Models for each category

INTERMEDIATE REGRESSION IN R

Richie Cotton

Data Evangelist at DataCamp

4 categories

```
unique(fish$species)
```

```
"Bream" "Roach" "Perch" "Pike"
```

Splitting the dataset

The smart way

- **base-R:** `split()` + `lapply()`
- `dplyr` : `nest_by()` + `mutate()`

The simple way

```
bream <- fish %>%
  filter(species == "Bream")
perch <- fish %>%
  filter(species == "Perch")
pike <- fish %>%
  filter(species == "Pike")
roach <- fish %>%
  filter(species == "Roach")
```

4 models

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

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

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

```
mdl_pike <- lm(mass_g ~ length_cm, data = pike)
```

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

Coefficients:
(Intercept)    length_cm
   -1540.82        53.19
```

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

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

Coefficients:
(Intercept)    length_cm
    -619.18        38.91
```

```
mdl_roach <- lm(mass_g ~ length_cm, data = roach)
```

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

Coefficients:
(Intercept)    length_cm
    -329.38        23.32
```

Explanatory data

```r
explanatory_data <- tibble(
  length_cm = seq(5, 60, 5)
)
```

Making predictions

```
prediction_data_bream <- explanatory_data %>%
  mutate(
    mass_g = predict(mdl_bream, explanatory_data),
    species = "Bream"
  )
```

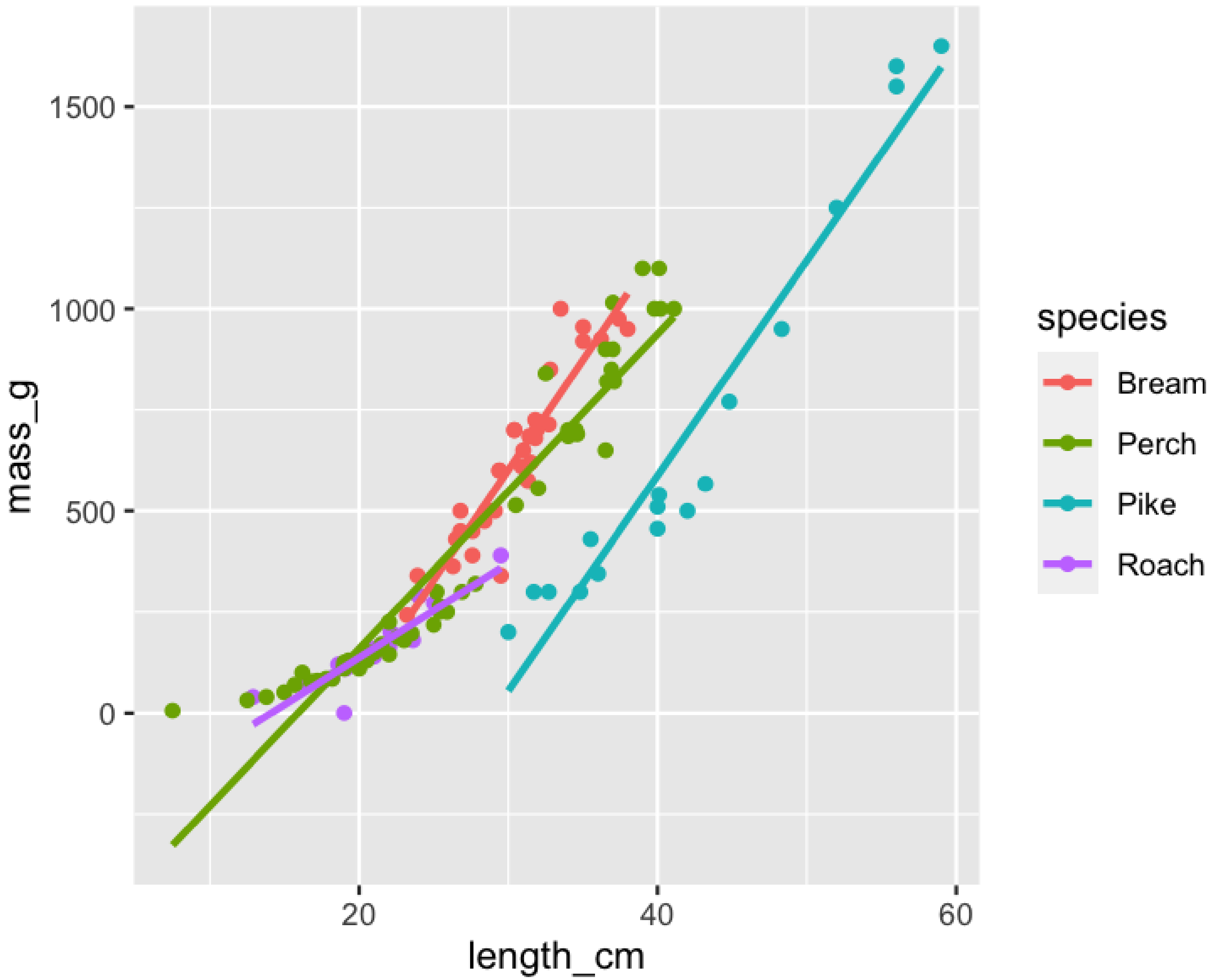
```
prediction_data_pike <- explanatory_data %>%
  mutate(
    mass_g = predict(mdl_perch, explanatory_data),
    species = "Perch"
  )
```

