

Making predictions

INTRODUCTION TO REGRESSION IN R



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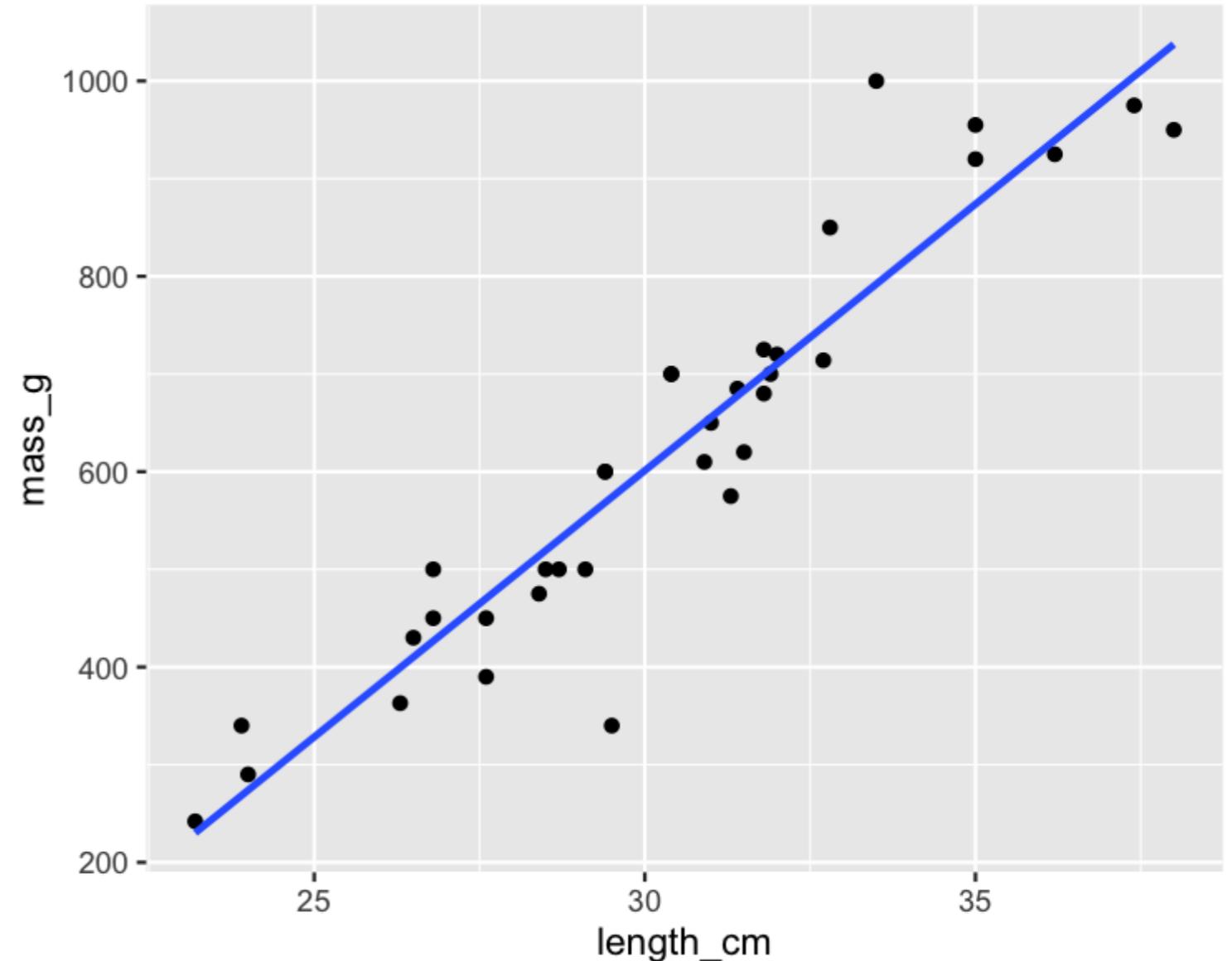
The fish dataset: bream

```
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()

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

