Parallel slopes linear regression

INTERMEDIATE REGRESSION WITH STATSMODELS IN PYTHON

Maarten Van den Broeck
Content Developer at DataCamp

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The previous course

This course assumes knowledge from **Introduction to Regression with statsmodels in Python**

From simple regression to multiple regression

Multiple regression is a regression model with more than one explanatory variable.

More explanatory variables can give **more insight** and **better predictions**.

The course contents

Chapter 1

- "Parallel slopes" regression

Chapter 2

- Interactions
- Simpson's Paradox

Chapter 3

- More explanatory variables
- How linear regression works

Chapter 4

- Multiple logistic regression
- The logistic distribution
- How logistic regression works

The fish dataset

mass_g	length_cm	species
242.0	23.2	Bream
5.9	7.5	Perch
200.0	30.0	Pike
40.0	12.9	Roach

- Each row represents a fish
- `mass_g` is the response variable
- 1 numeric, 1 categorical explanatory variable

One explanatory variable at a time

```
from statsmodels.formula.api import ols

mdl_mass_vs_length = ols("mass_g ~ length_cm",
                         data=fish).fit()
```

```
print(mdl_mass_vs_length.params)
```

```
Intercept   -536.223947
length_cm     34.899245
dtype: float64
```

- 1 intercept coefficient
- 1 slope coefficient

```
mdl_mass_vs_species = ols("mass_g ~ species + 0",
                          data=fish).fit()

print(mdl_mass_vs_species.params)
```

```
species[Bream]    617.828571
species[Perch]    382.239286
species[Pike]     718.705882
species[Roach]    152.050000
dtype: float64
```

- 1 intercept coefficient for each category

Both variables at the same time

```
mdl_mass_vs_both = ols("mass_g ~ length_cm + species + 0",
                       data=fish).fit()
```

```
print(mdl_mass_vs_both.params)
```

```
species[Bream]    -672.241866
species[Perch]    -713.292859
species[Pike]    -1089.456053
species[Roach]    -726.777799
length_cm           42.568554
dtype: float64
```

- 1 slope coefficient
- 1 intercept coefficient for each category

Comparing coefficients

```
print(mdl_mass_vs_length.params)
```

```
Intercept   -536.223947
length_cm     34.899245
```

```
print(mdl_mass_vs_species.params)
```