```
prediction_data_perch <- explanatory_data %>%
  mutate(
    mass_g = predict(mdl_pike, explanatory_data),
    species = "Pike"
  )
```

```
prediction_data_roach <- explanatory_data %>%
  mutate(
    mass_g = predict(mdl_roach, explanatory_data),
    species = "Roach"
  )
```

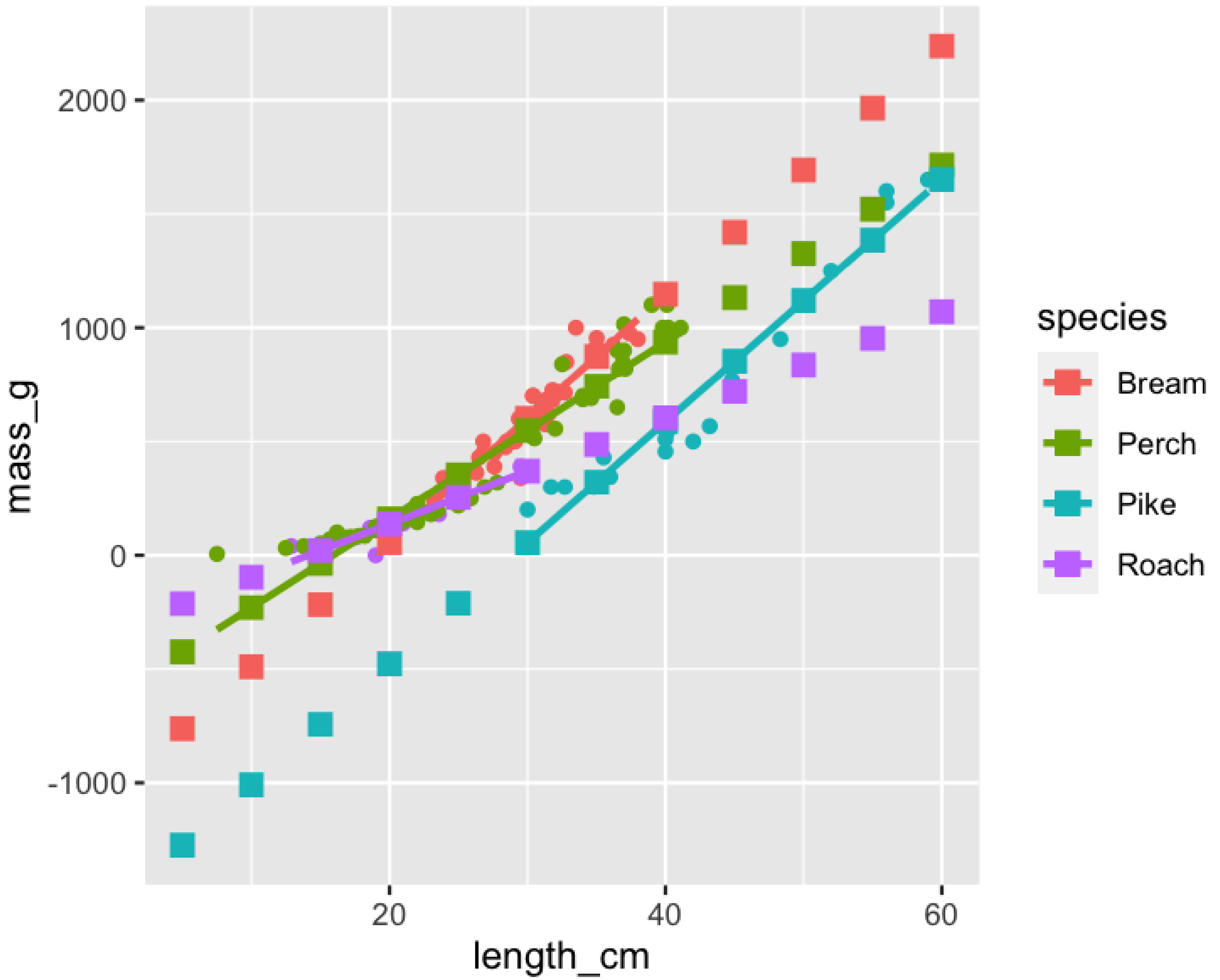
Visualizing predictions

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



Adding in your predictions

```
ggplot(fish,aes(length_cm, mass_g, color = species)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE) +
  geom_point(data = prediction_data_bream, size = 3, shape = 15) +
  geom_point(data = prediction_data_perch, size = 3, shape = 15) +
  geom_point(data = prediction_data_pike, size = 3, shape = 15) +
  geom_point(data = prediction_data_roach, size = 3, shape = 15)
```



Coefficient of determination

