Regression (Continued)

Today's Outline

- Conditional Distribution
- Simple Regression
 - Simple linear regression assumptions
 - Strict exogeneity
 - Heteroskedasticity
 - Error Normality
 - Standard Errors
 - Prediction vs Confidence intervals

Example Dataset

- Dataset used to investigate the relationship between CEO salary and sales
- Sample of data was reported in the May
 6, 1991 issue of Businessweek

1:

- · salary: 1990 salary, thousands \$
- pcsalary: percent change salary, 89-90
- sales: 1990 firm sales, millions \$
- roe: return on equity, 88-90 avg
- pcroe: percent change roe, 88-90
- ros: return on firm's stock, 88-90
- indus: =1 if industrial firm
- finance: =1 if financial firm
- · consprod: =1 if consumer product firm
- utility: =1 if transport. or utilties
- · Isalary: natural log of salary
- Isales: natural log of sales

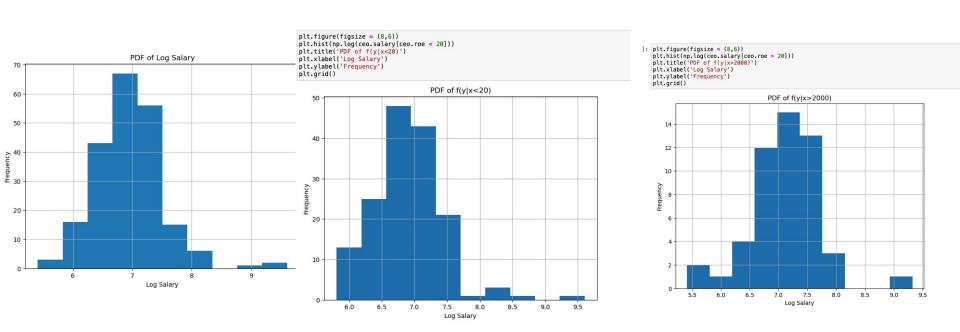
```
# import the wooldridge module
import wooldridge as woo

# use the .data() function to pull down the neccessary dataset
salary = woo.data('ceosal1')
salary.head()
```

102	salary	posalary	sales	roe	pcroe	ros	indus	finance	consprod	utility	Isalary	Isales
0	1095	20	27595.000000	14.1	106.400002	191	1	0	0	0	6.998509	10.225389
1	1001	32	9958.000000	10.9	-30.600000	13	1	0	0	0	6.908755	9.206132

Conditional Distributions

- A simple linear regression is based on assumptions about the conditional pdf of some dependent variable y (Salary) on an independent variable (x)
- We can use boolean indexing to get the pdf of salary from our data conditional on some value of return on equity



Regression and Residuals Plot

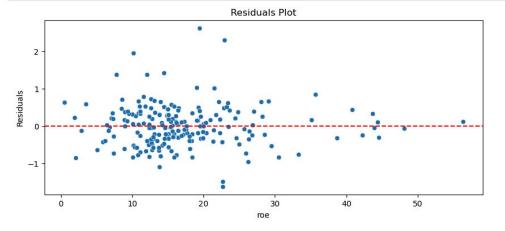
- We can also look at the estimates of our residuals (distance of our observations from the regression line)
- For a simple regression we will plot our dependent variable on the x-axis against the residuals on the y-axis
- This can be generated using any scatter plot, this will be useful for checking important properties of our regression

```
# fit a regression - note that we can add a log transform
# using numpy in the equation
reg = smf.ols('np.log(salary) ~ roe', data = ceo)
results = reg.fit()
results.params
```

```
Intercept 6.712169
roe 0.013863
dtype: float64
```

```
# fit regression to synthetic data
plt.figure(figsize = (10, 4))

# we can get the original data as an attribute as well as the residuals
sns.scatterplot(x = ceo.roe, y = results.resid)
plt.axhline(0, linestyle = '--', color = "red")
plt.ylabel("Residuals")
plt.title("Residuals Plot")
plt.show()
```



Simple Linear Regression Assumptions

- There are five classic assumptions for simple linear regression that will ensure our estimates of the slope and intercept are unbiased and the minimal possible variance
- The most important assumptions to pay attention to will be SLR
 4 and 5

- SLR.1: Linear population regression function: y = β₀ + β₁x + u
- SLR.2: Random sampling of x and y from the population
- SLR.3: Variation in the sample values x₁, ..., x_n
- SLR.4: Zero conditional mean: E(u|x) = 0
- SLR.5: Homoscedasticity: Var(u|x) = σ²
- Theorem 2.1: Under SLR.1 SLR.4, OLS parameter estimators are unbiased.
- Theorem 2.2: Under SLR.1 SLR.5, OLS parameter estimators have a specific sampling variance.