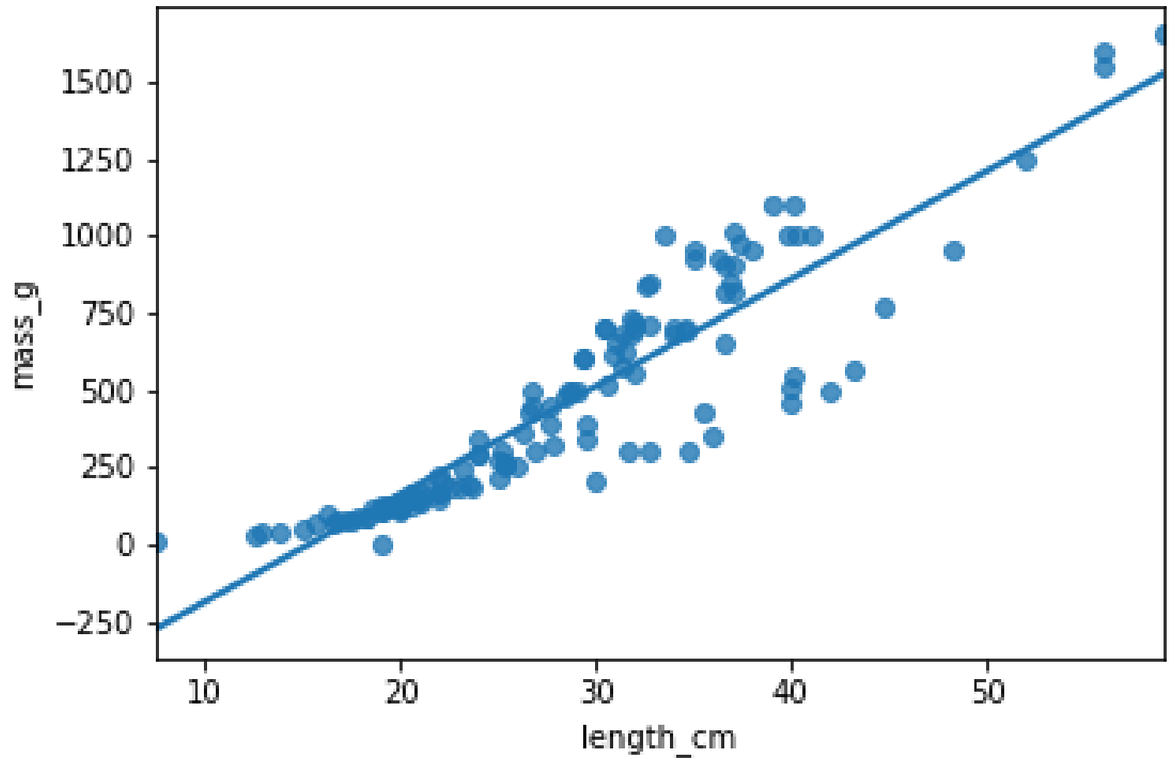
```
species[Bream]    617.828571
species[Perch]    382.239286
species[Pike]     718.705882
species[Roach]    152.050000
```

```
print(mdl_mass_vs_both.params)
```

```
species[Bream]    -672.241866
species[Perch]    -713.292859
species[Pike]    -1089.456053
species[Roach]    -726.777799
length_cm           42.568554
```

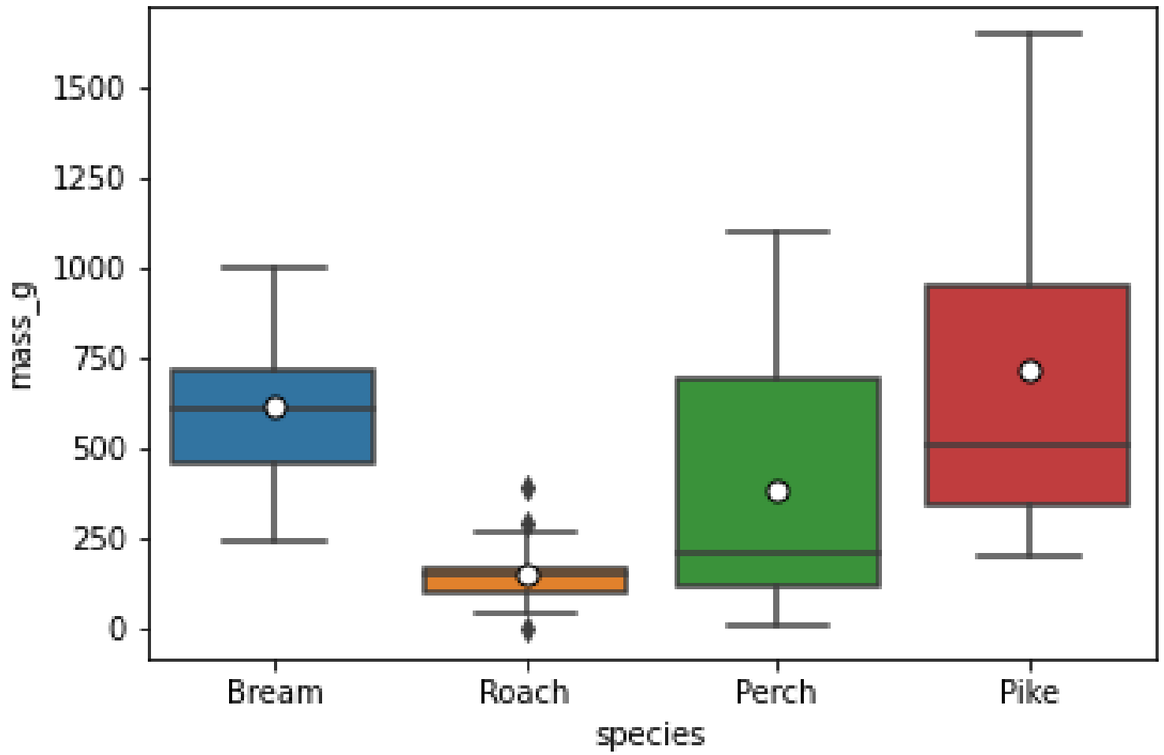
Visualization: 1 numeric explanatory variable

```
import matplotlib.pyplot as plt
import seaborn as sns

sns.regplot(x="length_cm",
            y="mass_g",
            data=fish,
            ci=None)

plt.show()
```