```
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

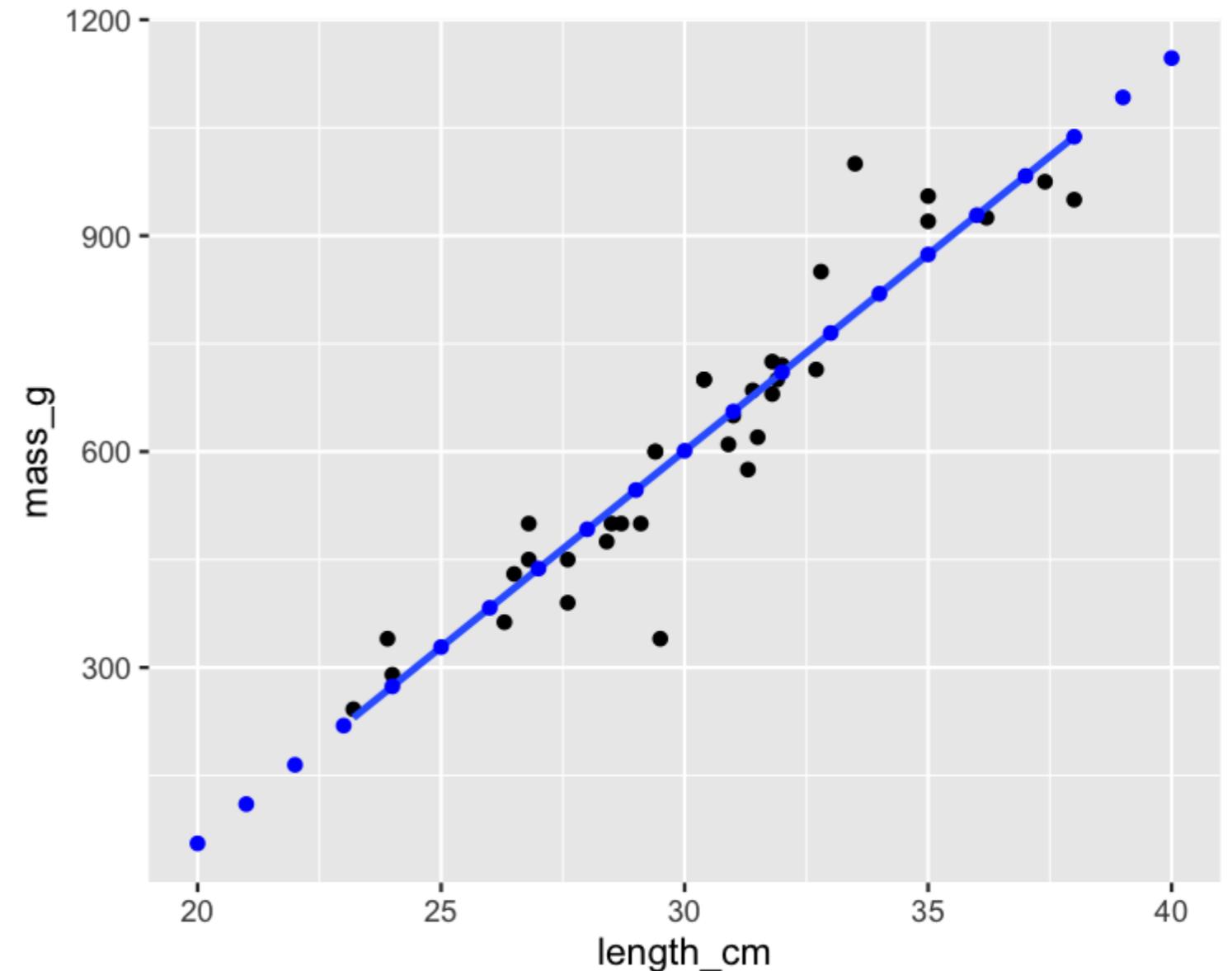
```
library(dplyr)
explanatory_data <- tibble(length_cm = 20:40)
```

```
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"  
  )
```