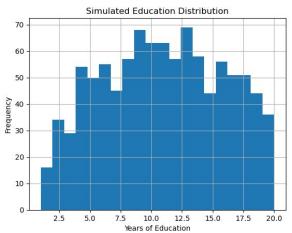
Strict Exogeneity

- SLR states that the value of the residuals should not be dependent on the value of your predictor
- If this assumption does not hold then your parameter estimates will be biased (interview question)

$$E[e_i|x_i] = 0$$

 For example, suppose the true relationship between income and education was:

Income (Thousands) =
$$40 + 5 *$$
 Education (years) + u



Simulated Exogeneity

 We can run the regression in the case where the errors (u) do not depend on education (x) to get an unbiased estimate of the population parameters

```
# add the true popultaion parameters
beta0 = 40
beta1 = 5
su = 20

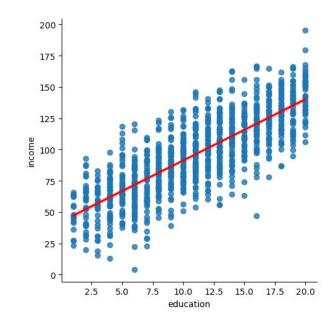
# create some noise and a dependent variable
u = np.random.normal(0, su, n)
education = nums

# create a synthetic y-variable
income = beta0 + beta1*education + u
```

```
results = smf.ols('income ~ education', data = data).fit()
results.params
```

Intercept 42.352327 education 4.884671

dtype: float64



Violation of SLR 4

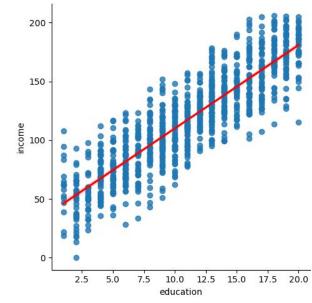
- However in the real world, there are likely factors in u that are correlated with x
 - Can you think of some examples? (factors that may effect education and income that may obscure the true estimate)
- If the value of u does depend somewhat on x, then our estimates will be biased
- What direction do you think the estimate of the effect of education on income would likely be biased?

```
# let the mean of the errors (u) depend on the value of x
u_x = (education*2)
# each draw from u will be based on twice the value of x
u = np.random.normal(u_x, su, n)
# note that we havent changed the coeffeicient for the population
# that creates the effect of educatioon on income
income = beta0 + beta1*education + u
```

```
results = smf.ols('income~education', data = data).fit()

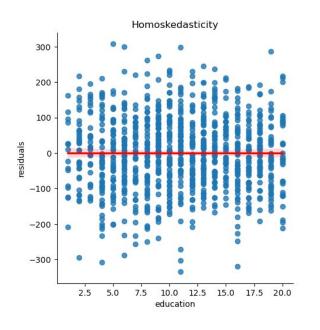
# The estimated effect of education on income is much higher results.params
```

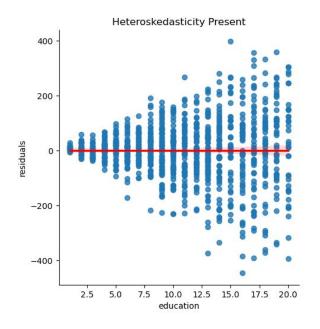
Intercept 39.106655 education 7.092376 dtype: float64



Heteroscedasticity (SLR 5)

- SLR 5 is the assumption that the variance of the residuals does not depend on x
 - SLR.5: Homoscedasticity: Var(u|x) = σ²
- Unlike for usual violations of SLR 4, we can often identify the presence of heteroskedasticity by looking at an X vs residuals plot for simple linear regression





Statistical Significance and P-Values in Python

- The consequence of heteroskedasticity on our regression will be present in our variance
- Variance is used for deciding whether the effect of our dependent variable on our independent variable is statistically significant
- We are testing the null hypothesis that:

$$H_0: \beta_k = 0 \text{ vs } H_1: \beta_k \neq 0$$

• In python we do this by looking at the p-values of the regression coefficient and commonly say a coefficient is statistically significant if it is less than .05 (lower is more restrictive

```
# Do we reject the null for the intercept?
# How about for education?
results.pvalues
```

