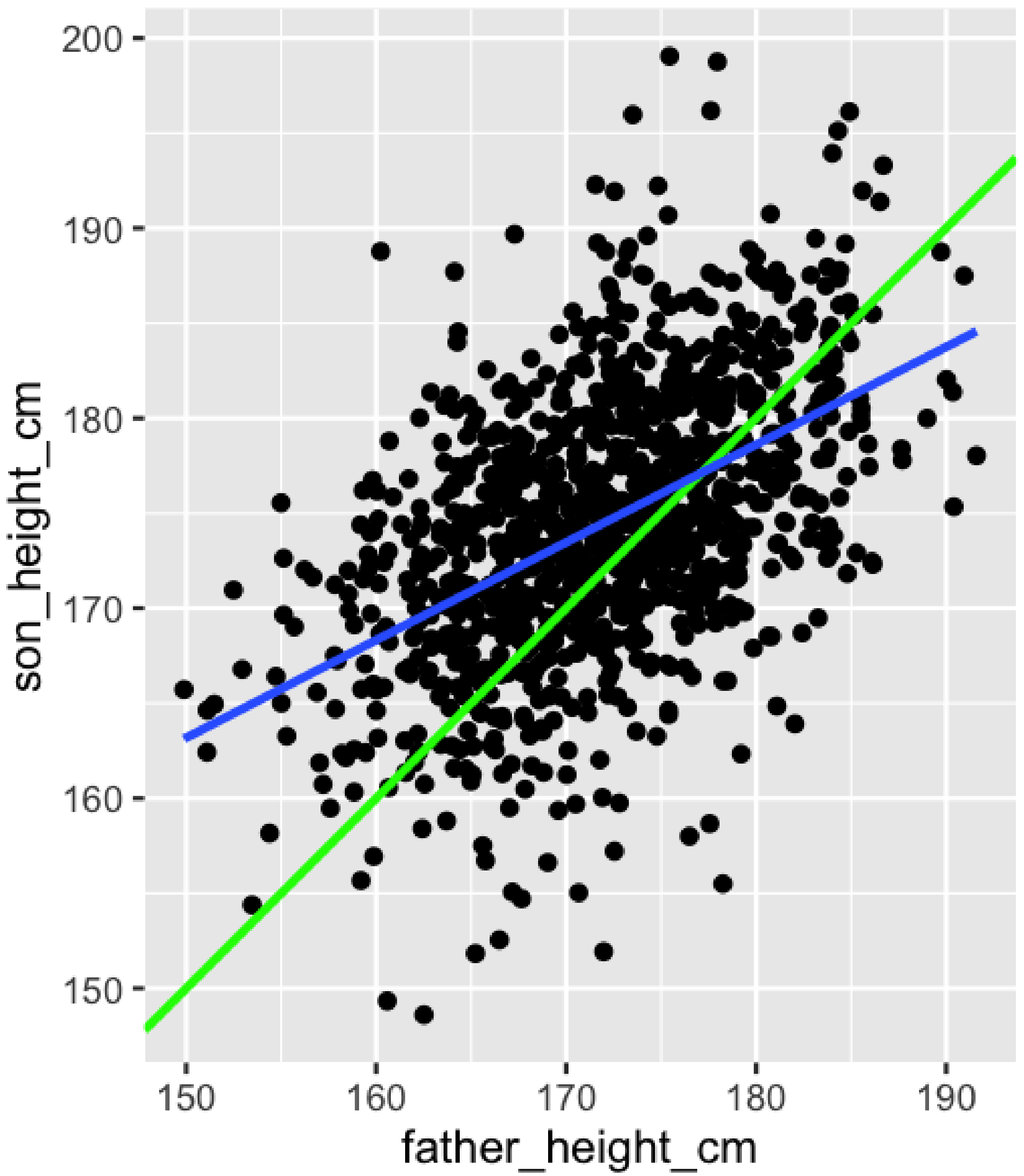
Scatter plot

```
plt_son_vs_father <- ggplot(
  father_son,
  aes(father_height_cm, son_height_cm)
) +
  geom_point() +
  geom_abline(color = "green", size = 1) +
  coord_fixed()
```



Adding a regression line

```
plt_son_vs_father +
  geom_smooth(method = "lm", se = FALSE)
```