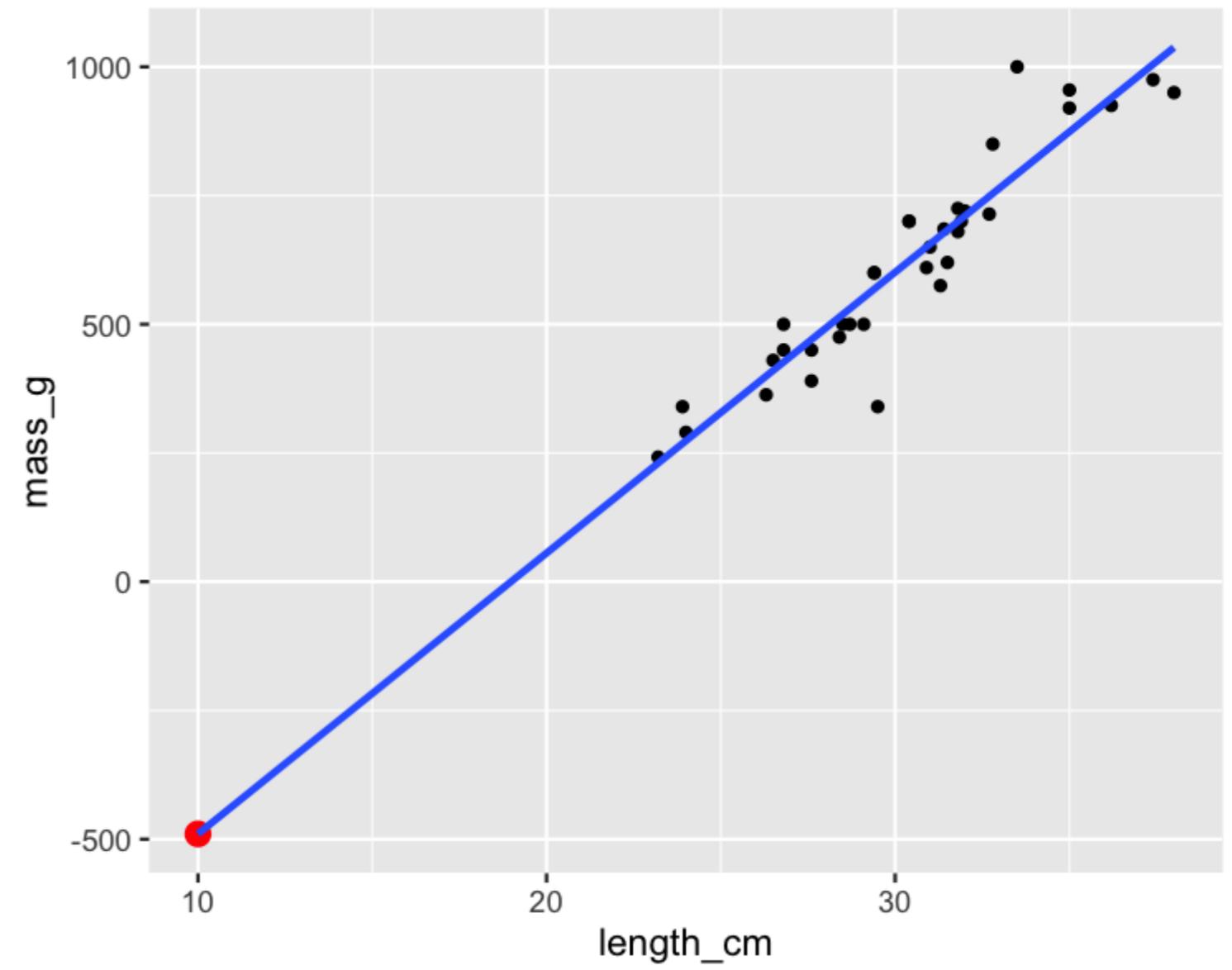


Extrapolating

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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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()

```
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(md1_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()

```
augment(md1_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(md1_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!

INTRODUCTION TO REGRESSION IN R

Regression to the mean

INTRODUCTION TO REGRESSION IN R



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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

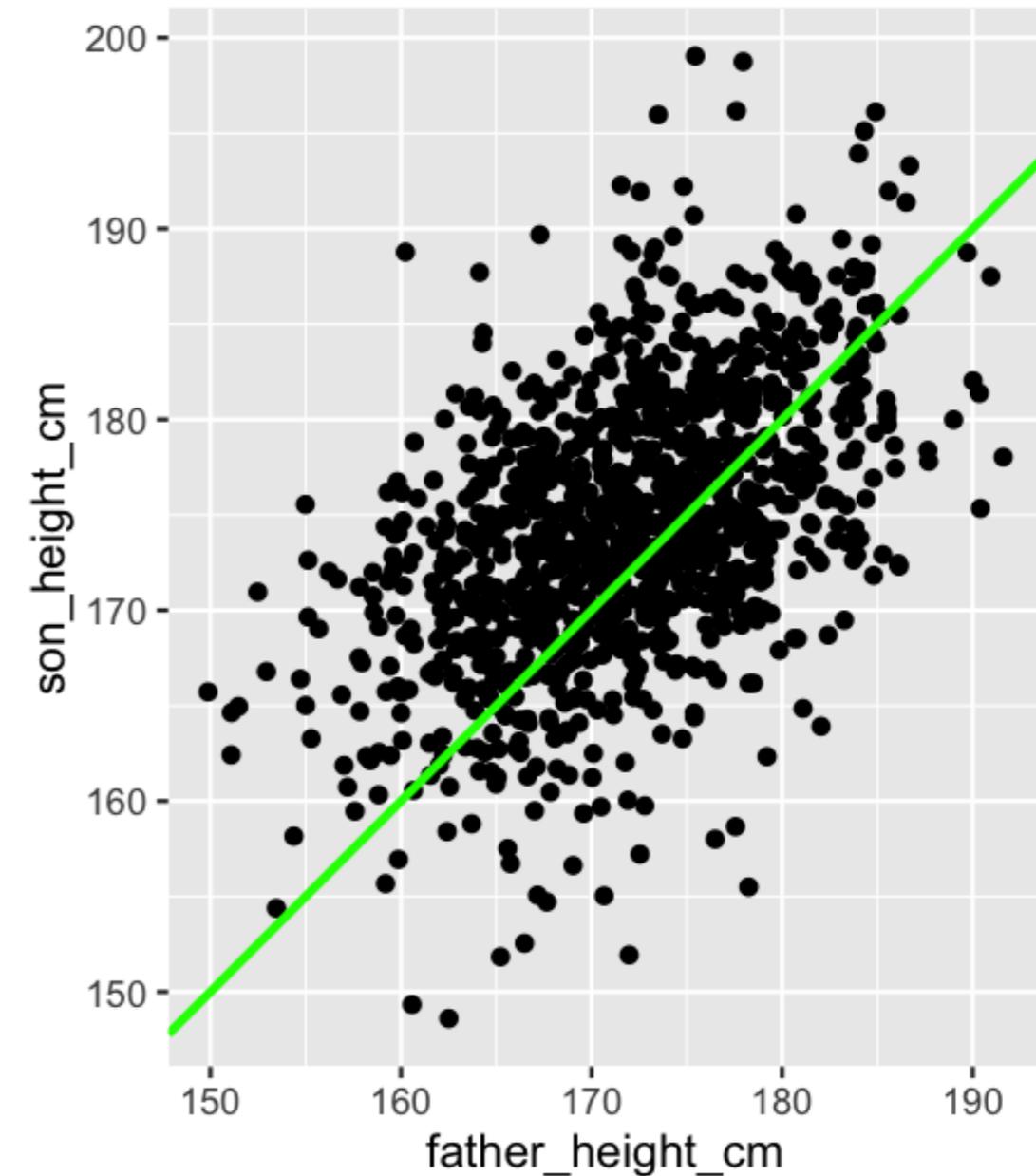
- 1078 father/son pairs
- Do tall fathers have tall sons?