```
mdl_fish <- lm(mass_g ~ length_cm + species, data = fish)

mdl_fish %>%
  glance() %>%
  pull(adj.r.squared)
```

```
0.917
```

```
mdl_bream %>% glance() %>% pull(adj.r.squared)
```

```
0.874
```

```
mdl_perch %>% glance() %>% pull(adj.r.squared)
```

```
0.917
```

```
mdl_pike %>% glance() %>% pull(adj.r.squared)
```

```
0.941
```

```
mdl_roach %>% glance() %>% pull(adj.r.squared)
```

```
0.815
```

Residual standard error

```
mdl_fish %>%
  glance() %>%
  pull(sigma)
```

```
103
```

```
mdl_bream %>% glance() %>% pull(sigma)
```

```
74.2
```

```
mdl_perch %>% glance() %>% pull(sigma)
```

```
100
```

```
mdl_pike %>% glance() %>% pull(sigma)
```

```
120
```

```
mdl_roach %>% glance() %>% pull(sigma)
```

```
38.2
```

Let's practice!

INTERMEDIATE REGRESSION IN R

One model with an interaction

INTERMEDIATE REGRESSION IN R

Richie Cotton
Data Evangelist at DataCamp

What is an interaction?

In the fish dataset

The effect of length on the expected mass is different for different species.

More generally

The effect of one explanatory variable on the expected response changes depending on the value of another explanatory variable.

Specifying interactions

No interactions

```
response ~ explntry1 + explntry2
```

With interactions (implicit)

```
response_var ~ explntry1 * explntry2
```

With interactions (explicit)

```
response ~ explntry1 + explntry2 + explntry1:explntry2
```

No interactions

```
mass_g ~ length_cm + species
```

With interactions (implicit)

```
mass_g ~ length_cm * species
```

With interactions (explicit)

```
mass_g ~ length_cm + species + length_cm:species
```

Running the model

```
lm(mass_g ~ length_cm * species, data = fish)
```

```
Call:
lm(formula = mass_g ~ length_cm * species, data = fish)

Coefficients:
           (Intercept)               length_cm            speciesPerch             speciesPike
             -1035.348                  54.550                 416.172                -505.477
          speciesRoach  length_cm:speciesPerch   length_cm:speciesPike  length_cm:speciesRoach
               705.971                 -15.639                  -1.355                 -31.231
```

Easier to understand coefficients

```r
mdl_inter <- lm(mass_g ~ species + species:length_cm + 0, data = fish)
```

```
Call:
lm(formula = mass_g ~ species + species:length_cm + 0, data = fish)

Coefficients:
          speciesBream            speciesPerch             speciesPike            speciesRoach
              -1035.35                 -619.18                -1540.82                 -329.38
speciesBream:length_cm  speciesPerch:length_cm   speciesPike:length_cm  speciesRoach:length_cm
                 54.55                   38.91                   53.19                   23.32
```

Familiar numbers

```
          speciesBream            speciesPerch             speciesPike            speciesRoach
              -1035.35                 -619.18                -1540.82                 -329.38
speciesBream:length_cm  speciesPerch:length_cm   speciesPike:length_cm  speciesRoach:length_cm
                 54.55                   38.91                   53.19                   23.32
```

```
coefficients(mdl_bream)
```

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

Let's practice!

Making predictions with interactions

INTERMEDIATE REGRESSION IN R

Richie Cotton

Data Evangelist at DataCamp

The model with the interaction

```
mdl_mass_vs_both_inter <- lm(mass_g ~ species + species:length_cm + 0, data = fish)
```

```
Call:
lm(formula = mass_g ~ species + species:length_cm + 0, data = fish)