Running a regression

```
mdl_son_vs_father <- lm(
  son_height_cm ~ father_height_cm,
  data = father_son
)
```

```
Call:
lm(formula = son_height_cm ~ father_height_cm, data = father_son)

Coefficients:
     (Intercept)  father_height_cm
          86.072             0.514
```

Making predictions

```r
really_tall_father <- tibble(
  father_height_cm = 190
)
predict(mdl_son_vs_father, really_tall_father)
```

```
183.7
```

```r
really_short_father <- tibble(
  father_height_cm = 150
)
predict(mdl_son_vs_father, really_short_father)
```

```
163.2
```

Let's practice!

INTRODUCTION TO REGRESSION IN R

Transforming variables

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Perch dataset

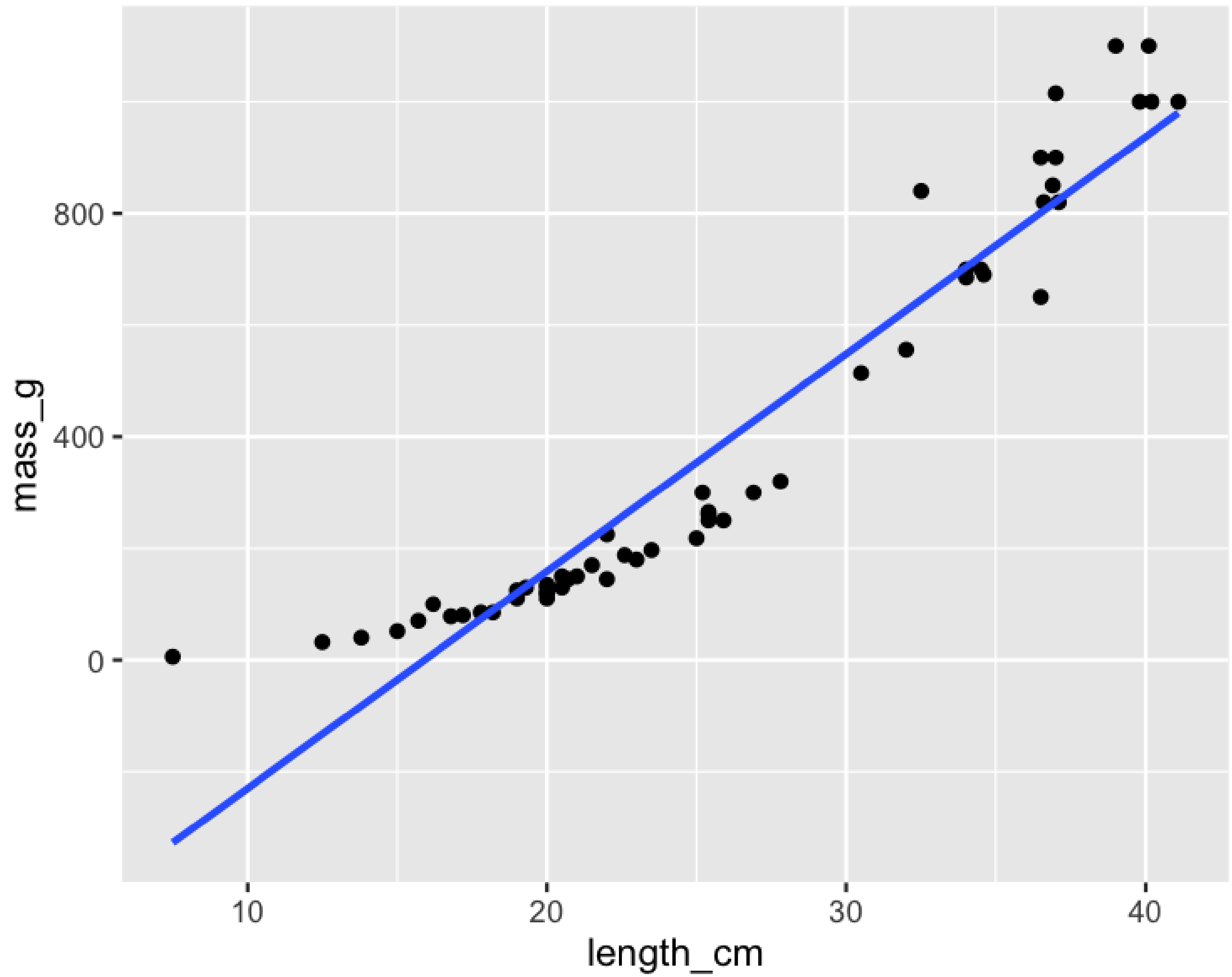
```
library(dplyr)

perch <- fish %>%
  filter(species == "Perch")
```