Visualization: 1 categorical explanatory variable

```
sns.boxplot(x="species",
            y="mass_g",
            data=fish,
            showmeans=True)
```



Visualization: both explanatory variables

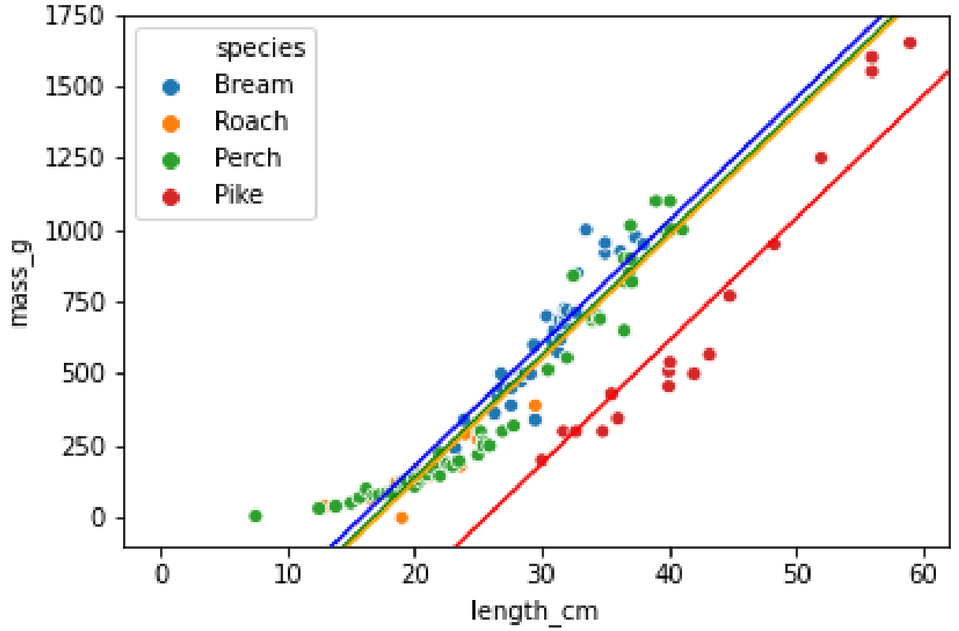
```
coeffs = mdl_mass_vs_both.params
print(coeffs)
```

```
species[Bream]    -672.241866
species[Perch]    -713.292859
species[Pike]    -1089.456053
species[Roach]    -726.777799
length_cm           42.568554
```

```
ic_bream, ic_perch, ic_pike, ic_roach, sl = coeffs
```

```
sns.scatterplot(x="length_cm",
                y="mass_g",
                hue="species",
                data=fish)
```

```
plt.axline(xy1=(0, ic_bream), slope=sl, color="blue")
plt.axline(xy1=(0, ic_perch), slope=sl, color="green")
plt.axline(xy1=(0, ic_pike), slope=sl, color="red")
plt.axline(xy1=(0, ic_roach), slope=sl, color="orange")
```



Let's practice!