Intercept 2.309339e-07 education 2.440591e-01

dtype: float64

Statistical Significance and Violations of Homoskedasticity

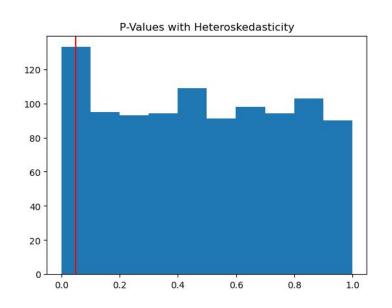
- Since heteroskedasticity will impact our variance, and p-values are a function of variance, we can no longer trust them
- We also cannot trust other measures based on variance like confidence intervals
- Heteroskedasticity may cause us to over or under reject our null hypothesis
- Below we simulate 1000 hypothesis test for the case where the variance of the errors depends on x (left) and when it does not(right)

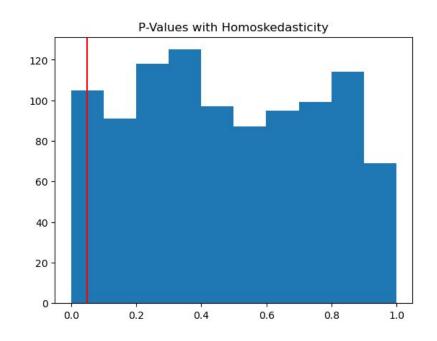
```
# add the true popultaion parameters
beta0 = 40
beta1 = .1
# A convenient number is chosen for this example
su = education * 9.2
outcome = []
for i in range(1000):
    # create some noise and a dependent variable
    u = np.random.normal(0, su, n)
    education = nums
    # create a synthetic y-variable
    income = beta0 + beta1*education + u
    data = pd.DataFrame([education,income,u]).T
    data.columns = ['education', 'income', 'u']
    results = smf.ols('income ~ education', data = data).fit()
    outcome.append(results.pvalues[1])
```

```
# add the true popultaion parameters
beta0 = 40
beta1 = .1
# A convenient number is chosen for this example
su = education * 9.2
outcome = []
for i in range(1000):
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    data.columns = ['education', 'income', 'u']
    results = smf.ols('income ~ education', data = data).fit()
    outcome.append(results.pvalues[1])
```

Statistical Significance and Violations of Homoskedasticity

- Below we plot histograms of the p-values from each experiment
- Note that we are much more likely (nearly 2x) to reject the null hypothesis when heteroskedasticity is present than when it is not





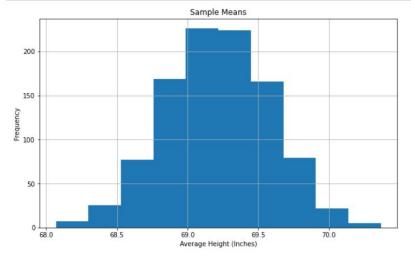
Simulating Sampling Variability

- Statistics such as our regression coefficients or sample mean are random variables
- Their values are dependent on a random sample
- We would like to understand how much the value of these statistics could vary between samples of the same size
- On the right I draw repeated samples from the theoretical distribution of male heights and find the mean

```
# example
mean_height = 69.2
sd_height = 2.66

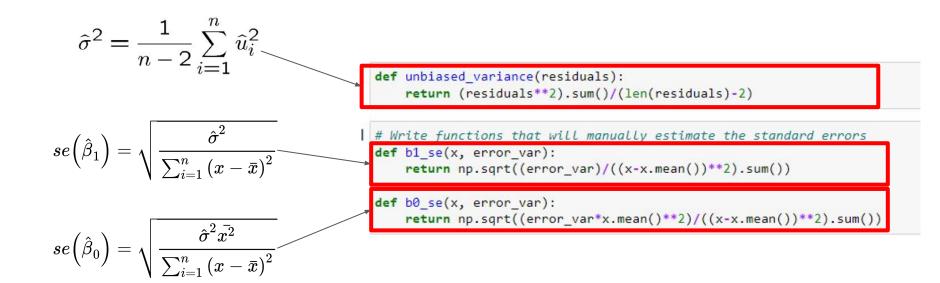
# simulate the process of calculating a mean over many different samples of size 50
sample_means = np.array([np.mean(np.random.normal(mean_height, sd_height, 50)) for i in range(1000)])

# simulate the process of calculating a mean over many different samples of size 50
plt.figure(figsize = (10, 6))
plt.hist(sample_means)
plt.xlabel("Sample Means")
plt.xlabel("Average Height (Inches)")
plt.ylabel("Frequency")
plt.grid()
```