Coefficients:
          speciesBream            speciesPerch             speciesPike            speciesRoach
              -1035.35                 -619.18                -1540.82                 -329.38
speciesBream:length_cm  speciesPerch:length_cm   speciesPike:length_cm  speciesRoach:length_cm
                 54.55                   38.91                   53.19                   23.32
```

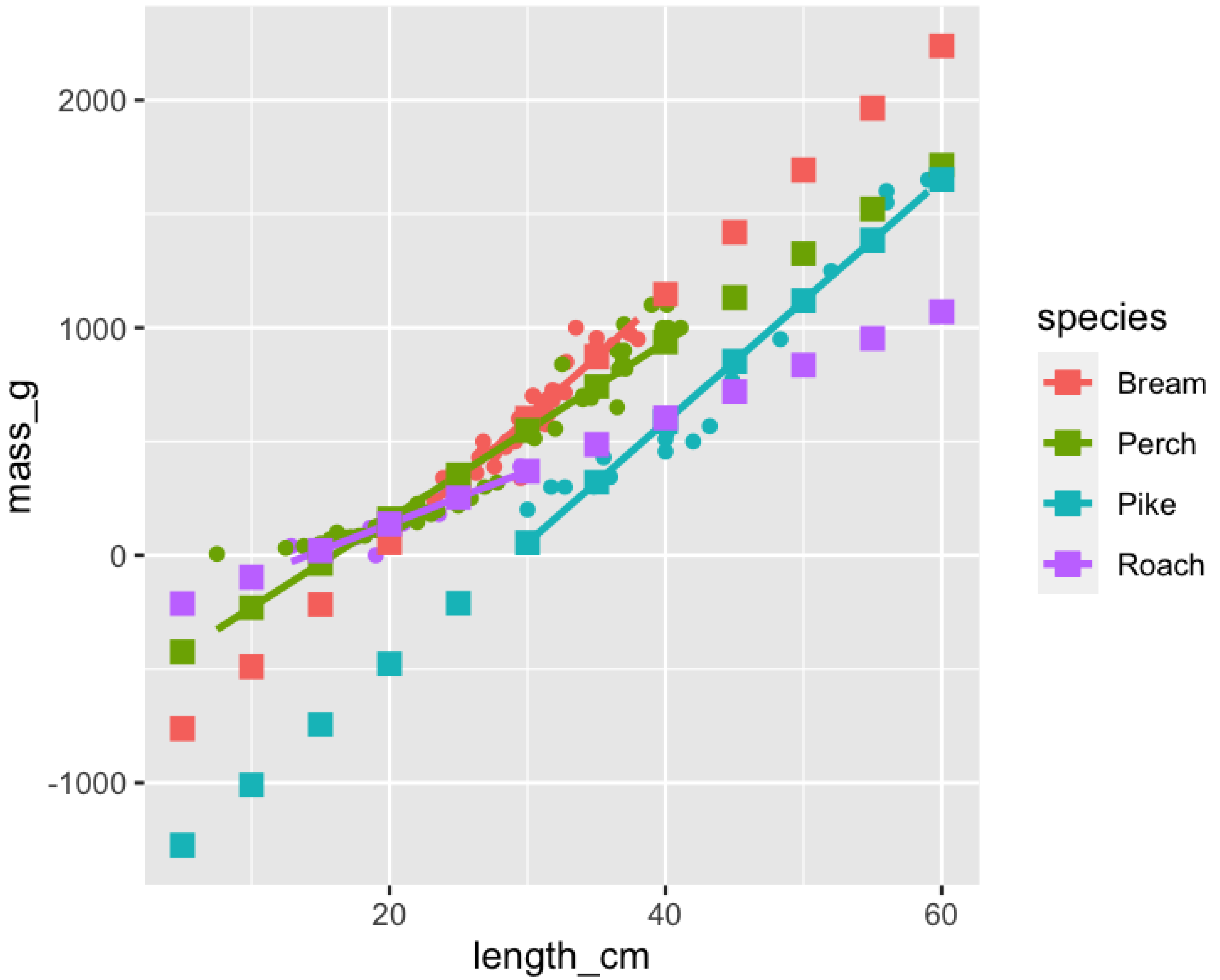
The prediction flow, again

```r
library(dplyr)
library(tidyr)
explanatory_data <- expand_grid(
  length_cm = seq(5, 60, 5),
  species = unique(fish$species)
)

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

Visualizing the predictions

```
ggplot(fish, aes(length_cm, mass_g, color = species)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE) +
  geom_point(data = prediction_data, size = 3, shape = 15)
```



Manually calculating the predictions

```
coeffs <- coefficients(mdl_mass_vs_both_inter)
```

```
          speciesBream           speciesPerch            speciesPike           speciesRoach
           -1035.34757             -619.17511            -1540.82427             -329.37621
speciesBream:length_cm speciesPerch:length_cm  speciesPike:length_cm speciesRoach:length_cm
              54.54998               38.91147               53.19487               23.31926
```

```
intercept_bream <- coeffs[1]
intercept_perch <- coeffs[2]
intercept_pike <- coeffs[3]
intercept_roach <- coeffs[4]
```

```
slope_bream <- coeffs[5]
slope_perch <- coeffs[6]
slope_pike <- coeffs[7]
slope_roach <- coeffs[8]
```

Manually calculating the predictions

```
explanatory_data %>%
  mutate(
    mass_g = case_when(



    )
  )
```

Manually calculating the predictions

```
explanatory_data %>%
  mutate(
    mass_g = case_when(
      species == "Bream" ~



    )
  )
```

Manually calculating the predictions

```r
explanatory_data %>%
  mutate(
    mass_g = case_when(
      species == "Bream" ~ intercept_bream + slope_bream * length_cm




    )
  )
```

Manually calculating the predictions

```
explanatory_data %>%
  mutate(
    mass_g = case_when(
      species == "Bream" ~ intercept_bream + slope_bream * length_cm,
      species == "Perch" ~ intercept_perch + slope_perch * length_cm,
      species == "Pike" ~ intercept_pike + slope_pike * length_cm,
      species == "Roach" ~ intercept_roach + slope_roach * length_cm
    )
  )
```

Let's practice!

INTERMEDIATE REGRESSION IN R

Simpson's Paradox

INTERMEDIATE REGRESSION IN R

Richie Cotton
Data Evangelist at DataCamp

A most ingenious paradox!