INTERMEDIATE REGRESSION WITH STATSMODELS IN PYTHON

Predicting parallel slopes

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The prediction workflow

```
import pandas as pd
import numpy as np
expl_data_length = pd.DataFrame(
  {"length_cm": np.arange(5, 61, 5)})
print(expl_data_length)
```

```
    length_cm
0           5
1          10
2          15
3          20
4          25
5          30
6          35
7          40
8          45
9          50
10         55
11         60
```

The prediction workflow

```
[A, B, C] x [1, 2] ==> [A1, B1, C1, A2, B2, C2]
```

```
from itertools import product
product(["A", "B", "C"], [1, 2])
```

```
length_cm = np.arange(5, 61, 5)
species = fish["species"].unique()

p = product(length_cm, species)

expl_data_both = pd.DataFrame(p,
                              columns=['length_cm',
                                       'species'])
print(expl_data_both)
```

```
    length_cm species
0           5   Bream
1           5   Roach
2           5   Perch
3           5    Pike
4          10   Bream
5          10   Roach
6          10   Perch
...
41         55   Roach
42         55   Perch
43         55    Pike
44         60   Bream
45         60   Roach
46         60   Perch
47         60    Pike
```

The prediction workflow

Predict `mass_g` from length_cm only

```
prediction_data_length = expl_data_length.assign(
    mass_g = mdl_mass_vs_length.predict(expl_data)
)
```

```
    length_cm     mass_g
0           5  -361.7277
1          10  -187.2315
2          15   -12.7353
3          20   161.7610
4          25   336.2572
5          30   510.7534
... # number of rows: 12
```

Predict `mass_g` from both explanatory variables

```
prediction_data_both = expl_data_both.assign(
    mass_g = mdl_mass_vs_both.predict(expl_data)
)
```

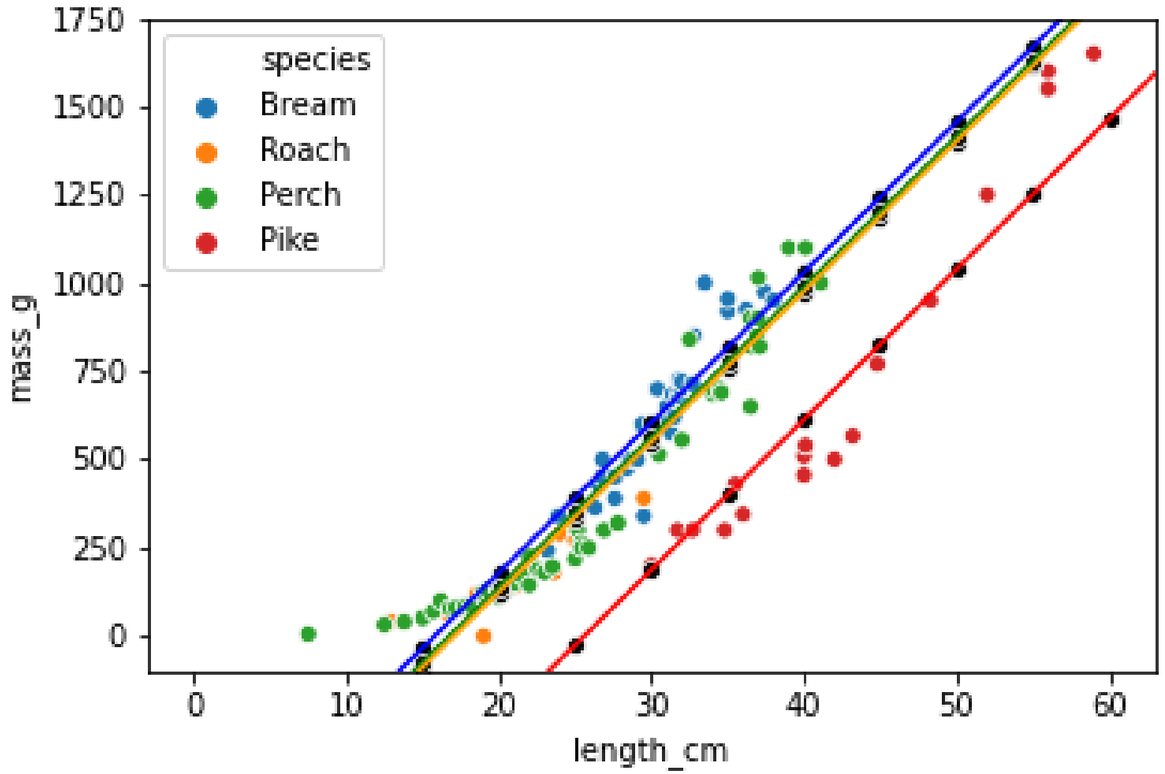
```
    length_cm species     mass_g
0           5   Bream  -459.3991
1           5   Roach  -513.9350
2           5   Perch  -500.4501
3           5    Pike  -876.6133
4          10   Bream  -246.5563
5          10   Roach  -301.0923
... # number of rows: 48
```