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>

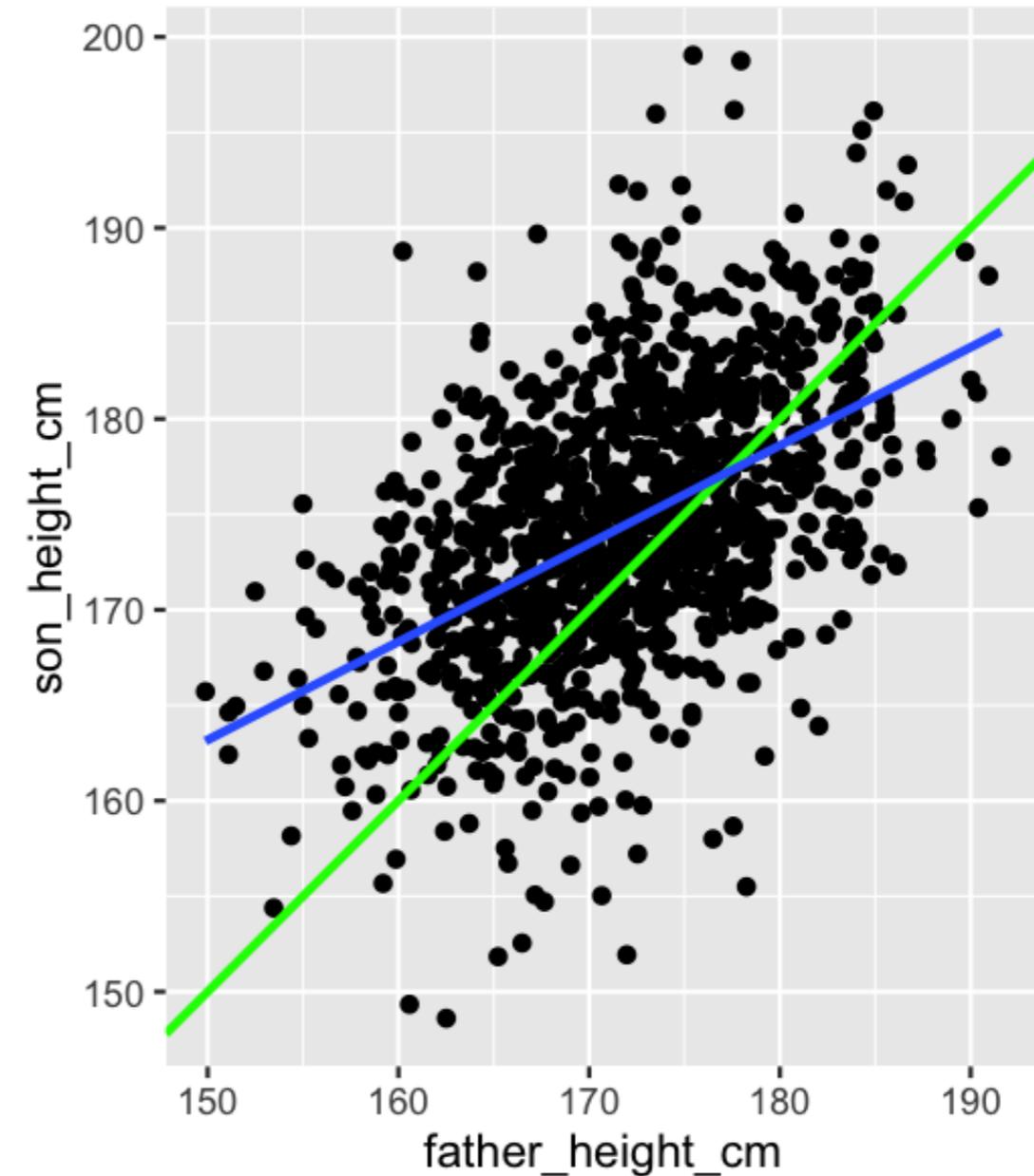
Scatter plot

```
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

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

183.7

