Quantifying model fit

INTRODUCTION TO REGRESSION WITH STATSMODELS IN PYTHON

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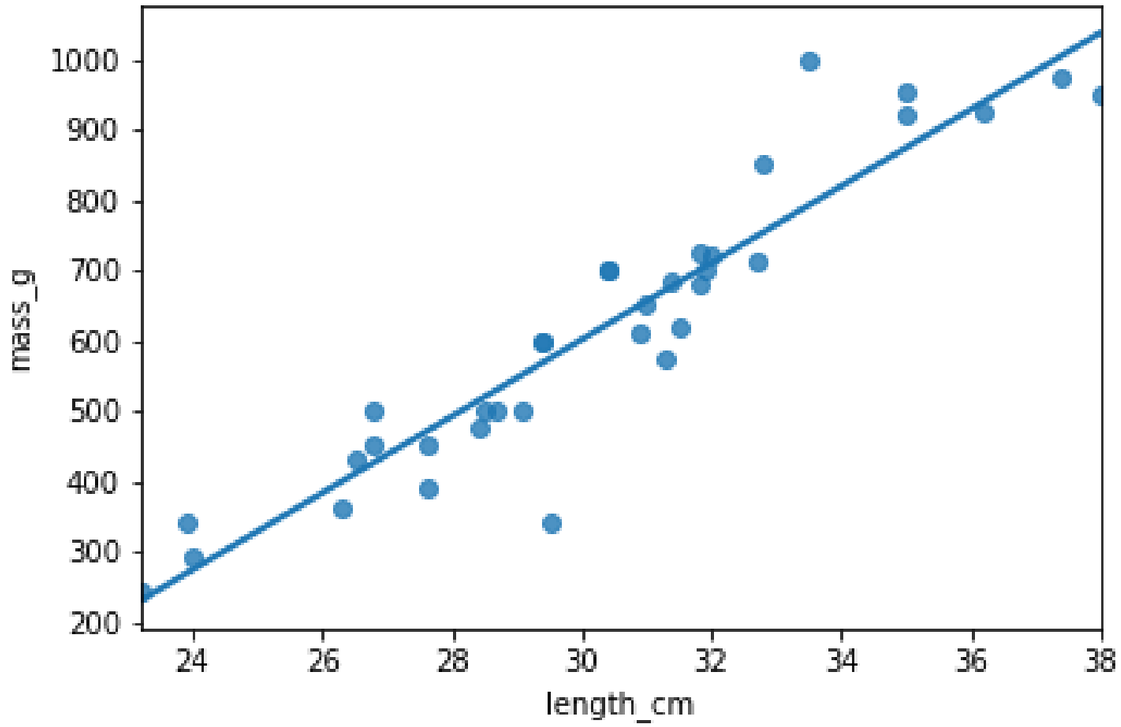
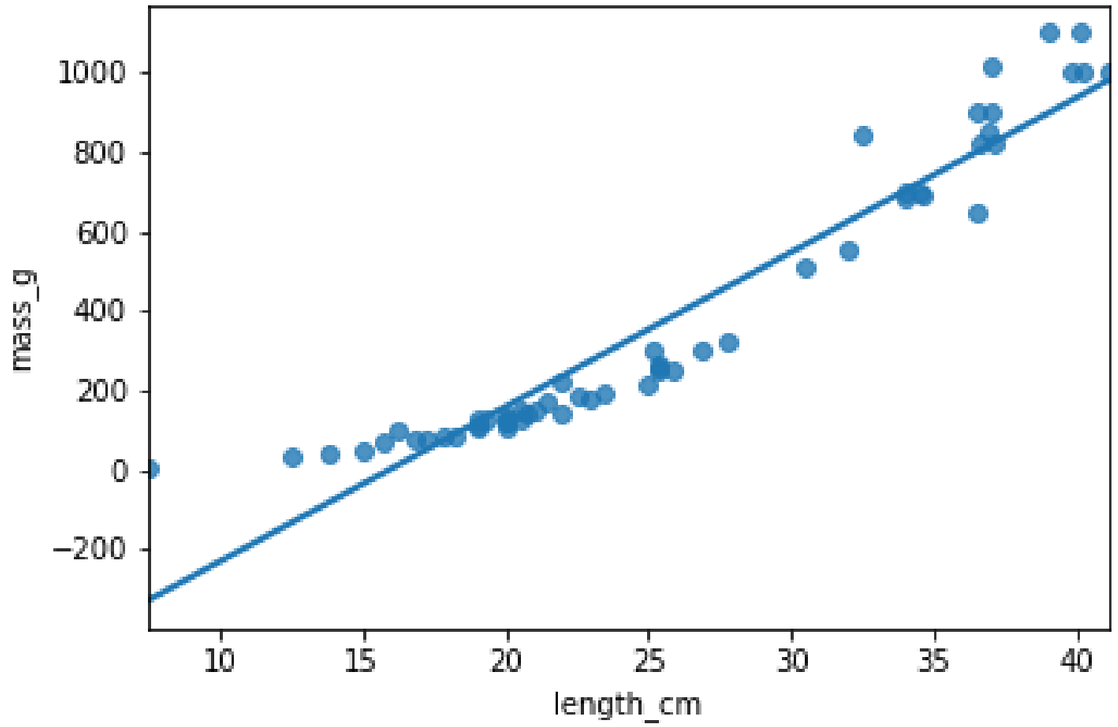
Bream and perch models

Bream



Perch



Coefficient of determination

Sometimes called "r-squared" or "R-squared".

> The proportion of the variance in the response variable that is predictable from the explanatory variable

- `1` means a perfect fit
- `0` means the worst possible fit

.summary()

Look at the value titled "R-Squared"

```
mdl_bream = ols("mass_g ~ length_cm", data=bream).fit()
```

```
print(mdl_bream.summary())
```

```
# Some lines of output omitted


                            OLS Regression Results
Dep. Variable:                     mass_g   R-squared:                       0.878
Model:                             OLS      Adj. R-squared:                  0.874
Method:                  Least Squares      F-statistic:                     237.6
```