Visualizing the predictions

```
plt.axline(xy1=(0, ic_bream), slope=sl, color="blue")
plt.axline(xy1=(0, ic_perch), slope=sl, color="green")
plt.axline(xy1=(0, ic_pike), slope=sl, color="red")
plt.axline(xy1=(0, ic_roach), slope=sl, color="orange")

sns.scatterplot(x="length_cm",
                y="mass_g",
                hue="species",
                data=fish)
```

```
sns.scatterplot(x="length_cm",
                y="mass_g",
                color="black",
                data=prediction_data)
```



Manually calculating predictions for linear regression

```
coeffs = mdl_mass_vs_length.params
print(coeffs)
```

```
Intercept   -536.223947
length_cm     34.899245
```

```
intercept, slope = coeffs
```

```
explanatory_data = pd.DataFrame(
{"length_cm": np.arange(5, 61, 5)})

prediction_data = explanatory_data.assign(
    mass_g = intercept + slope * explanatory_data
    )
```

```
print(prediction_data)
```

```
    length_cm       mass_g
0           5  -361.727721
1          10  -187.231494
2          15   -12.735268
3          20   161.760959
4          25   336.257185
5          30   510.753412
...
9          50  1208.738318
10         55  1383.234545
11         60  1557.730771
```

Manually calculating predictions for multiple regression

```
coeffs = mdl_mass_vs_both.params
print(coeffs)
```

```
species[Bream]    -672.241866
species[Perch]    -713.292859
species[Pike]    -1089.456053
species[Roach]    -726.777799
length_cm           42.568554
```

```
ic_bream, ic_perch, ic_pike, ic_roach, slope = coeffs
```

np.select()

```
conditions = [
      condition_1,
      condition_2,
      # ...
      condition_n
]

choices = [list_of_choices] # same length as conditions

np.select(conditions, choices)
```

Choosing an intercept with np.select()

```
conditions = [
    explanatory_data["species"] == "Bream",
    explanatory_data["species"] == "Perch",
    explanatory_data["species"] == "Pike",
    explanatory_data["species"] == "Roach"
]
```

```
choices = [ic_bream, ic_perch, ic_pike, ic_roach]
```

```
intercept = np.select(conditions, choices)
```

```
print(intercept)
```

```
[ -672.24  -726.78  -713.29 -1089.46
  -672.24  -726.78  -713.29 -1089.46
  -672.24  -726.78  -713.29 -1089.46
  -672.24  -726.78  -713.29 -1089.46
  -672.24  -726.78  -713.29 -1089.46
  -672.24  -726.78  -713.29 -1089.46
  -672.24  -726.78  -713.29 -1089.46
  -672.24  -726.78  -713.29 -1089.46
  -672.24  -726.78  -713.29 -1089.46
  -672.24  -726.78  -713.29 -1089.46
  -672.24  -726.78  -713.29 -1089.46
  -672.24  -726.78  -713.29 -1089.46]
```