```
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

INTRODUCTION TO REGRESSION IN R



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Perch dataset

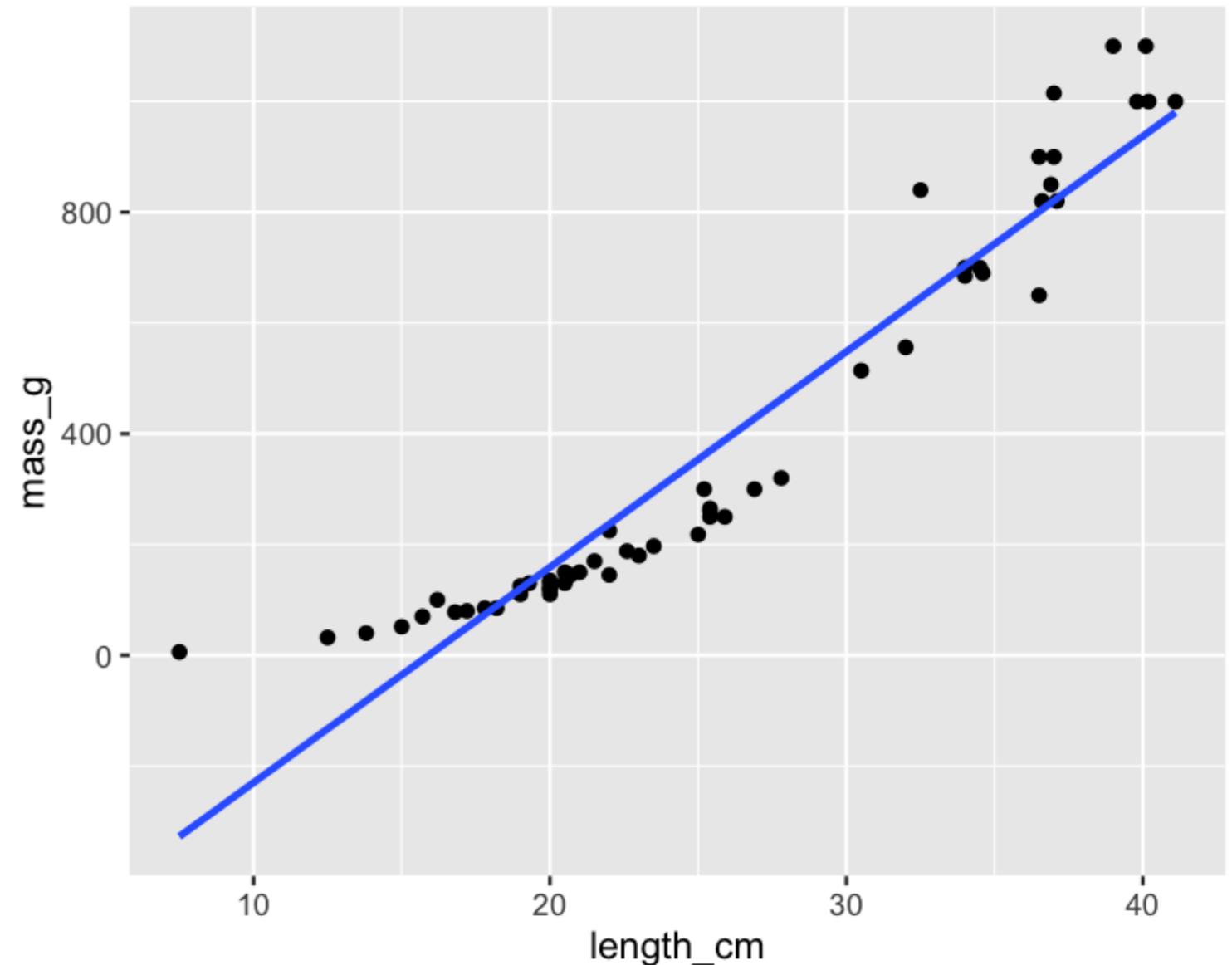
```
library(dplyr)

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

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

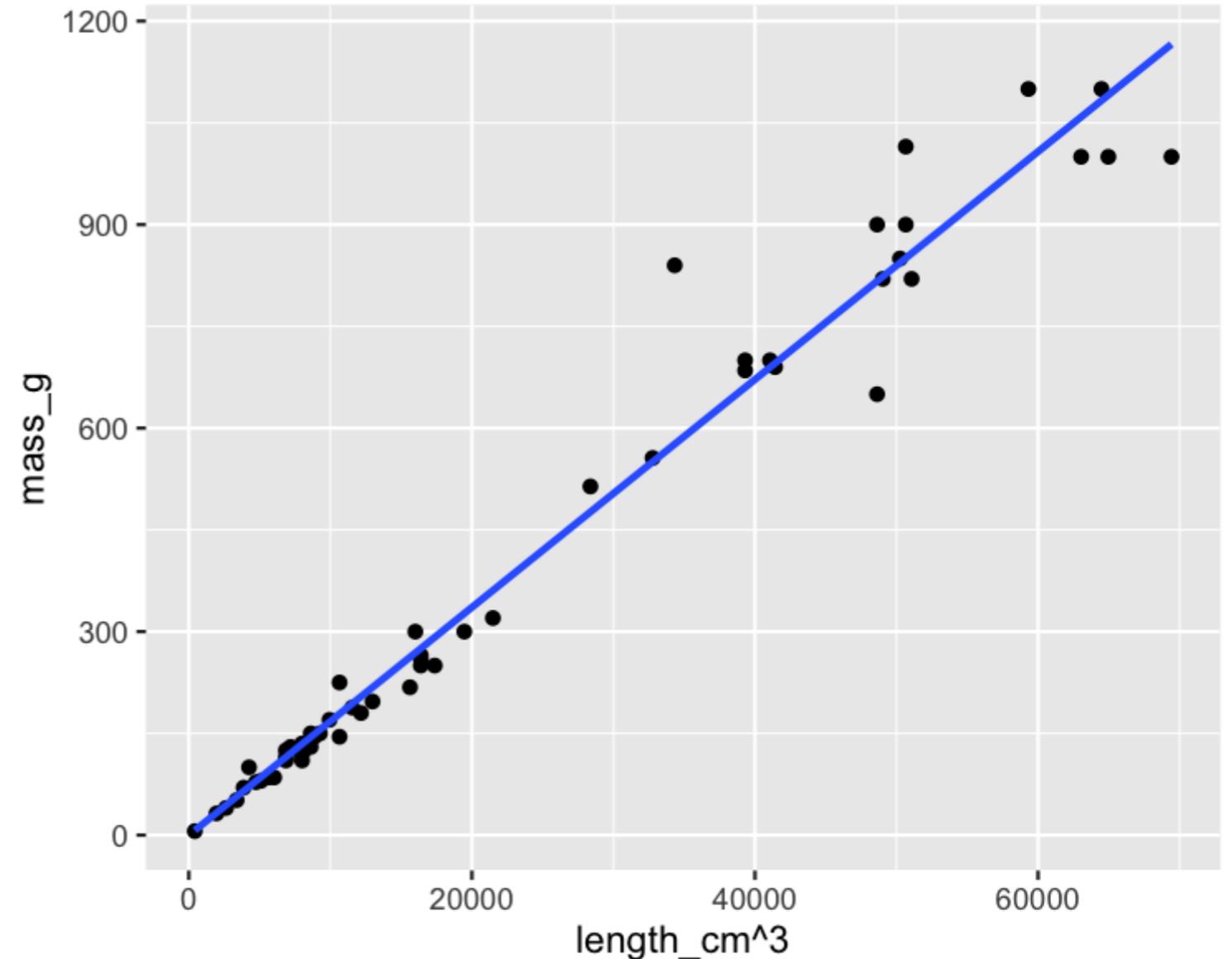


Bream vs. perch



Plotting mass vs. length cubed