species	mass_g	length_cm
Perch	5.9	7.5
Perch	32.0	12.5
Perch	40.0	13.8
Perch	51.5	15.0
Perch	70.0	15.7
...	...	...

It's not a linear relationship

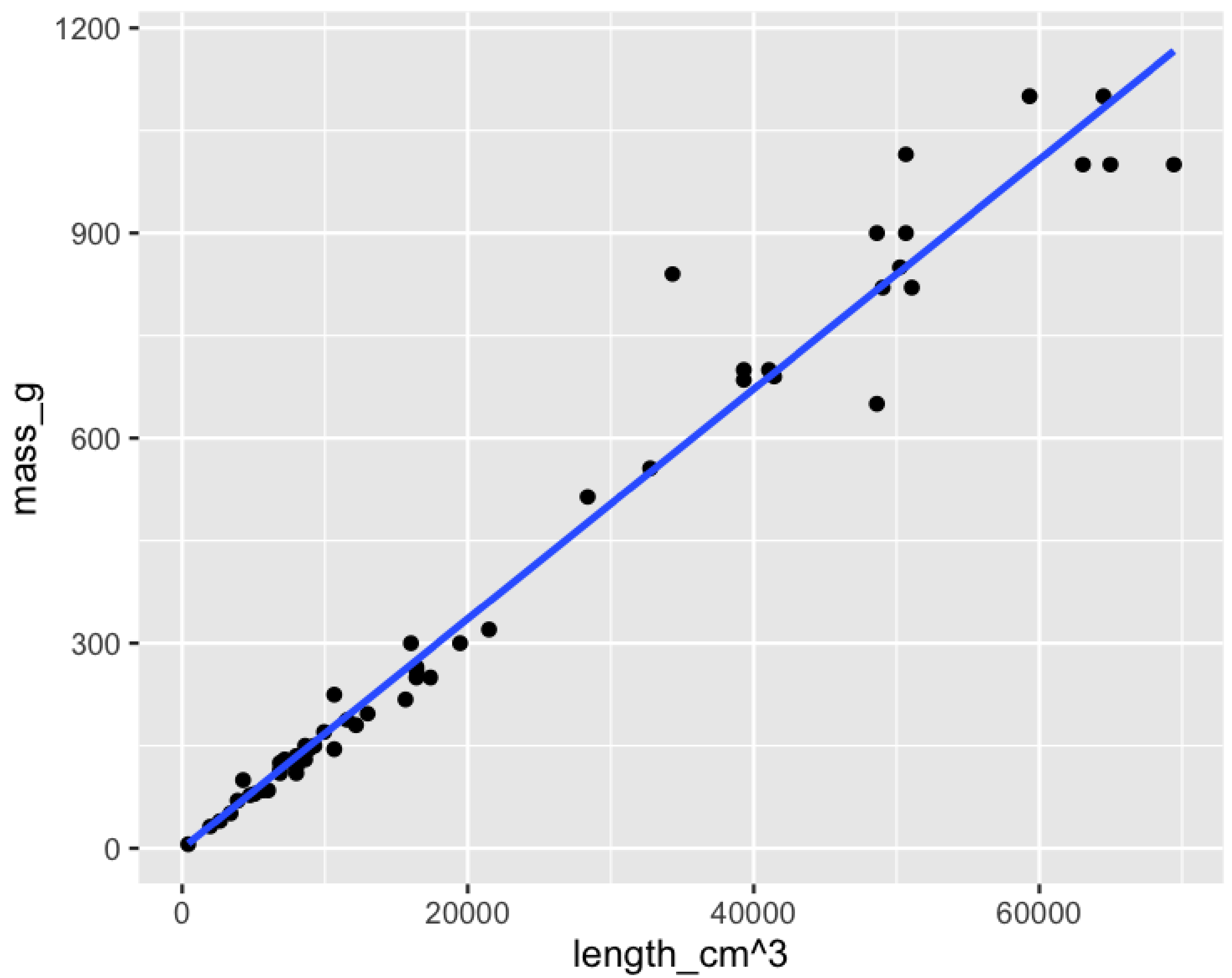
```r
ggplot(perch, aes(length_cm, mass_g)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE)
```