.rsquared attribute

```
print(mdl_bream.rsquared)
```

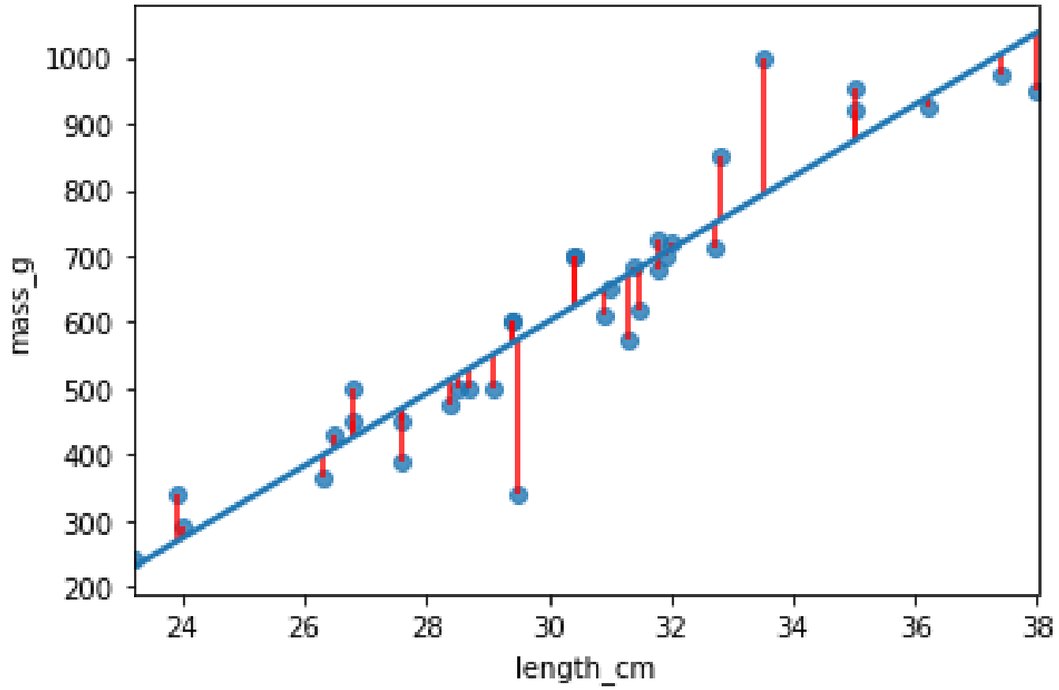
```
0.8780627095147174
```

It's just correlation squared

```
coeff_determination = bream["length_cm"].corr(bream["mass_g"]) ** 2
print(coeff_determination)
```

```
0.8780627095147173
```

Residual standard error (RSE)



- A "typical" difference between a prediction and an observed response
- It has the same unit as the response variable.
- MSE = RSE2

.mse_resid attribute

```
mse = mdl_bream.mse_resid
print('mse: ', mse)
```

```
mse:  5498.555084973521
```

```
rse = np.sqrt(mse)
print("rse: ", rse)
```

```
rse:  74.15224261594197
```

Calculating RSE: residuals squared

```
residuals_sq = mdl_bream.resid ** 2

print("residuals sq: \n", residuals_sq)
```

```
residuals sq:
0       138.957118
1       260.758635
2      5126.992578
3      1318.919660
4       390.974309
     ...
30     2125.047026
31     6576.923291
32      206.259713
33      889.335096
34     7665.302003
Length: 35, dtype: float64
```

Calculating RSE: sum of residuals squared

```
residuals_sq = mdl_bream.resid ** 2

resid_sum_of_sq = sum(residuals_sq)

print("resid sum of sq :",
      resid_sum_of_sq)
```

```
resid sum of sq : 181452.31780412616
```

Calculating RSE: degrees of freedom

```
residuals_sq = mdl_bream.resid ** 2

resid_sum_of_sq = sum(residuals_sq)

deg_freedom = len(bream.index) - 2

print("deg freedom: ", deg_freedom)
```

```
deg freedom:  33
```

Degrees of freedom equals the number of observations minus the number of model coefficients.

Calculating RSE: square root of ratio

```
residuals_sq = mdl_bream.resid ** 2

resid_sum_of_sq = sum(residuals_sq)

deg_freedom = len(bream.index) - 2

rse = np.sqrt(resid_sum_of_sq/deg_freedom)

print("rse :", rse)
```

```
rse : 74.15224261594197
```

Interpreting RSE

`mdl_bream` has an RSE of `74`.

> The difference between predicted bream masses and observed bream masses is typically about 74g.

Root-mean-square error (RMSE)

```
residuals_sq = mdl_bream.resid ** 2

resid_sum_of_sq = sum(residuals_sq)

deg_freedom = len(bream.index) - 2

rse = np.sqrt(resid_sum_of_sq/deg_freedom)

print("rse :", rse)
```

```
rse : 74.15224261594197
```

```
residuals_sq = mdl_bream.resid ** 2

resid_sum_of_sq = sum(residuals_sq)

n_obs = len(bream.index)

rmse = np.sqrt(resid_sum_of_sq/n_obs)

print("rmse :", rmse)
```

```
rmse : 72.00244396727619
```

Let's practice!

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Visualizing model fit

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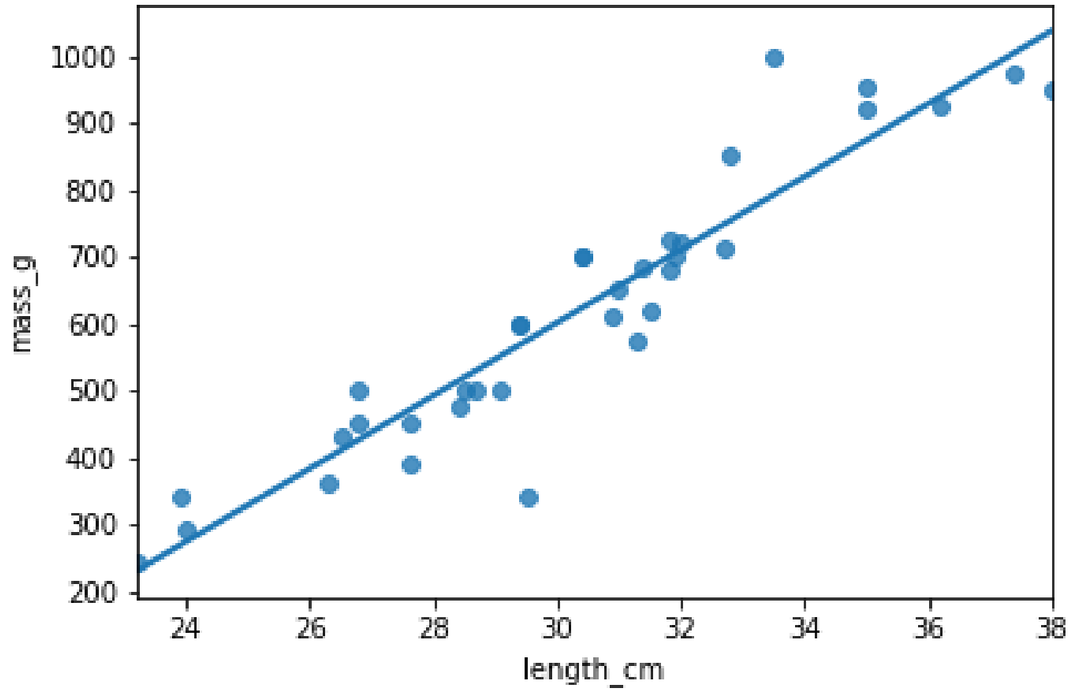
Residual properties of a good fit