```
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

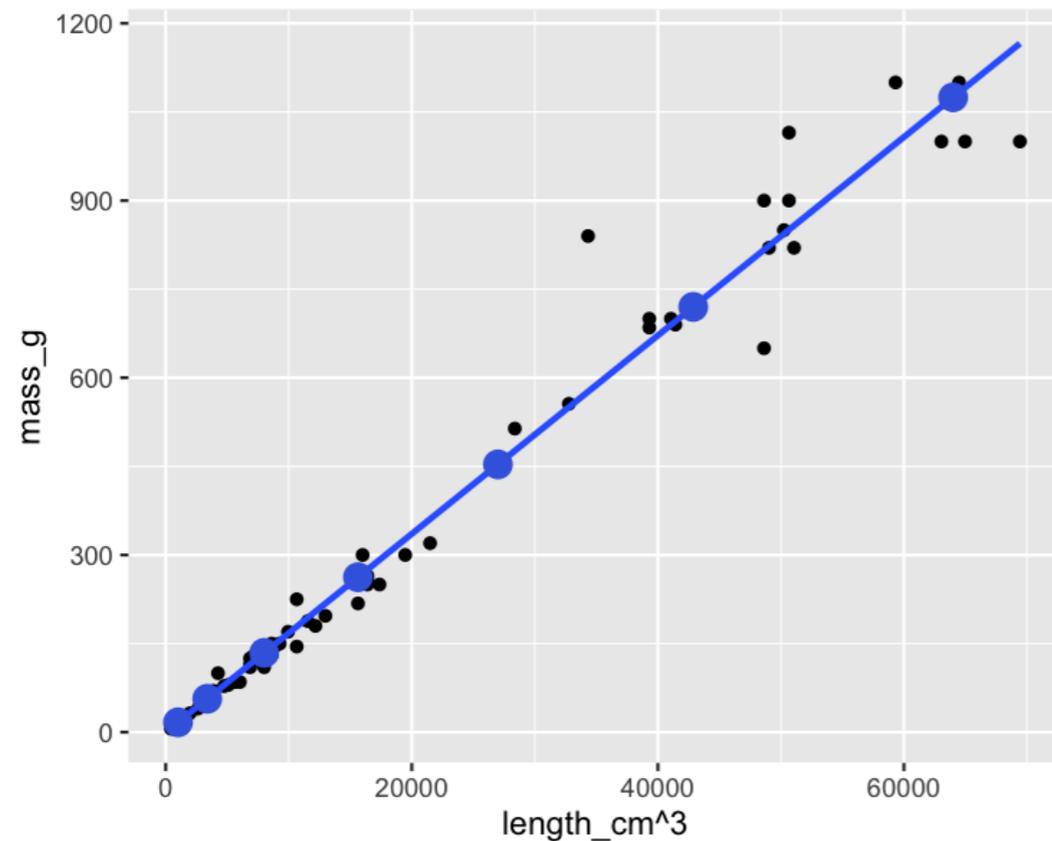
```
explanatory_data <- tibble(  
  length_cm = seq(10, 40, 5)  
)
```