Simpson's Paradox occurs when the trend of a model on the whole dataset is very different from the trends shown by models on subsets of the dataset.

trend = slope coefficient

Synthetic Simpson data

x	y	group
62.24344	70.60840	D
52.33499	14.70577	B
56.36795	46.39554	C
66.80395	66.17487	D
66.53605	89.24658	E
62.38129	91.45260	E

- 5 groups of data, labeled "A" to "E"

[1] https://www.rdocumentation.org/packages/datasauRus/topics/simpsons_paradox

Linear regressions

Whole dataset

```
mdl_whole <- lm(
  y ~ x,
  data = simpsons_paradox
)
coefficients(mdl_whole)
```

```
(Intercept)            x
    -38.554        1.751
```

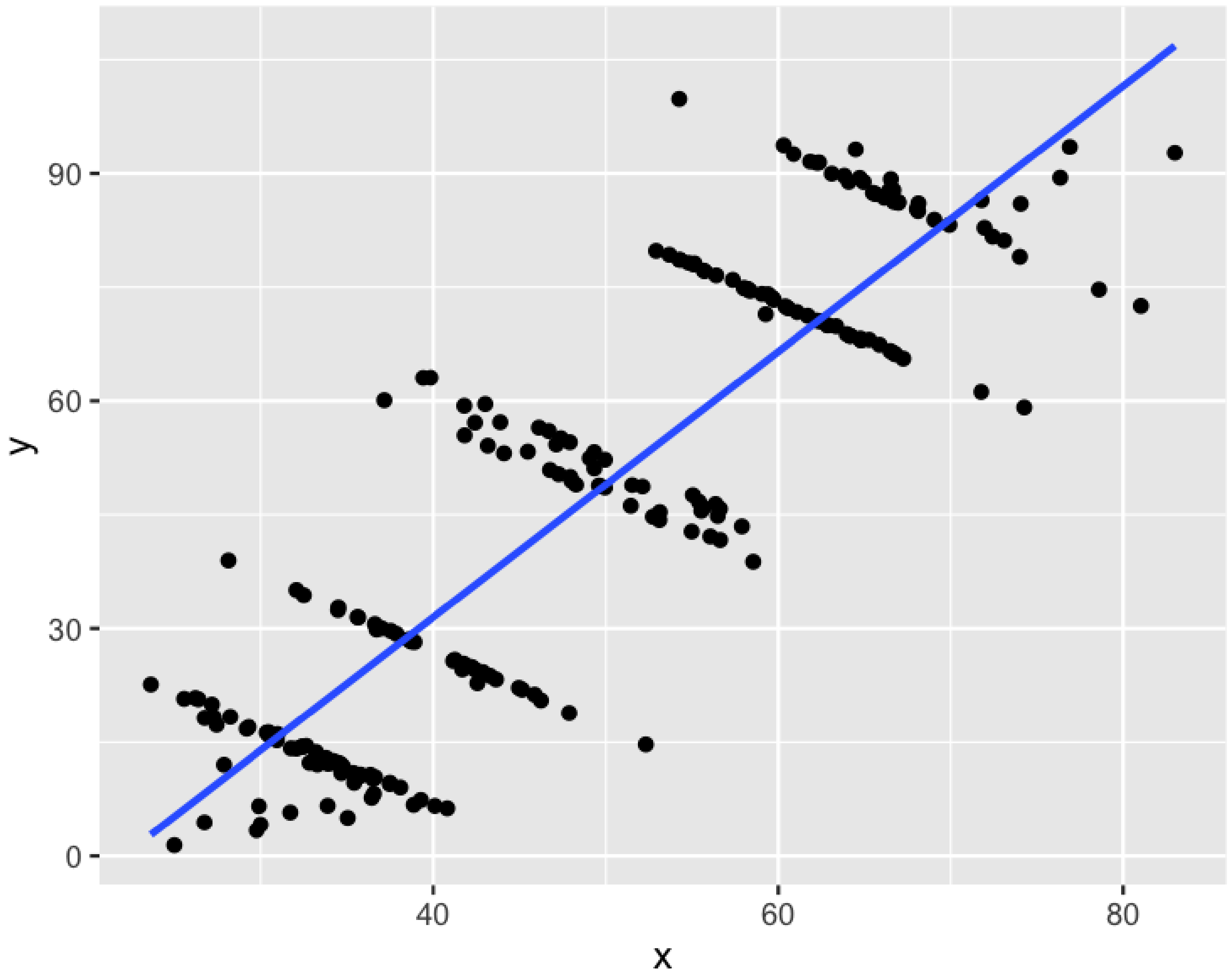
By group

```
mdl_by_group <- lm(
  y ~ group + group:x + 0,
  data = simpsons_paradox
)
coefficients(mdl_by_group)
```

```
  groupA    groupB    groupC    groupD    groupE
 32.5051   67.3886   99.6333  132.3932  123.8242
groupA:x  groupB:x  groupC:x  groupD:x  groupE:x
 -0.6266   -1.0105   -0.9940   -0.9908   -0.5364
```