- Residuals are normally distributed
- The mean of the residuals is zero

Bream and perch again

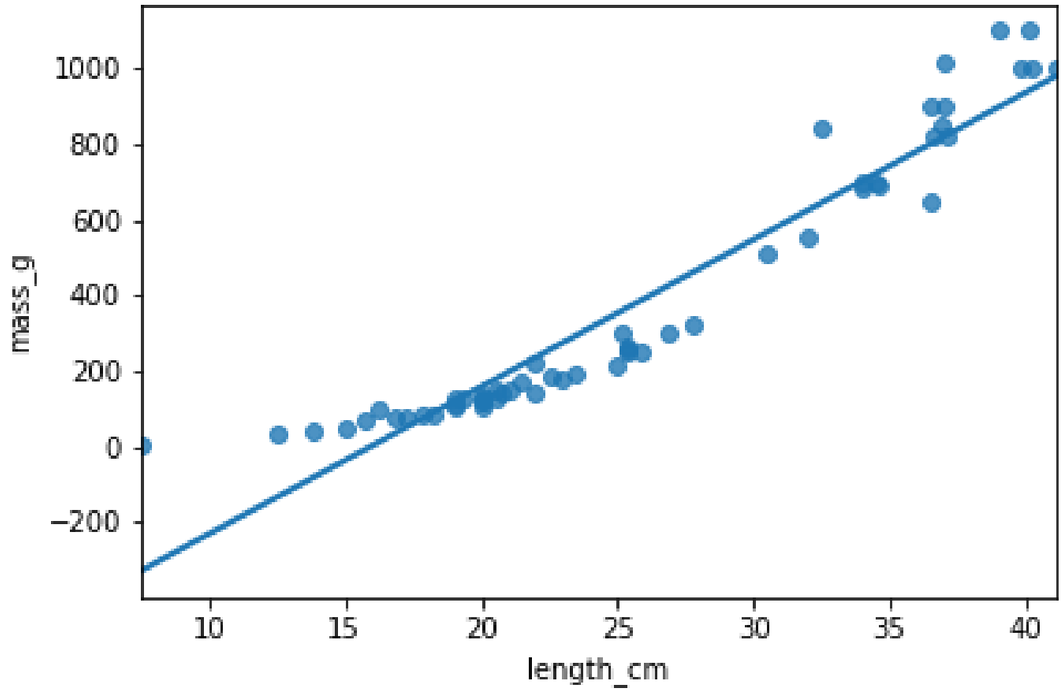
Bream: the "good" model

```
mdl_bream = ols("mass_g ~ length_cm", data=bream).fit()
```



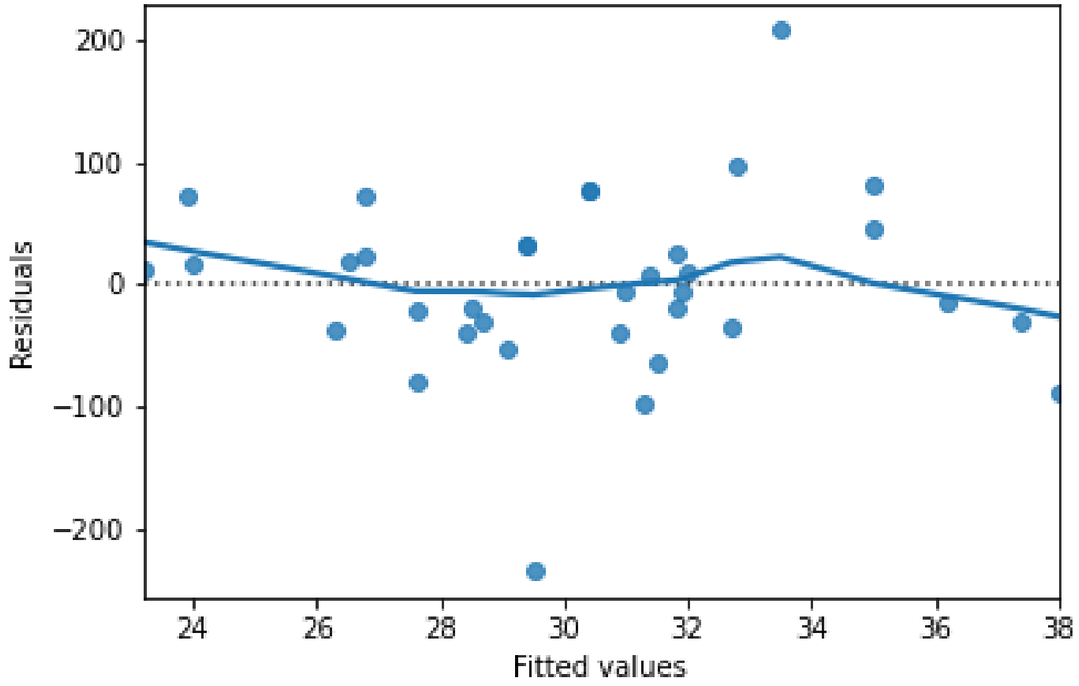
Perch: the "bad" model

```
mdl_perch = ols("mass_g ~ length_cm", data=perch).fit()
```