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

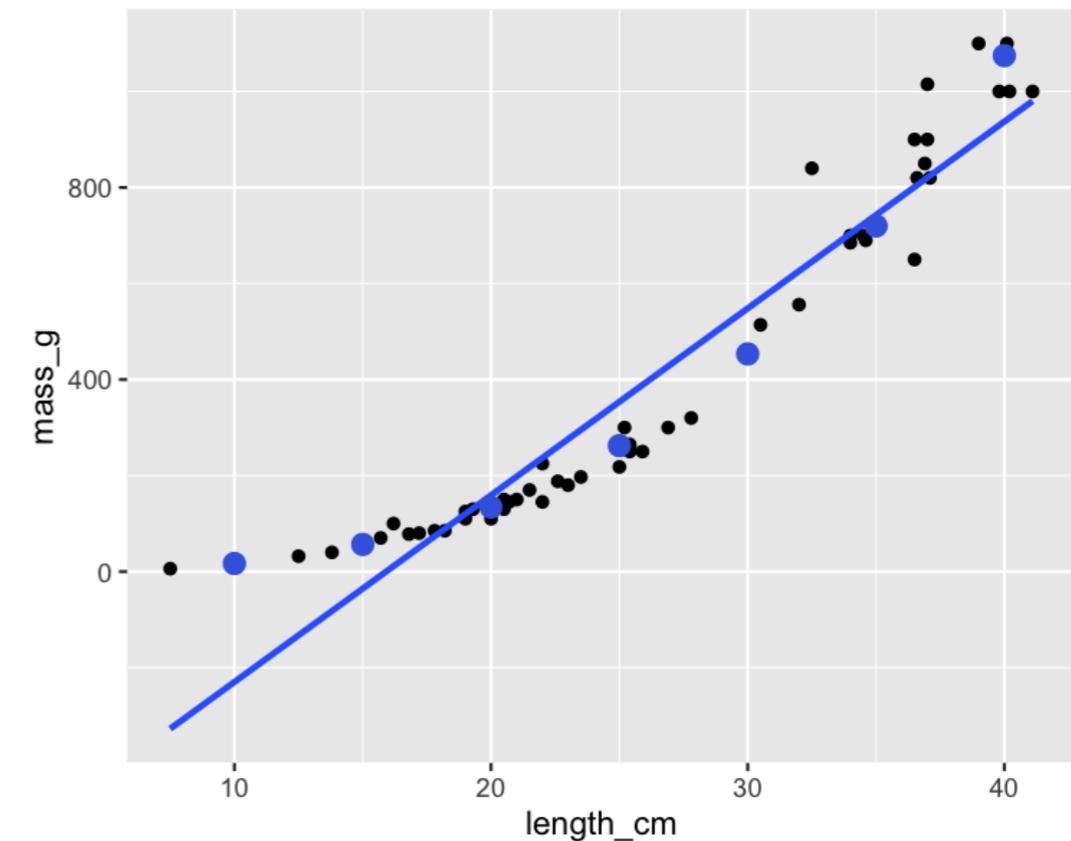
```
# A tibble: 7 x 2  
  length_cm mass_g  
    <dbl> <dbl>  
1      10  16.7  
2      15  56.6  
3      20 134.  
4      25 262.  
5      30 453.  
6      35 720.  
7      40 1075.
```

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

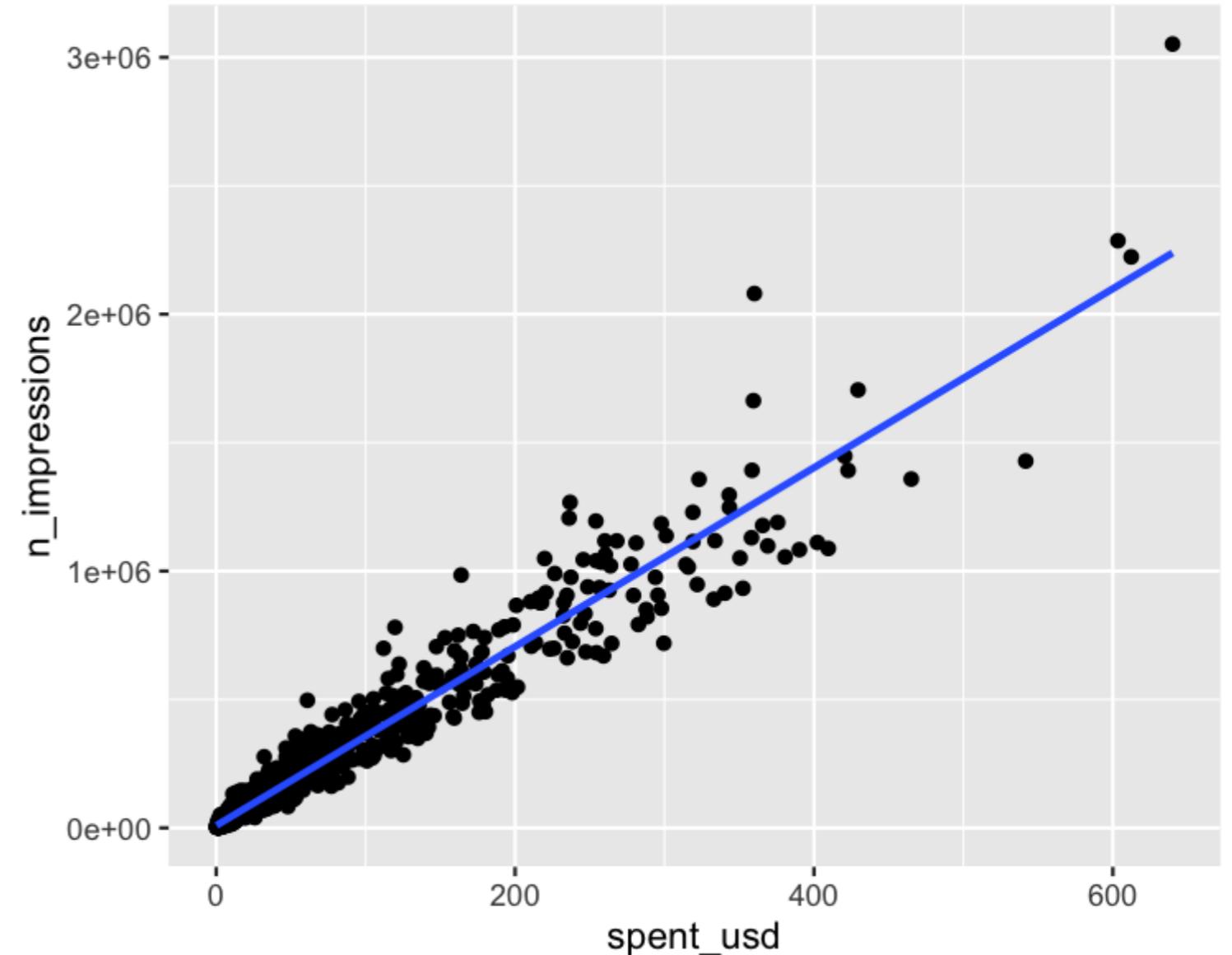
1. Pay Facebook to shows ads.
2. People see the ads ("impressions").
3. Some people who see it, click it.