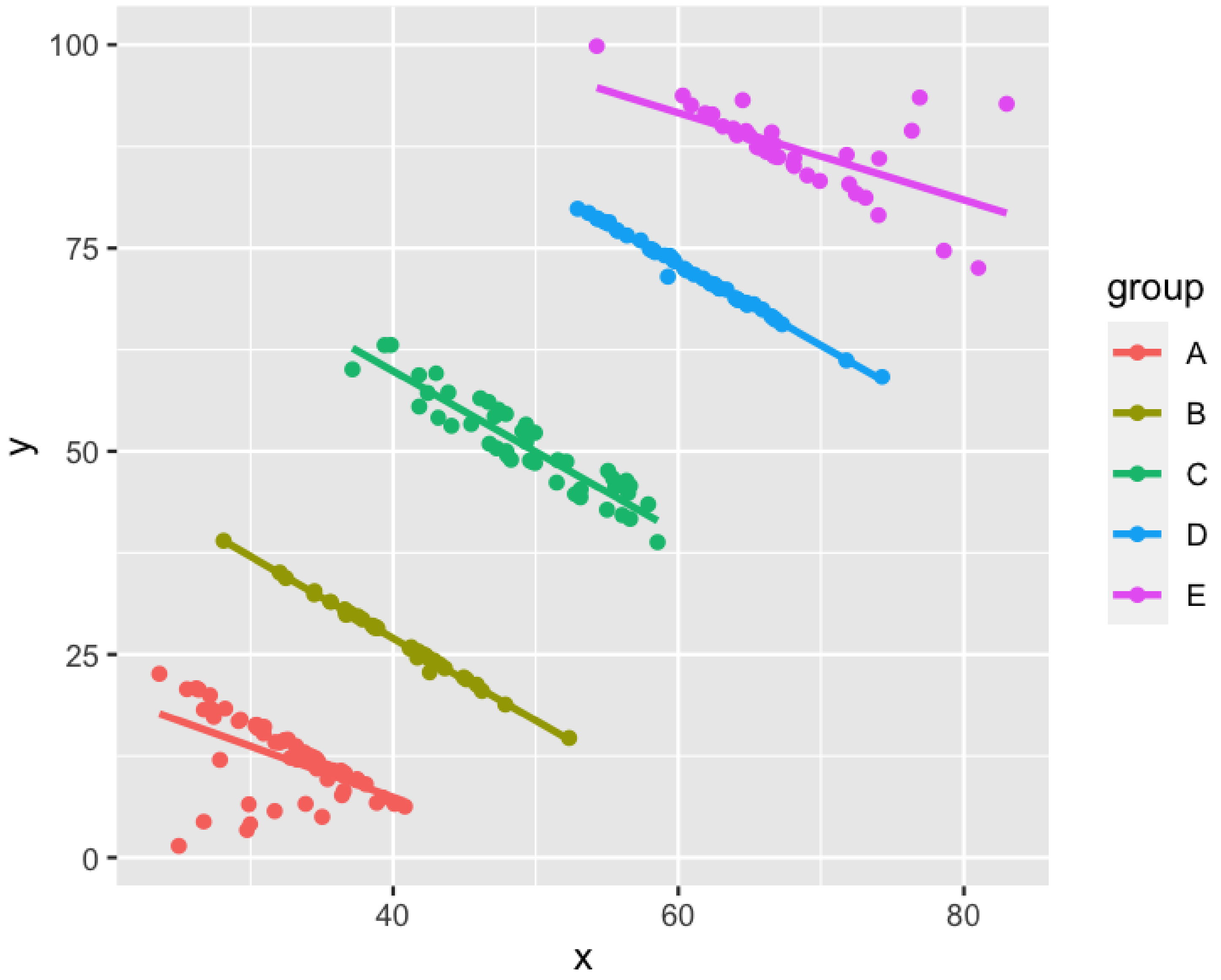
Plotting the whole dataset

```r
ggplot(simpsons_paradox, aes(x, y)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE)
```



Plotting by group

```
ggplot(simpsons_paradox, aes(x, y, color = group)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE)
```



Reconciling the difference

Good advice

If possible, try to plot the dataset.