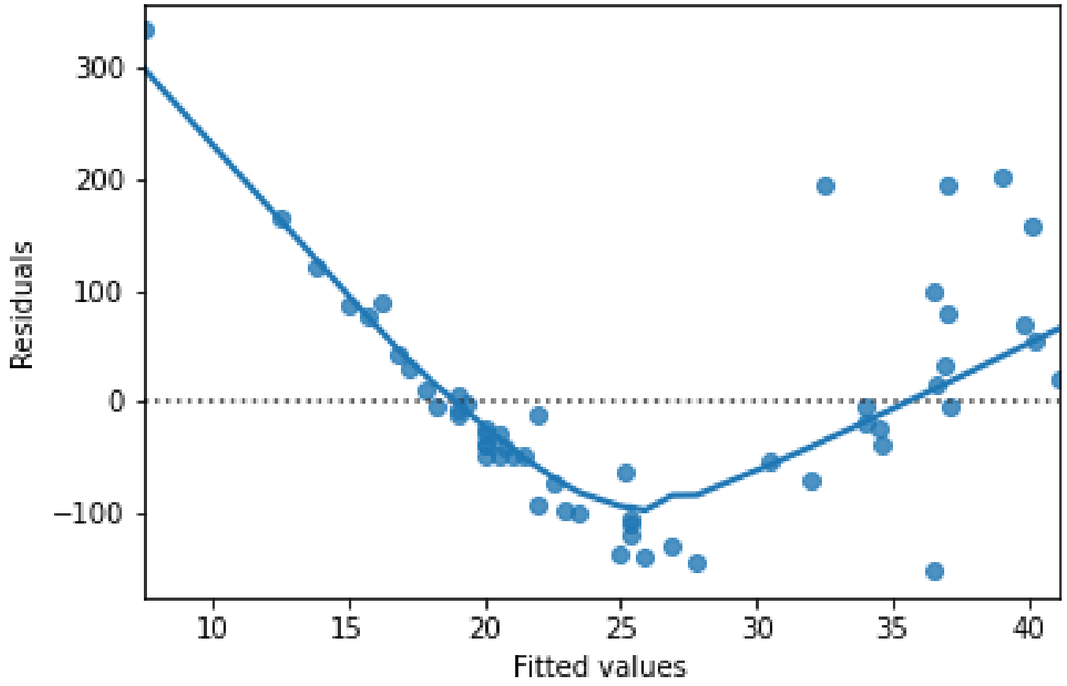


Residuals vs. fitted

Bream

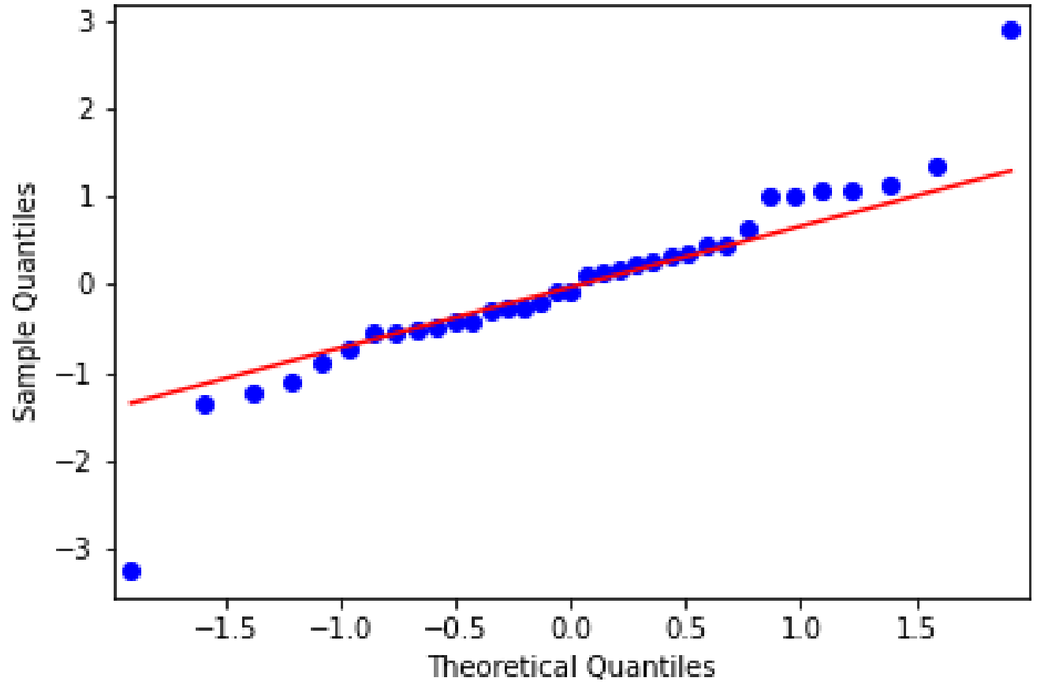


Perch

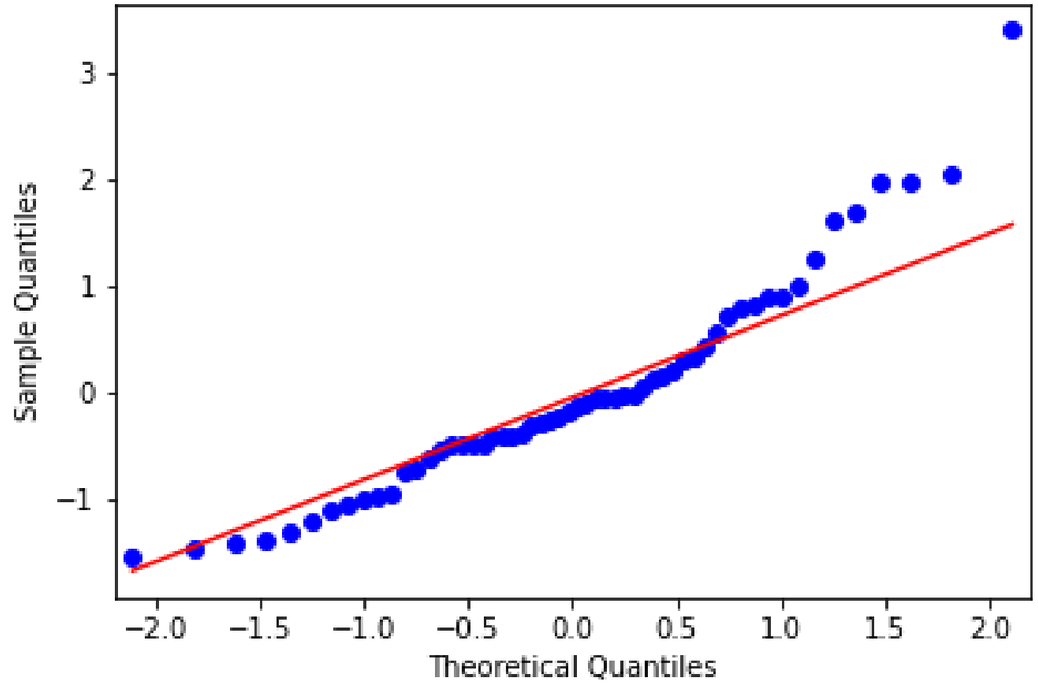


Q-Q plot

Bream

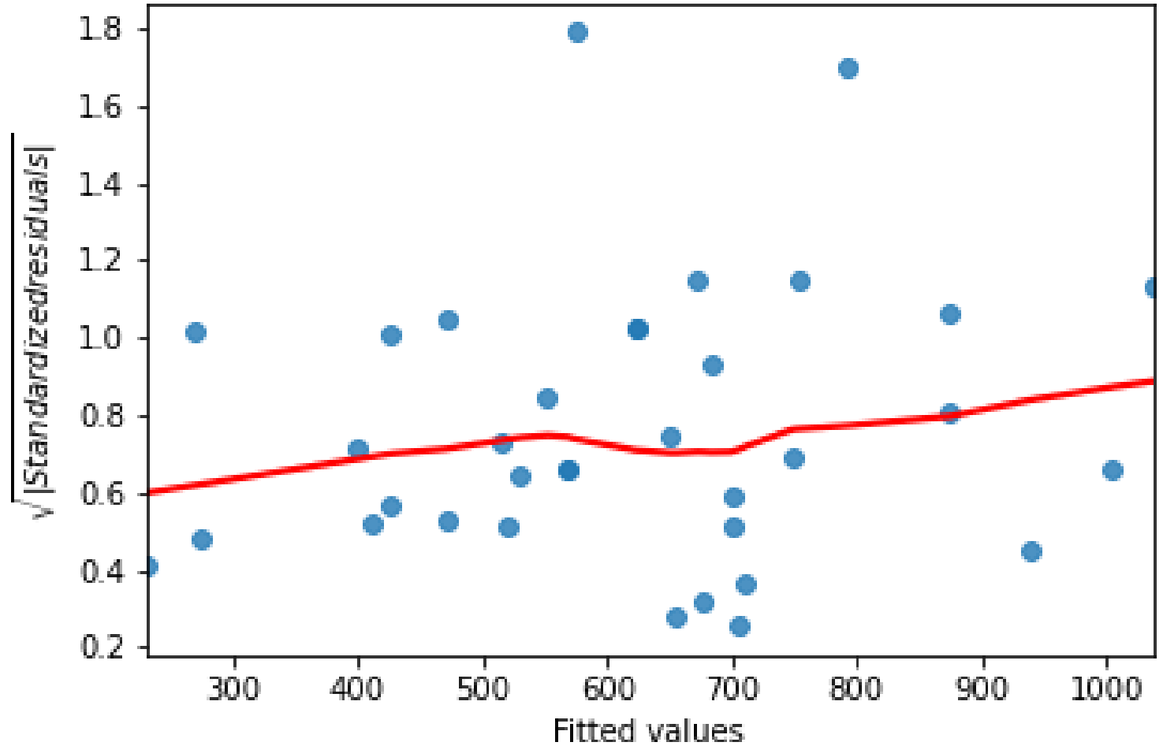


Perch

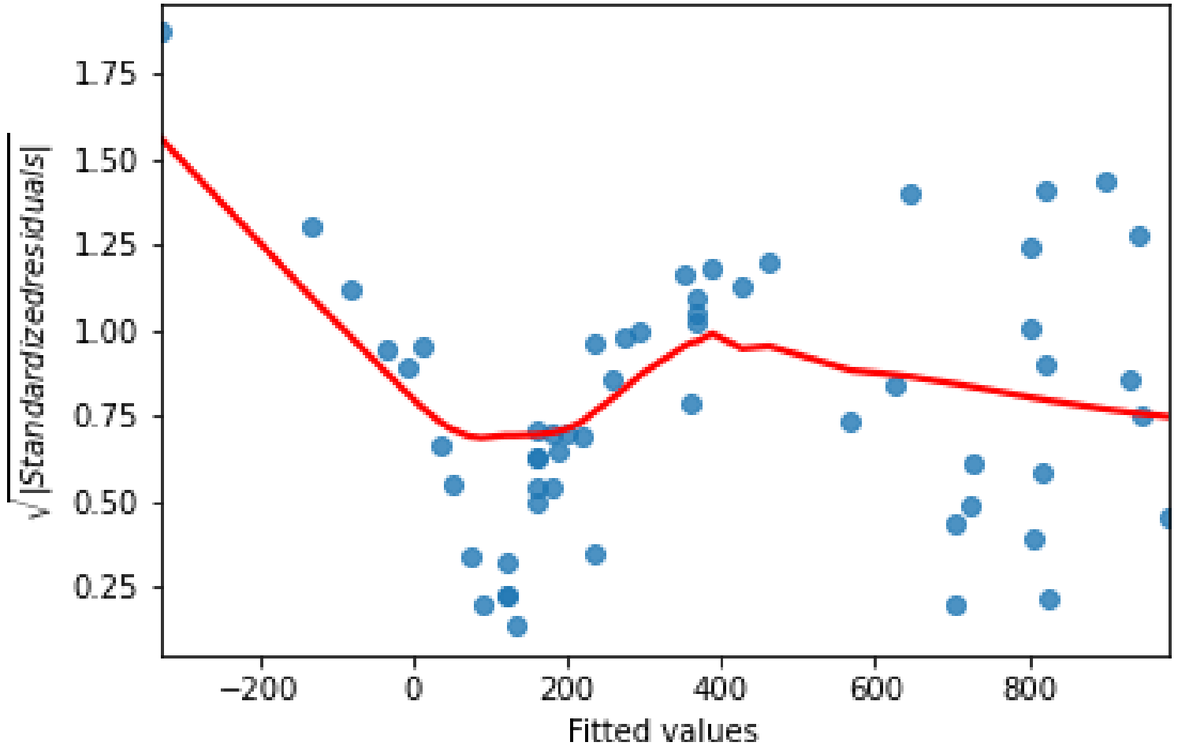


Scale-location plot

Bream

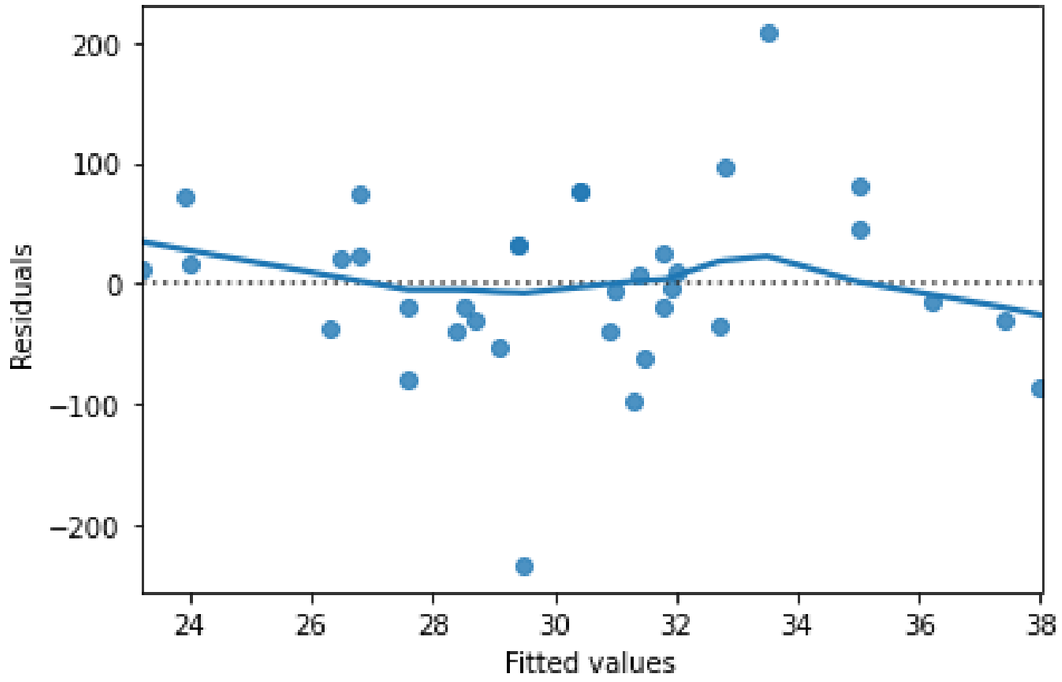


Perch