- 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
...

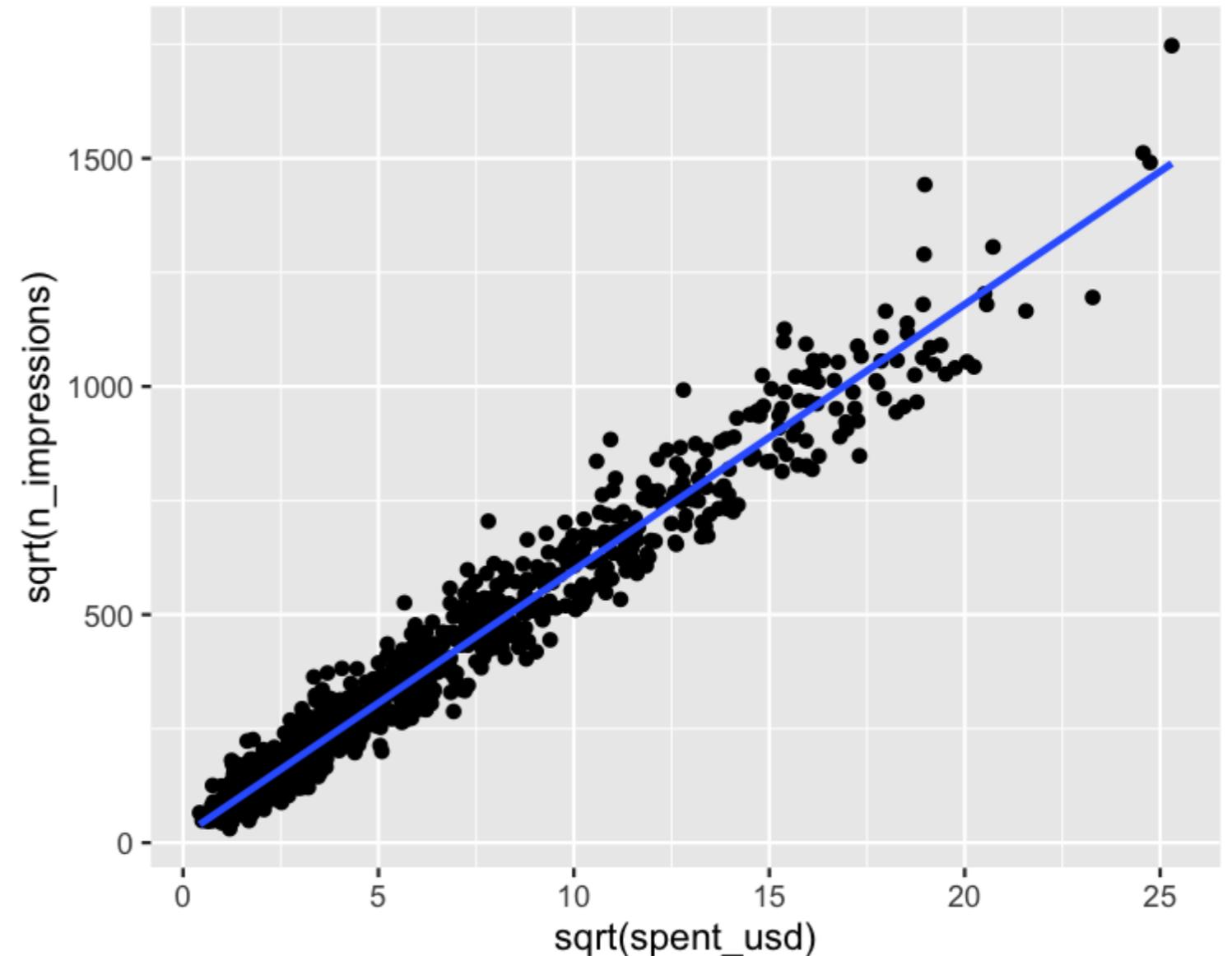
Plot is cramped

```
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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