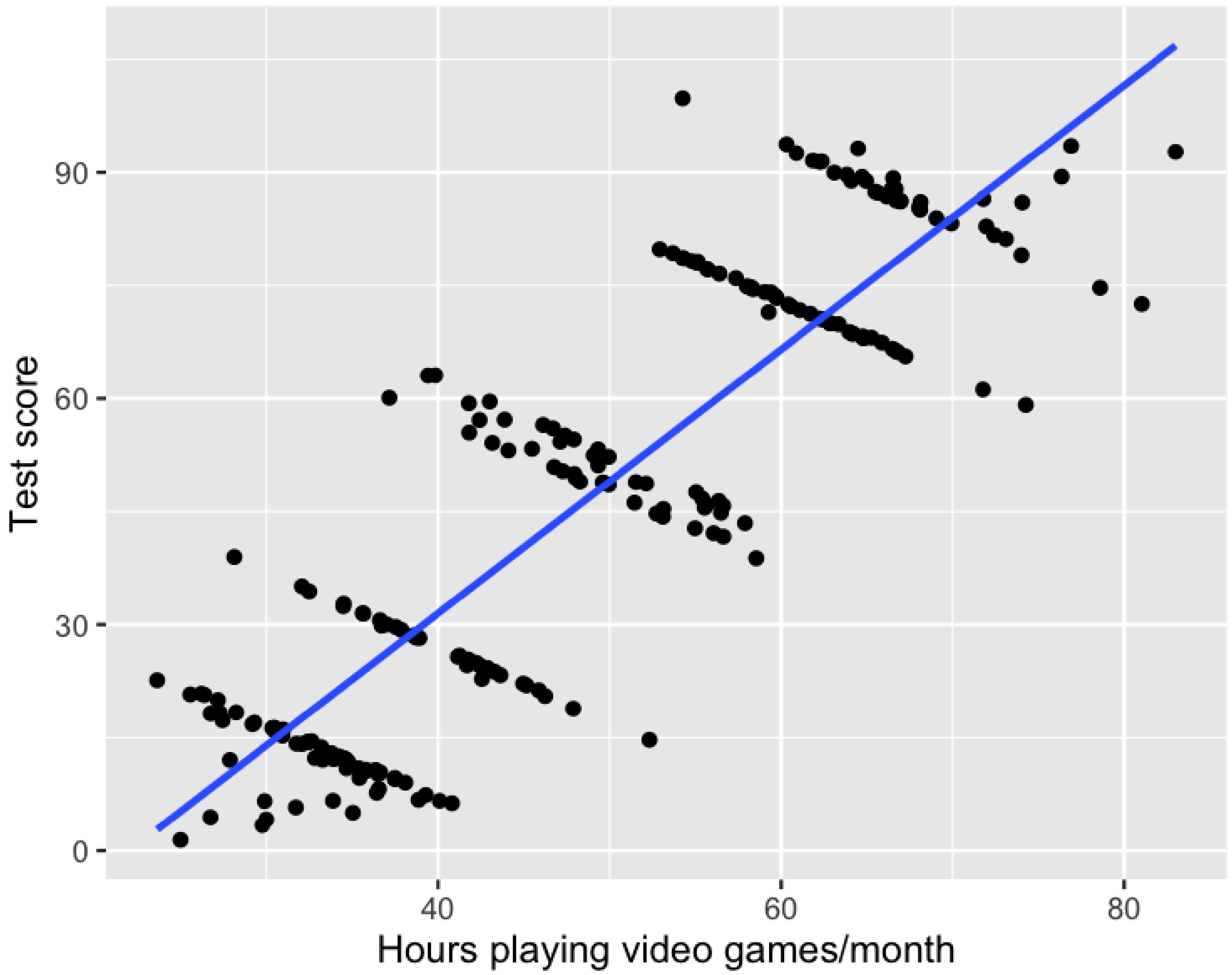
Common advice

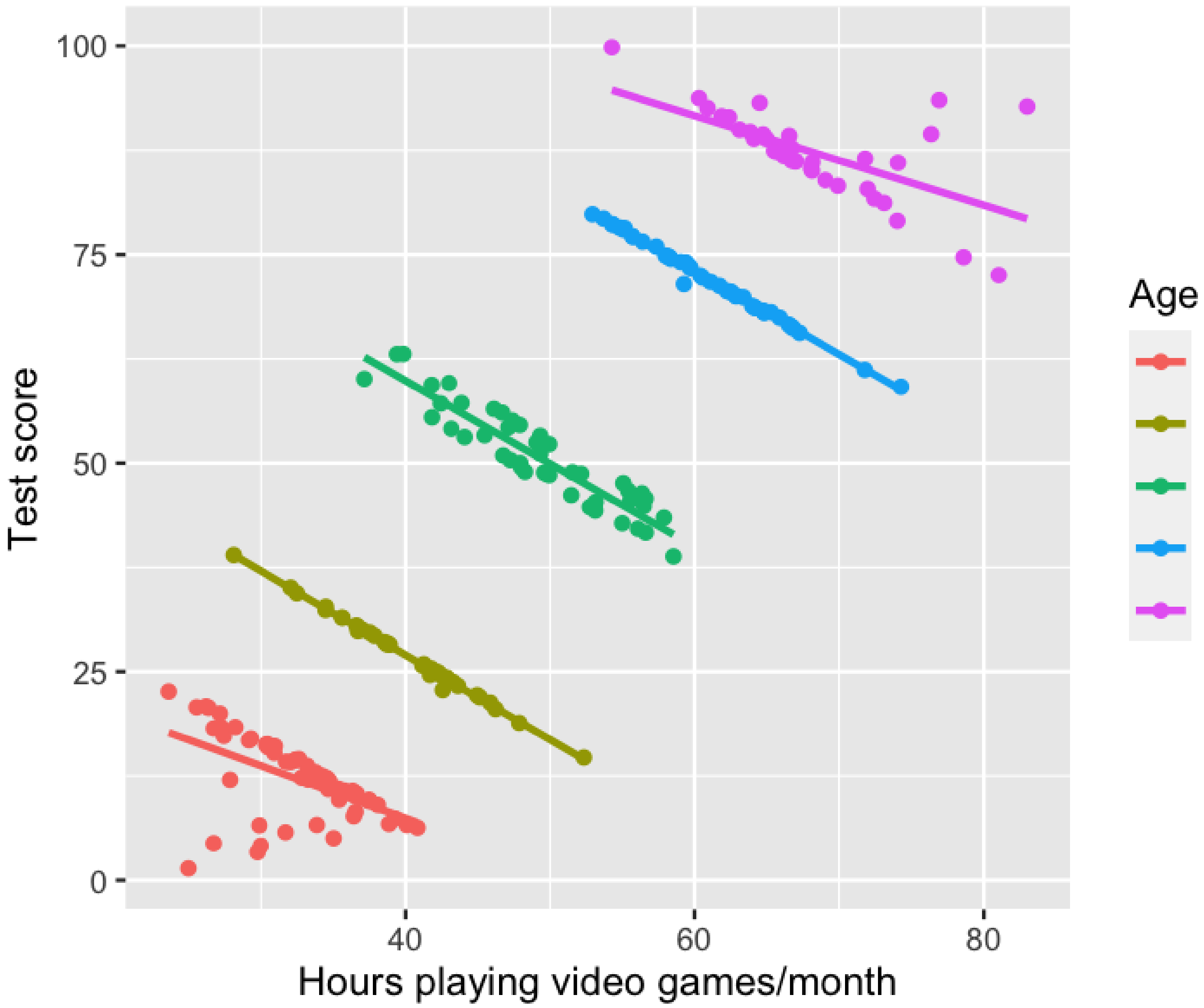
You can't choose the best model in general—it depends on the dataset and the question you are trying to answer.