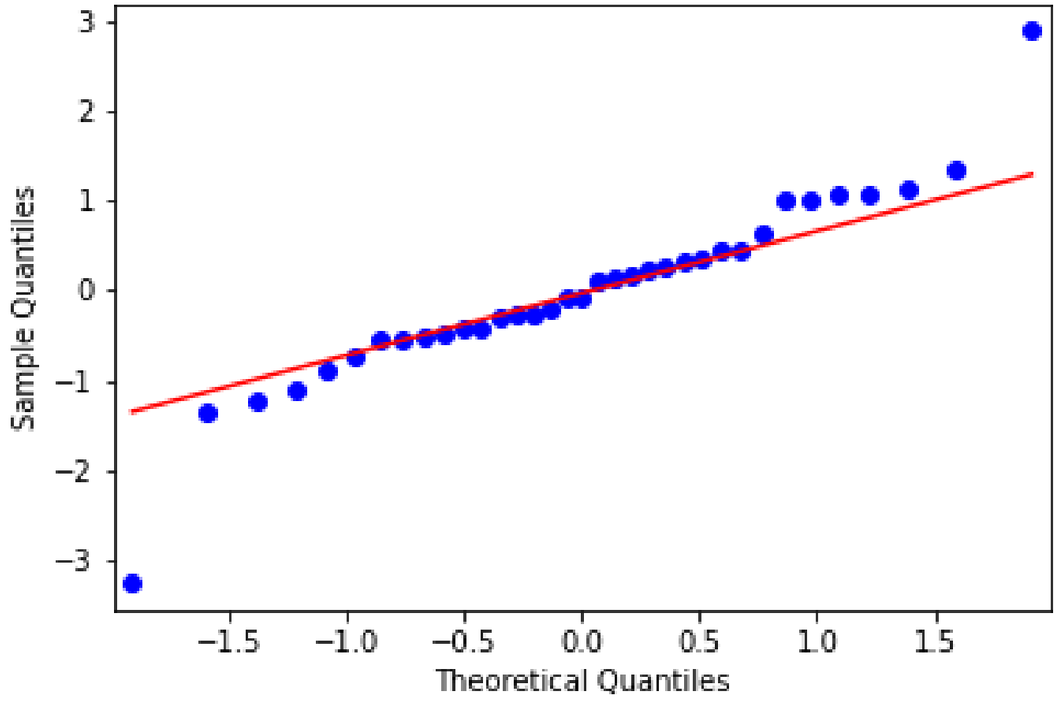
residplot()

```
sns.residplot(x="length_cm", y="mass_g", data=bream, lowess=True)
plt.xlabel("Fitted values")
plt.ylabel("Residuals")
```



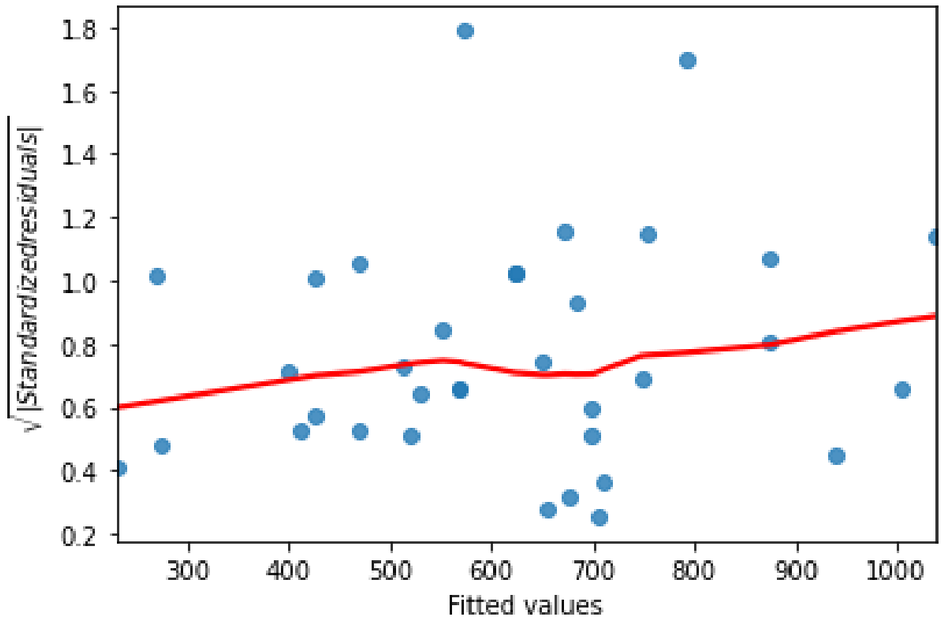
qqplot()

```
from statsmodels.api import qqplot
qqplot(data=mdl_bream.resid, fit=True, line="45")
```



Scale-location plot

```
model_norm_residuals_bream = mdl_bream.get_influence().resid_studentized_internal
model_norm_residuals_abs_sqrt_bream = np.sqrt(np.abs(model_norm_residuals_bream))
sns.regplot(x=mdl_bream.fittedvalues, y=model_norm_residuals_abs_sqrt_bream, ci=None, lowess=True)
plt.xlabel("Fitted values")
plt.ylabel("Sqrt of abs val of stdized residuals")
```



Let's practice!