Error Variance and Standard Errors

- Below we generate functions designed to estimate the:
 - Error variance (how much variation there is in the unobservables affecting y)
 - Standard error of beta1
 - Standard error of beta2



Error Variance and Standard Errors (Calculation)

0.288340

0.034517

: Intercept np.log(sales)

dtype: float64

- Below I print the error variance and standard errors of each coefficient for a log-log regression of ceo salary on sales
- Note the standard errors and error variance can be pulled from the regression results

```
# estimate error variance
 unbiased variance(results2.resid)
: 0.25437679009205144
                                                                                              # Error variance from statsmodels
# run each of the functions to estimate standard errors
                                                                                              # note that the square root will give you
  slope se = b1 se(np.log(ceo["sales"]),unbiased variance(results2.resid))
                                                                                              # the standard error of the rearession
 int se = b0 se(np.log(ceo["sales"]),unbiased variance(results2.resid))
                                                                                              results2.scale
 # display result
                                                                                              0.25437679009205144
 print("Slope Standard Error:", slope se, "Intercept Standard Error: ", int se)
 Slope Standard Error: 0.03451666142779875 Intercept Standard Error: 0.28622129679708264
# print them out form statsmodels
 results2.bse
```

Jarque-Bera Test

- Normality of your residuals is nice to have, especially when the sample isn't large
- Certain transformations can help make residuals more normal
- The Jarque-Bera test can help us determine whether the residuals are likely to be normal
- The null hypothesis is H_0: JB = 0, why?

$$JB = \frac{N}{6}(S^2 + \frac{(k-3)^2}{4})$$

Running Jarque-Bera Test

- The formula is simple to implement directly
 - Outputs test statistic
- Scipy.stats also has a function that can implement the test
 - Outputs the test statistic and p-value

```
def jarque_bera(results):
    uhat = results.resid

# Pull variables

S = stats.skew(uhat)
    k = stats.kurtosis(uhat, fisher = False)

N = len(uhat)

# calculate

JB = (N/6)*(S**2+((k-3)**2)/4)

return JB
```

```
jarque_bera(results)
```

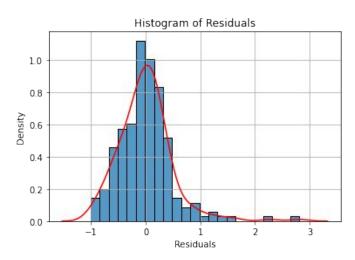
: 403.8308938784628

```
1 import scipy.stats as stats
2 stats.jarque_bera(results.resid)
```

Jarque_beraResult(statistic=403.8308938784628, pvalue=0.0)

Jarque-Bera Test in Summary

- The summary module also outputs several useful statistics about the residuals
 - Skew
 - Kurtosis
 - JB test



1 results.summary()

OLS Regression Results

Skew:

Kurtosis:

1.507

9.106

Dep. Varia	able:		np.log(s	alary)	R	-squared	: 0.	211
Mo	del:			OLS	Adj. R	-squared	: 0.2	207
Met	hod:	L	east Sq	uares	F	-statistic	: 55	5.30
	ate:	Thu	ı, 13 Oct	2022	Prob (F-	sta <mark>t</mark> istic)	: 2.70e	-12
Т		13:	49:07	Log-Li	-152.50			
No. Observations:				209		: 309.0		
Df Residuals:				207		315.7		
Df Model:				1				
Covariance Type:			nonr	obust				
		pef	std err	t	P> t	[0.025	0.975]	
Intercept	4.82	220	0.288	16.723	0.000	4.254	5.390	
np.log(sales)	0.25	67	0.035	7.436	0.000	0.189	0.325	
Omnibu	is: 8	34.15	1 Du	ı <mark>rbin-W</mark> a	itson:	1.860		
Prob(Omnibus	s):	0.00	0 Jarq	ue-Bera	ra (JB): 403.83			
124	20870			<u></u>				

Prob(JB): 2.04e-88

70.0

Cond. No.