Bream vs. perch

Plotting mass vs. length cubed

```r
ggplot(perch, aes(length_cm ^ 3, mass_g)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE)
```



Modeling mass vs. length cubed

```
mdl_perch <- lm(mass_g ~ I(length_cm ^ 3), data = perch)
```

```
Call:
lm(formula = mass_g ~ I(length_cm^3), data = perch)


Coefficients:
   (Intercept)  I(length_cm^3)
       -0.1175          0.0168
```

Predicting mass vs. length cubed

```
explanatory_data <- tibble(
  length_cm = seq(10, 40, 5)
)
```

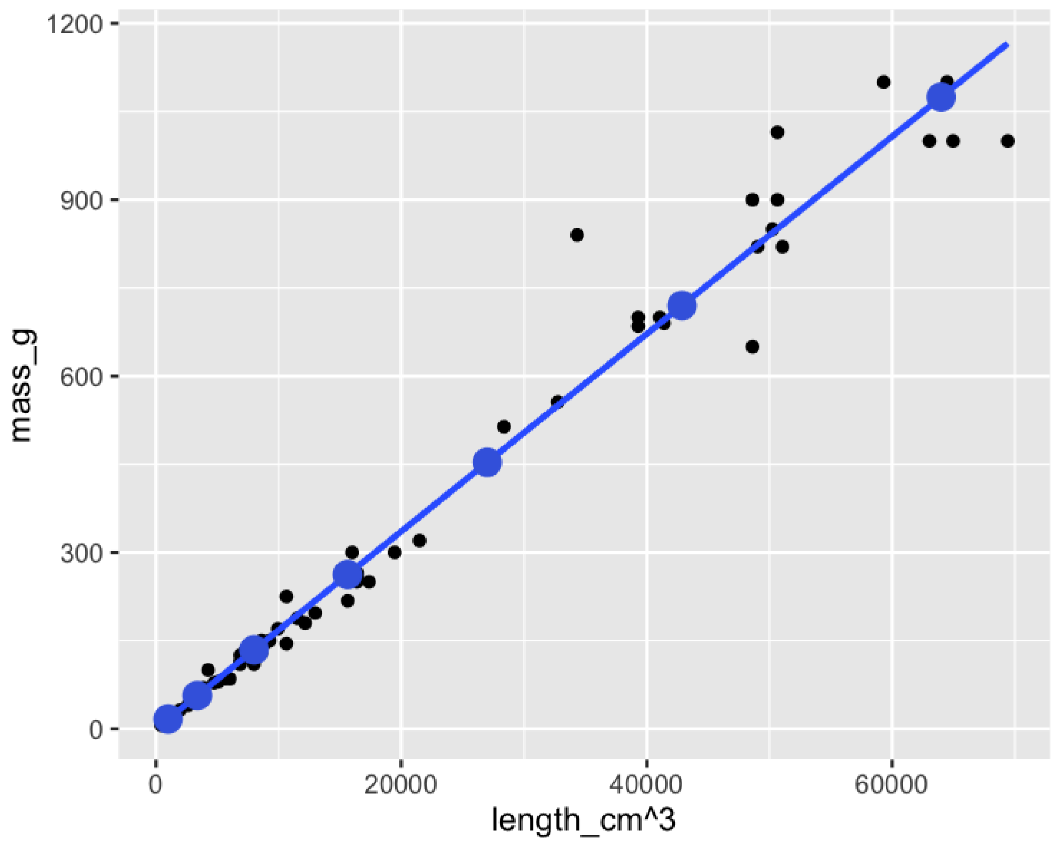
```
prediction_data <- explanatory_data %>%
  mutate(
    mass_g = predict(mdl_perch, explanatory_data)
  )
```