INTRODUCTION TO REGRESSION WITH STATSMODELS IN PYTHON

Outliers, leverage, and influence

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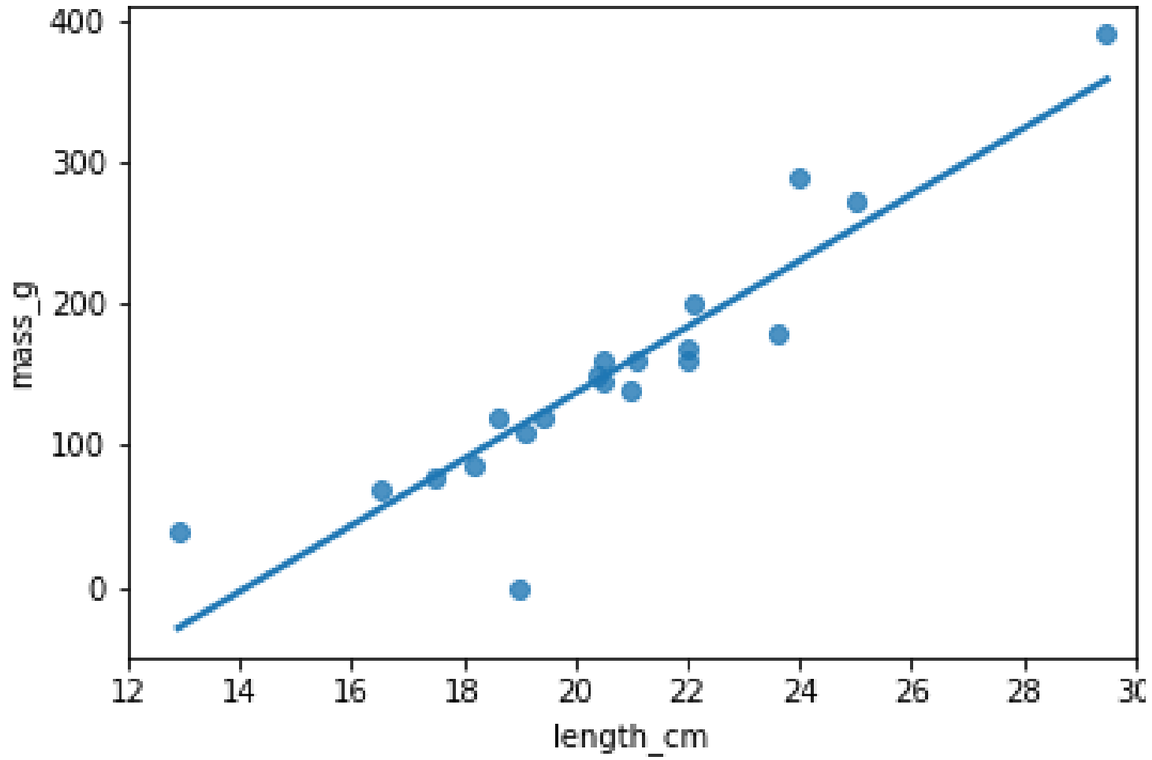
Roach dataset

```
roach = fish[fish['species'] == "Roach"]
print(roach.head())
```

```
    species  mass_g  length_cm
35    Roach    40.0       12.9
36    Roach    69.0       16.5
37    Roach    78.0       17.5
38    Roach    87.0       18.2
39    Roach   120.0       18.6
```

Which points are outliers?

```
sns.regplot(x="length_cm",
            y="mass_g",
            data=roach,
            ci=None)
plt.show()
```

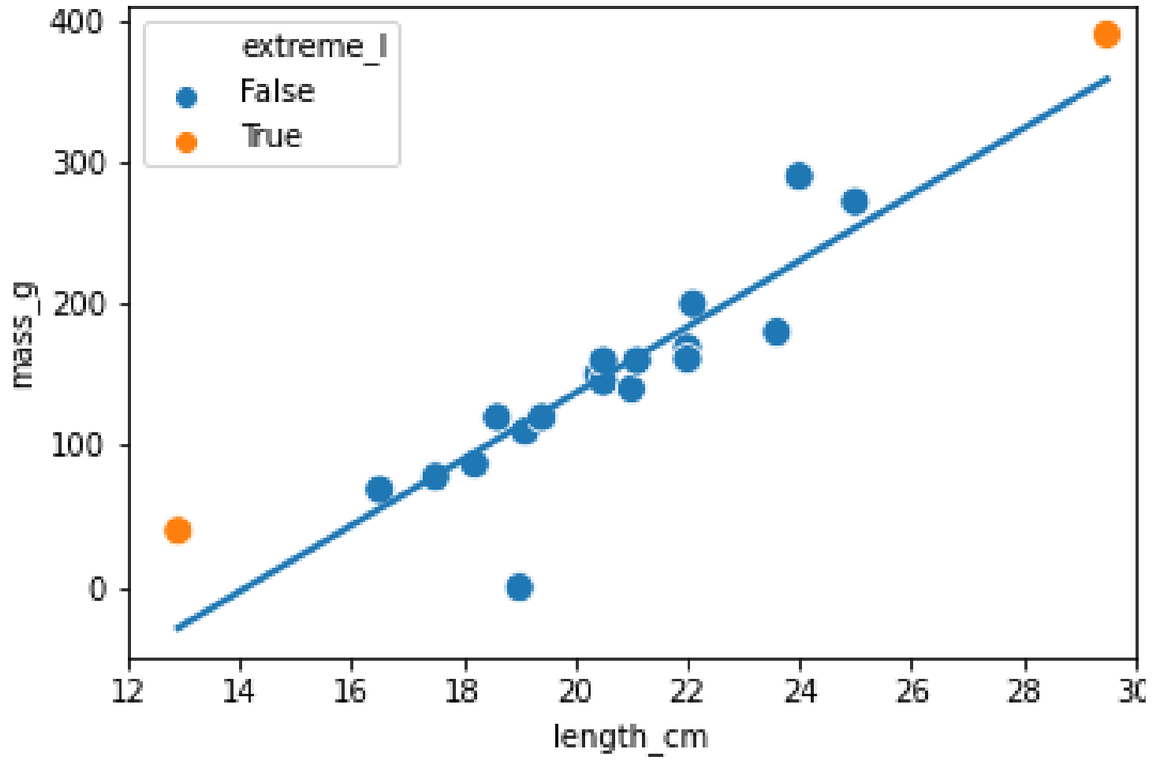


Extreme explanatory values

```
roach["extreme_l"] = ((roach["length_cm"] < 15) |
                      (roach["length_cm"] > 26))

fig = plt.figure()
sns.regplot(x="length_cm",
            y="mass_g",
            data=roach,
            ci=None)

sns.scatterplot(x="length_cm",
                y="mass_g",
                hue="extreme_l",
                data=roach)
```