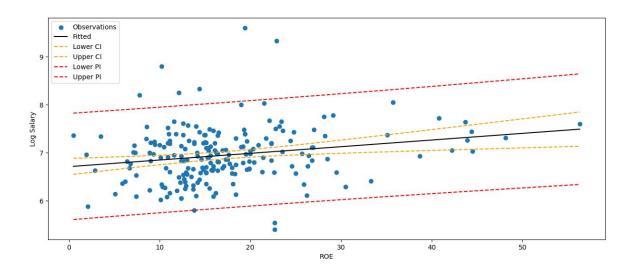
Exercises: Normality and Intervals

- Regress log(wage) on education
- Determine whether the residuals of this regression are normally distributed
- Generate a summary frame containing the confidence and prediction intervals
- (optional) visualize the confidence and prediction intervals along with the regression line and observations

- · wage: average hourly earnings
- · educ: years of education
- · exper: years potential experience
- tenure: years with current employer
- nonwhite: =1 if nonwhite
- · female: =1 if female
- married: =1 if married
- · numdep: number of dependents
- smsa: =1 if live in SMSA
- northcen: =1 if live in north central U.S.
- · south: =1 if live in southern region
- . west: =1 if live in western region
- construc: =1 if work in construc. indus.
- · ndurman: =1 if in nondur, manuf, indus.
- . trcommpu: =1 if in trans, commun, pub ut
- . trade: =1 if in wholesale or retail
- . services: =1 if in services indus.
- · profserv: =1 if in prof. serv. indus.
- profocc: =1 if in profess. occupation
- · clerocc: =1 if in clerical occupation
- servocc: =1 if in service occupation
- Iwage: log(wage)
- expersq: exper^2
- tenursq: tenure^2

Prediction and Confidence Intervals

- Confidence Intervals: Concerned with estimating the population means for a given value of X
- Prediction Intervals: Predicts the range in which an observation for a given value of X is likely to fall
 - Prediction intervals include the uncertainty inherent to confidence intervals and thus are always wider



Producing Prediction and Confidence Intervals

predictions

- Generate an array of evenly spaced values over the range of X
- Use results.get_prediction() to get the predicted value for each x in the range
- 3. Use the predictions.summary_frame() method to get the intervals

```
# get xrange
xrange = np.linspace(ceo.roe.min(), ceo.roe.max(), 200)

# Put in format that works with get_predictions()
new_data = pd.DataFrame(xrange, columns = ["roe"])

# Generate predictions over range
predictions = results.get_prediction(new_data)

# Generate table with intervals for each x
predictions = predictions.summary_frame(alpha=0.05)
```

	mean	mean_se	mean_ci_lower	mean_ci_upper	obs_ci_lower	obs_ci_upper
0	6.719100	0.084625	6.552263	6.885937	5.611764	7.826436
1	6.722987	0.083497	6.558372	6.887601	5.615984	7.829990
2	6.726874	0.082374	6.564474	6.889274	5.620198	7.833550

Plotting Prediction and Confidence Intervals

- Four different elements are included in thuis plot:
 - Observed values for each actual x
 - The predicted mean value for each x in xrange (in the "mean" column)
 - The confidence intervals for the regression line (mean_ci_lower and mean_ci_upper)
 - The confidence intervals for the predictions (obs_ci_lower and obs_ci_upper)

```
plt.figure(figsize = (15, 6))
plt.scatter(ceo.roe, np.log(ceo.salary))
plt.plot(xrange, predictions["mean"], color = "black")

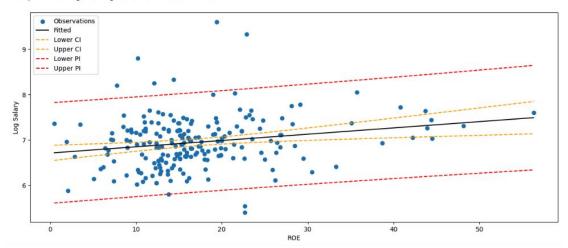
plt.xlabel("ROE")
plt.ylabel("Log Salary")

# confidence Intervals
plt.plot(xrange, predictions["mean_ci_lower"], color = "orange", linestyle = '--')
plt.plot(xrange, predictions["mean_ci_upper"], color = "orange", linestyle = '--')

# prediction Intervals
plt.plot(xrange, predictions["obs_ci_lower"], color = "red", linestyle = '--')
plt.plot(xrange, predictions["obs_ci_upper"], color = "red", linestyle = '--')

# Fun fact - the legend is labelled in the order you draw each plot element!
plt.legend(["Observations", "Fitted", "Lower CI", "Upper CI", "Lower PI", "Upper PI"])
```