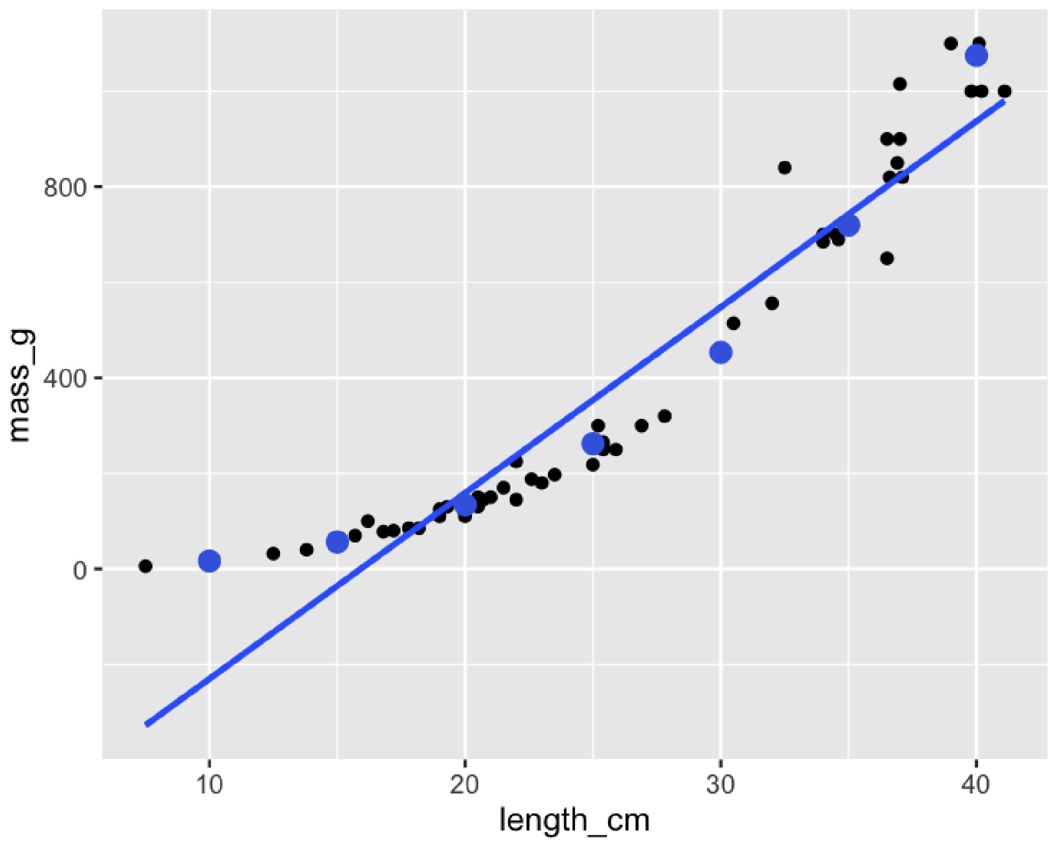
```
# A tibble: 7 x 2
  length_cm mass_g
      <dbl>  <dbl>
1        10   16.7
2        15   56.6
3        20  134.
4        25  262.
5        30  453.
6        35  720.
7        40 1075.
```

Plotting mass vs. length cubed

```
ggplot(perch, aes(length_cm ^ 3, mass_g)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE) +
  geom_point(data = prediction_data, color = "blue")
```

```
ggplot(perch, aes(length_cm, mass_g)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE) +
  geom_point(data = prediction_data, color = "blue")
```