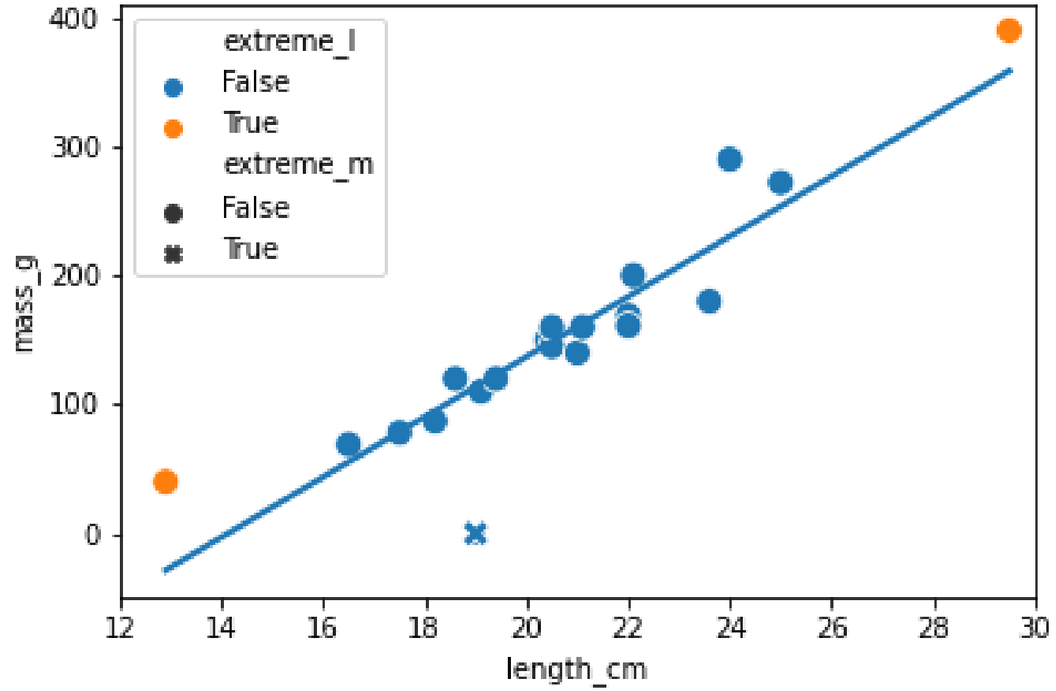


Response values away from the regression line

```
roach["extreme_m"] = roach["mass_g"] < 1

fig = plt.figure()
sns.regplot(x="length_cm",
            y="mass_g",
            data=roach,
            ci=None)

sns.scatterplot(x="length_cm",
                y="mass_g",
                hue="extreme_l",
                style="extreme_m",
                data=roach)
```



Leverage and influence

Leverage is a measure of how extreme the explanatory variable values are.

Influence measures how much the model would change if you left the observation out of the dataset when modeling.

.get_influence() and .summary_frame()

```
mdl_roach = ols("mass_g ~ length_cm", data=roach).fit()
summary_roach = mdl_roach.get_influence().summary_frame()
roach["leverage"] = summary_roach["hat_diag"]

print(roach.head())
```

```
   species  mass_g  length_cm  leverage
35   Roach    40.0       12.9  0.313729
36   Roach    69.0       16.5  0.125538
37   Roach    78.0       17.5  0.093487
38   Roach    87.0       18.2  0.076283
39   Roach   120.0       18.6  0.068387
```

Cook's distance

Cook's distance is the most common measure of influence.

```
roach["cooks_dist"] = summary_roach["cooks_d"]
print(roach.head())
```

```
    species  mass_g  length_cm  leverage  cooks_dist
35    Roach    40.0       12.9  0.313729    1.074015
36    Roach    69.0       16.5  0.125538    0.010429
37    Roach    78.0       17.5  0.093487    0.000020
38    Roach    87.0       18.2  0.076283    0.001980
39    Roach   120.0       18.6  0.068387    0.006610
```

Most influential roaches

```
print(roach.sort_values("cooks_dist", ascending = False))
```

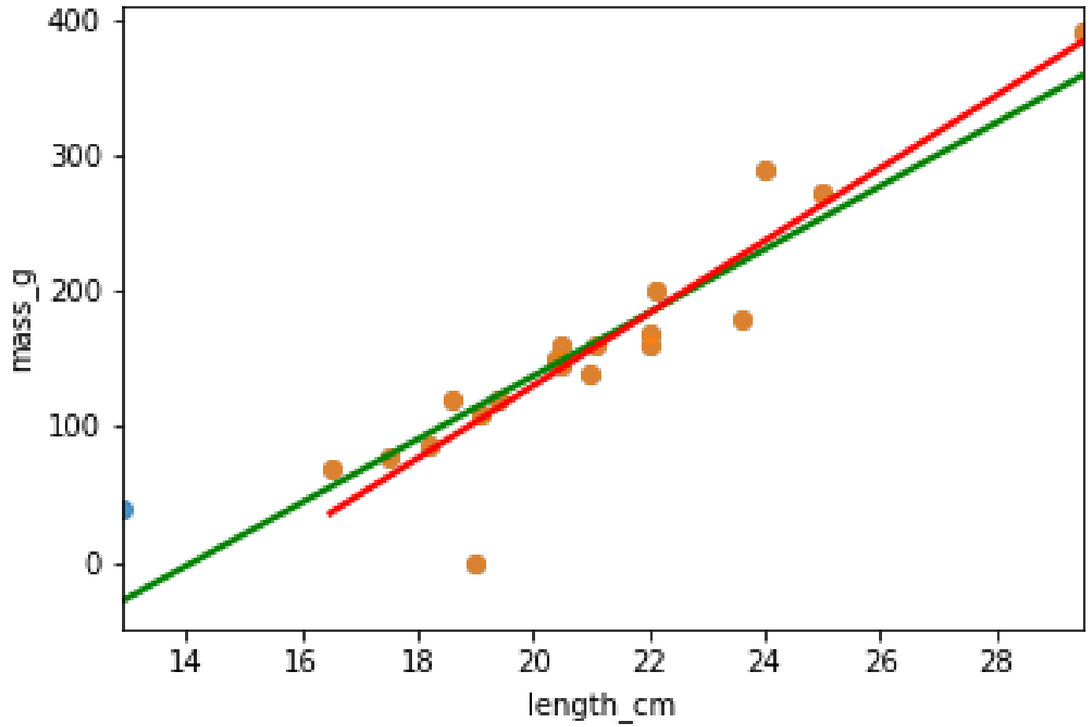
```
   species  mass_g  length_cm  leverage  cooks_dist
35   Roach    40.0       12.9  0.313729    1.074015 # really short roach
54   Roach   390.0       29.5  0.394740    0.365782 # really long roach
40   Roach     0.0       19.0  0.061897    0.311852 # roach with zero mass
52   Roach   290.0       24.0  0.099488    0.150064
51   Roach   180.0       23.6  0.088391    0.061209
..     ...     ...        ...       ...         ...
43   Roach   150.0       20.4  0.050264    0.000257
44   Roach   145.0       20.5  0.050092    0.000256
42   Roach   120.0       19.4  0.056815    0.000199
47   Roach   160.0       21.1  0.050910    0.000137
37   Roach    78.0       17.5  0.093487    0.000020
```

Removing the most influential roach

```
roach_not_short = roach[roach["length_cm"] != 12.9]

sns.regplot(x="length_cm",
            y="mass_g",
            data=roach,
            ci=None,
            line_kws={"color": "green"})

sns.regplot(x="length_cm",
            y="mass_g",
            data=roach_not_short,
            ci=None,
            line_kws={"color": "red"})
```



Let's practice!

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