More good advice

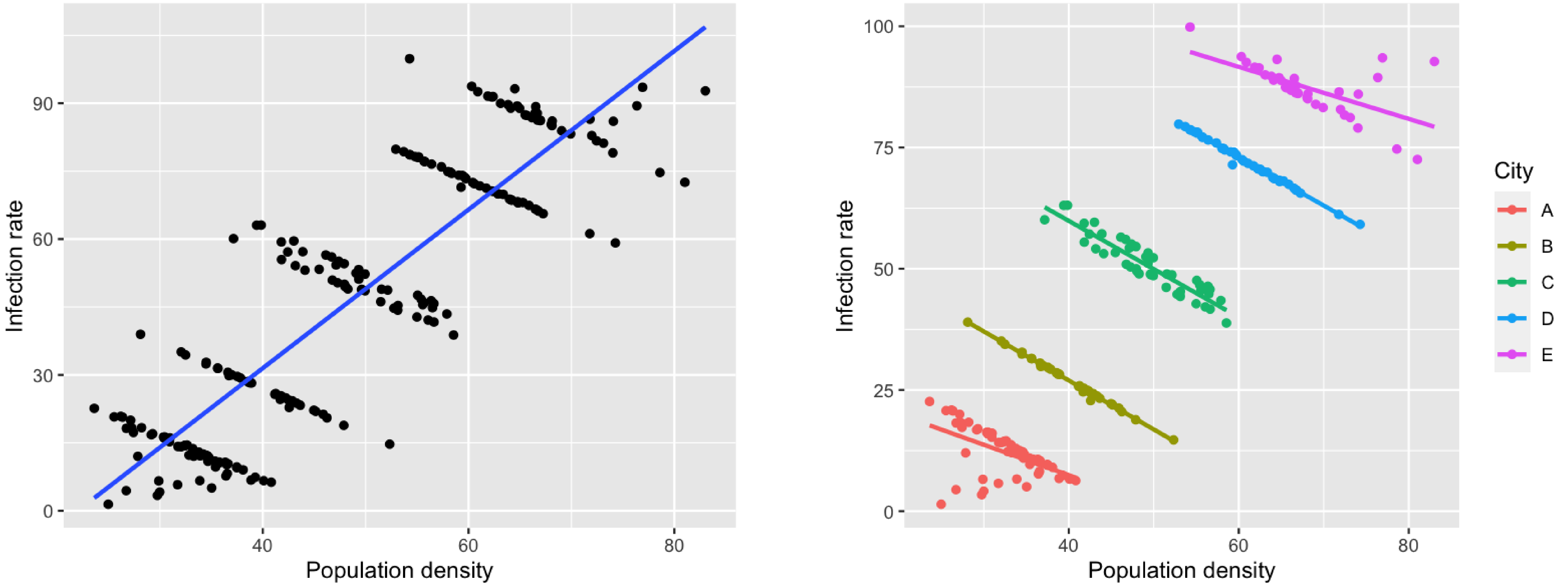
Articulate a question before you start modeling.

Test score example





Infectious disease example



[1] https://stats.stackexchange.com/questions/478463/examples-of-simpsons-paradox-being-resolved-by-choosing-the-aggregate-data

Reconciling the difference, again

- Usually (but not always) the grouped model contains more insight.
- Are you missing explanatory variables?
- Context is important.

Simpson's paradox in real datasets

- The paradox is usually less obvious.
- You may see a zero slope rather than a complete change in direction.
- It may not appear in every group.

Let's practice!

INTERMEDIATE REGRESSION IN R