Facebook advertising dataset

How advertising works

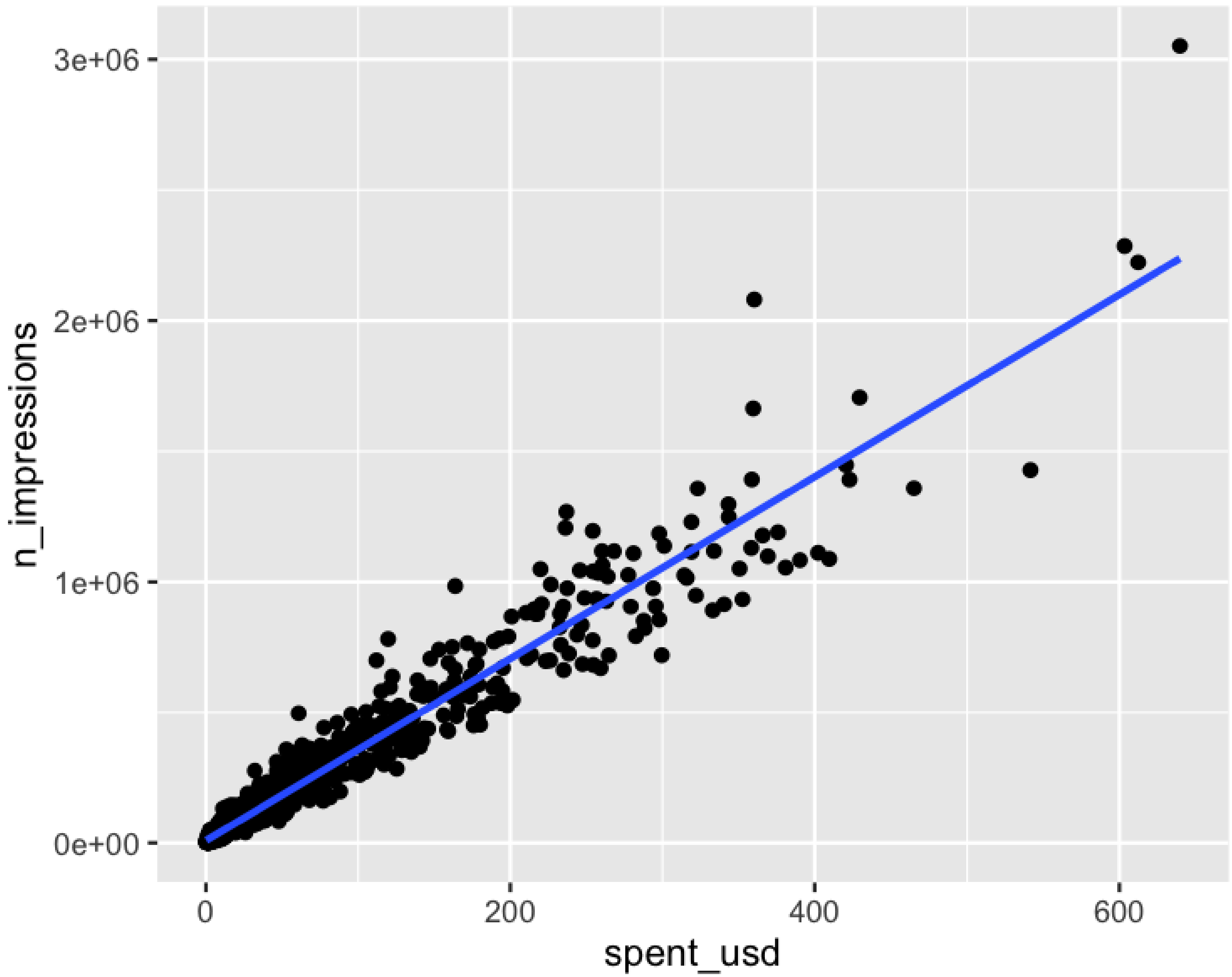
1. Pay Facebook to shows ads.
2. People see the ads ("impressions").
3. Some people who see it, click it.

- 936 rows
- Each row represents 1 advert

spent_usd	n_impressions	n_clicks
1.43	7350	1
1.82	17861	2
1.25	4259	1
1.29	4133	1
4.77	15615	3
...	...	...