The final prediction step

```
prediction_data = explanatory_data.assign(
    intercept = np.select(conditions, choices),
    mass_g = intercept + slope * explanatory_data["length_cm"])

print(prediction_data)
```

```
    length_cm species  intercept     mass_g
0           5   Bream  -672.2419  -459.3991
1           5   Roach  -726.7778  -513.9350
2           5   Perch  -713.2929  -500.4501
3           5    Pike -1089.4561  -876.6133
4          10   Bream  -672.2419  -246.5563
5          10   Roach  -726.7778  -301.0923
6          10   Perch  -713.2929  -287.6073
7          10    Pike -1089.4561  -663.7705
8          15   Bream  -672.2419   -33.7136
...
40         55   Bream  -672.2419  1669.0286
41         55   Roach  -726.7778  1614.4927
42         55   Perch  -713.2929  1627.9776
43         55    Pike -1089.4561  1251.8144
44         60   Bream  -672.2419  1881.8714
45         60   Roach  -726.7778  1827.3354
46         60   Perch  -713.2929  1840.8204
47         60    Pike -1089.4561  1464.6572
```

Compare to .predict()

```
mdl_mass_vs_both.predict(explanatory_data)
```

```
0     -459.3991
1     -513.9350
2     -500.4501
3     -876.6133
4     -246.5563
5     -301.0923
...
43    1251.8144
44    1881.8714
45    1827.3354
46    1840.8204
47    1464.6572
```

Let's practice!

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Assessing model performance

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Model performance metrics

- *Coefficient of determination (R-squared)*: how well the linear regression line fits the observed values.
  - Larger is better.
- *Residual standard error (RSE)*: the typical size of the residuals.
  - Smaller is better.

Getting the coefficient of determination

```
print(mdl_mass_vs_length.rsquared)
```

```
0.8225689502644215
```

```
print(mdl_mass_vs_species.rsquared)
```

```
0.25814887709499157
```

```
print(mdl_mass_vs_both.rsquared)
```

```
0.9200433561156649
```

Adjusted coefficient of determination

- More explanatory variables increases R^2.
- Too many explanatory variables causes overfitting.
- *Adjusted coefficient of determination* penalizes more explanatory variables.
- $\bar{R}^2 = 1 - (1 - R^2)\frac{n_{obs} - 1}{n_{obs} - n_{var} - 1}$
- Penalty is noticeable when R^2 is small, or n_{var} is large fraction of n_{obs}.
- In `statsmodels`, it's contained in the `rsquared_adj` attribute.

Getting the adjusted coefficient of determination

```
print("rsq_length: ", mdl_mass_vs_length.rsquared)
print("rsq_adj_length: ", mdl_mass_vs_length.rsquared_adj)
```

```
rsq_length:  0.8225689502644215
rsq_adj_length:  0.8211607673300121
```

```
print("rsq_species: ", mdl_mass_vs_species.rsquared)
print("rsq_adj_species: ", mdl_mass_vs_species.rsquared_adj)
```

```
rsq_species:  0.25814887709499157
rsq_adj_species:  0.24020086605696722
```

```
print("rsq_both: ", mdl_mass_vs_both.rsquared
print("rsq_adj_both: ", mdl_mass_vs_both.rsquared_adj)
```

```
rsq_both:  0.9200433561156649
rsq_adj_both:  0.9174431400543857
```

Getting the residual standard error

```
rse_length = np.sqrt(mdl_mass_vs_length.mse_resid)
print("rse_length: ", rse_length)
```

```
rse_length:  152.12092835414788
```

```
rse_species = np.sqrt(mdl_mass_vs_species.mse_resid)
print("rse_species: ", rse_species)
```

```
rse_species:  313.5501156682592
```

```
rse_both = np.sqrt(mdl_mass_vs_both.mse_resid)
print("rse_both: ", rse_both)
```

```
rse_both:  103.35563303966488
```

Let's practice!

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