<matplotlib.legend.Legend at 0x7feb092f2fd0>



K-Fold Cross Validation

- K-fold cross validation splits our data up into k subsets
- Train our model on k-1 subsets and predict on the one that's left out
- Repeat over all combinations of subsets
- Helpful to measure overfitting and optimizing model parameters
- On the right I show the first step of 5-fold cross validation where the first 20 observations are used to train and the last 5 are used to test

 Train

 (step 1)

1095 20 27595.000000 6.998509 1122 578 6.359574 1368 0 7.221105 1145 1078 6.997596 1237 567 933 11 6.838405 12 1339 0 7.199678 10.597809 937 2513 800049 22 299999 2011 0 7.606388 1585 0 7.368340 1058 922 759 6.632002 1414 7.254178 23 1041

1 ceo[:25]

Test (Step 1)

K-Fold Cross Validation (sklearn)



- Sklearn is the premiers ML library for most models
- Includes tools for testing, tuning, and cross validation
- The kfold submodule will automatically split your data into k subsets
- This is a generator function that we can iterate through in a loop
- Can be combined with other compatible functions
- We can also set shuffle = True if we suspect our data isn't arranged randomly

```
1 from sklearn, model selection import KFold # import KFold
  for train index, test_index in kf.split(ceo):
       print("TRAIN:", train index, "TEST:", test index)
158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175
176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193
194 195 196 197 198 199 200 201 202 203 204 205 206 207 208
```

Manual Cross Validation

- Cross validation can be implemented manually in the following steps:
 - Train model over training indices
 - Make predictions over the test indices
 - Calculate a test metric (MSE, MAPE, RMSE, etc) to evaluate the model's performance against the observed testing values
 - Store the performance for each fold

```
# split the data into 5 subsets
kf = KFold(n_splits = 5)

mse = []
for train_index, test_index in kf.split(ceo):
    # train data over training set
    results = smf.ols('np.log(salary) ~ np.log(sales)', ceo.iloc[train_index]).fit()

# test over last split
s = ((np.log(ceo.iloc[test_index]["salary"]) - results.predict(ceo.iloc[test_index]))**2).mean()

# append test metric
mse.append(s)
```

```
1 mse

[0.12340491612500952,

0.13110902468036287,

0.2573800924128631,

0.34446212923335046,

0.4873535250351009]
```

Sklearn Cross Validation

- Cross validation is straightforward in sklearn
- Requires us to use the sklearn regression functions for compatibility
- Cross_val_score has us specify:
 - o The model
 - Dependent/independent variables
 - The scoring method
 - Number of folds
- Sklearn seeks to maximize each metric, so this is why the negative is taken of some metrics (like MSE and RMSE)
- Why do we square? Why prefer MSE over RMSE?

```
from sklearn.linear_model import LinearRegression
from sklearn.model_selection import cross_val_score

x = np.log(ceo[['sales']])
y = np.log(ceo[['salary']])

regr = LinearRegression()
scores = cross_val_score(regr, x, y, cv=5, scoring='neg_mean_squared_error')
print('5-Fold CV MSE Scores:', scores)

5-Fold CV MSE Scores: [-0.12340492 -0.13110902 -0.25738009 -0.34446213 -0.48735353]
```

```
Regression
                                      metrics.explained variance score
'explained_variance'
'max error'
                                     metrics.max error
'neg_mean_absolute_error'
                                     metrics.mean absolute error
'neg_mean_squared_error'
                                     metrics.mean squared error
'neg_root_mean_squared_error'
                                     metrics.mean_squared_error
'neg_mean_squared_log_error'
                                     metrics.mean_squared_log_error
'neg_median_absolute_error'
                                     metrics.median_absolute error
                                     metrics.r2 score
'neg_mean_poisson_deviance'
                                      metrics.mean poisson deviance
'neg_mean_gamma_deviance'
                                     metrics.mean gamma deviance
'neg_mean_absolute_percentage_error
                                     metrics.mean absolute percentage error
'd2_absolute_error_score'
                                     metrics.d2 absolute error score
'd2_pinball_score'
                                     metrics.d2 pinball score
'd2_tweedie_score'
                                     metrics.d2 tweedie score
```