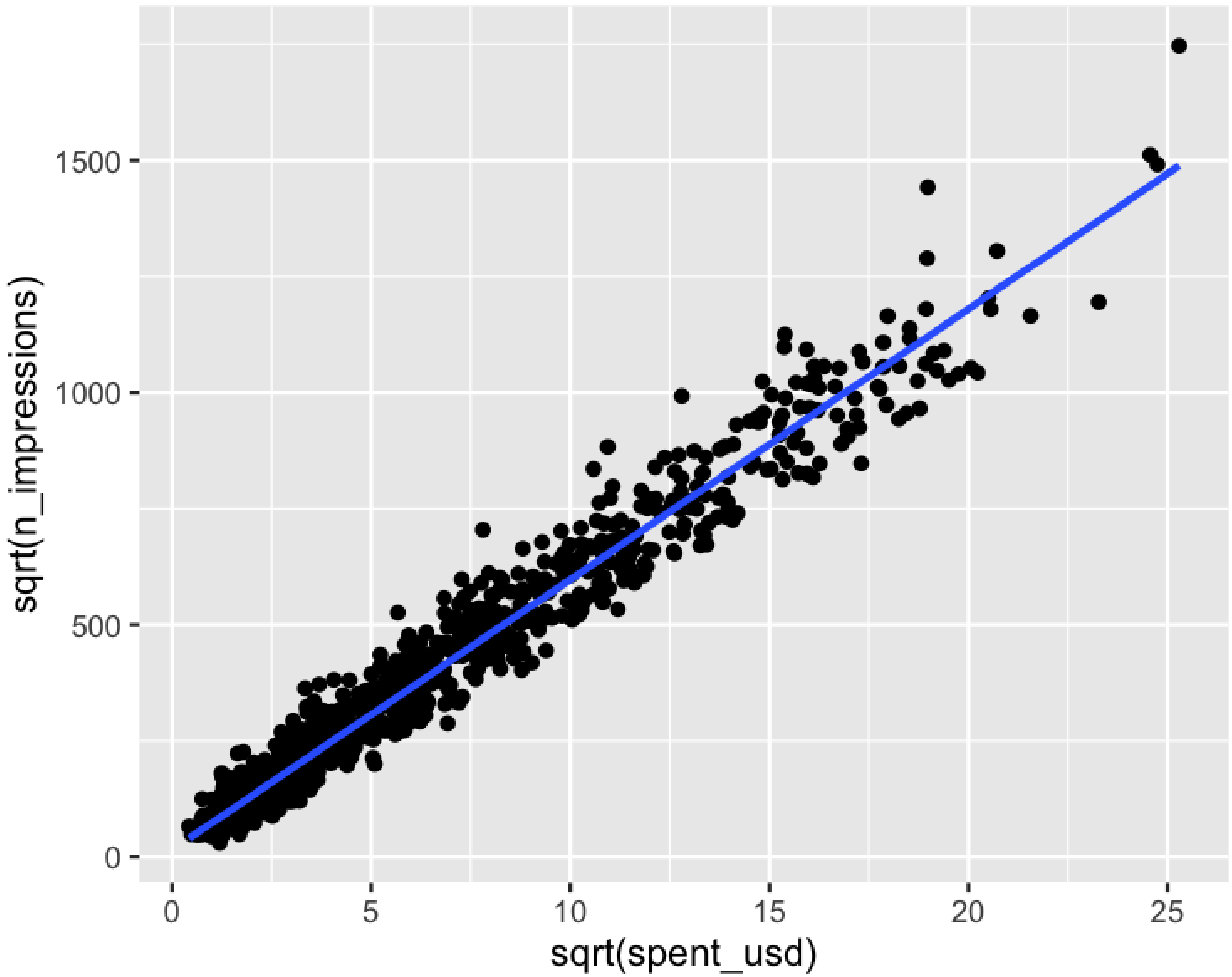
Plot is cramped

```
ggplot(
  ad_conversion,
  aes(spent_usd, n_impressions)
) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE)
```



Square root vs square root

```
ggplot(
  ad_conversion,
  aes(sqrt(spent_usd), sqrt(n_impressions))
) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE)
```



Modeling and predicting

```
mdl_ad <- lm(
  sqrt(n_impressions) ~ sqrt(spent_usd),
  data = ad_conversion
)
```

```
explanatory_data <- tibble(
  spent_usd = seq(0, 600, 100)
)
```

```
prediction_data <- explanatory_data %>%
  mutate(
    sqrt_n_impressions = predict(
      mdl_ad, explanatory_data
    ),
    n_impressions = sqrt_n_impressions ^ 2
  )
```

```
# A tibble: 7 x 3
  spent_usd sqrt_n_impressions n_impressions
      <dbl>              <dbl>         <dbl>
1         0               15.3          235.
2       100              598.       357289.
3       200              839.       703890.
4       300             1024.      1048771.
5       400             1180.      1392762.
6       500             1318.      1736184.
7       600             1442.      2079202.
```

Let's practice!

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