Practice Exercise – Preprocessing

The first rule in preprocessing is: **know your data!**

Therefore, you are going to explore your data over several dimensions and views to bring your raw data to a state of processed data, ready to be used for your model.

The **TBLF** approach is suggested:

- **Try:** Explore the problem (in this case, explore your data)
- **Broken?:** What is broken? (Do you see something wrong in your data)
- **Learn:** Why is it wrong? (What is wrong with this data? How can you solve it?)
- **Fix:** Fix the problem (What can I do to bring the wrong data to an acceptable solution?)

Business scenario

You are in charge of preprocessing the data your company wants to use in a new machine learning model. The model will be used to predict average influence of a journal, based on journal/publishing information coming from a variety of sources, including researchers, web scraping, and the publishers themselves.

You've received raw data related to the business problem to solve. Your task is to better understand the data using some descriptive statistics. Once you understand the data, you will clean and reshape it. You will use the final processed dataset in your model.

Learning objectives

1. Understand a business scenario and corresponding dataset by analyzing the data using descriptive statistics
2. Use visualization tools to support this analysis:
   - Scatter plots to spot correlations between features
   - Box and whisker plots and histograms to understand the distribution of your data
3. Use statistics tools to support previous analysis, such as a correlation matrix to quantify those relationships
4. Based on the analysis conclusions, prepare a processed dataset for the model by:
   - Dealing with outliers
   - Dealing with missing values
   - Cleaning the data

In [1]:
```
%%capture

%pip install -U pandas sparkmagic -q
%pip uninstall matplotlib -y
```

```
%pip uninstall seaborn -y
%pip install matplotlib==3.6.1
%pip install seaborn
%pip install mkl
%matplotlib inline
%pip uninstall numpy -y
%pip install numpy==1.26.4
```

Restart the Kernel by running the following command. Note: after running the code, the cell will not indicate that it has been run.

In [ ]:
```
# restart the kernel to apply the changes
from IPython.display import display_html
def restartkernel() :
    display_html("<script>Jupyter.notebook.kernel.restart()</script>",raw=True)

restartkernel()
```

After the kernel restarts, import your packages.

In [1]:
```
import pandas as pd
import numpy as np
from matplotlib import pyplot as plt
import seaborn as sns

pd.set_option('display.max_colwidth', None)
```

Dataset

The data comes from a variety of sources, including researchers, web scraping, and the publishers themselves. The data has been manipulated to be suited for this preprocessing task.

Data schema

A dataset on journal/publisher information with estimated-article-influence-scores:

- journal_name: Name of the journal
- issn: Unique publication code
- citation_count_sum: Sum of the number of citations for each journal
- paper_count_sum: Sum of the number of papers for each journal
- avg_cites_per_paper: Average number of citations per paper
- ranking: Artificial label created for the exercise (possible values: A, B, C, D)
- proj_ai: Projected average influence

Start by loading the file.

In [2]:
```
df_journals = pd.read_csv("estimated-article-influence-scores-Exerc2.csv", sep="
del df_journals["Unnamed: 0"]
```

First glance at your data

Learn

How many features do you have?

```
In [3]: print("Number of features: {}".format(df_journals.shape[1]))
```

```
Number of features: 7
```

How many samples do you have?

```
In [5]: print("Number of samples: {}".format(df_journals.shape[0]))
```

```
Number of samples: 3615
```

> ## Question 1
>
> ### Try
>
> Print the first 10 rows to see what the data looks like. Apply the `head` function (documentation) to your dataset.

```
In [6]: # Enter your code here
        df_journals.head(10)
```

Out[6]:

	issn	journal_name	citation_count_sum	paper_count_sum	avg_cites_per_paper	ranking	pr
0	2092-6731	3d research	151.0	106.0	1.424528	D	
1	1530-9932	aaps pharmscitech	2208.0	801.0	2.756554	D	
2	1687-0409	abstract and applied analysis	3005.0	2923.0	1.028053	B	
3	1545-7230	academic psychiatry	537.0	490.0	1.095918	NaN	
4	1936-4709	academic questions	40.0	67.0	0.597015	A	
5	1432-0517	accreditation and quality assurance	255.0	331.0	0.770393	A	
6	1839-2571	acoustics australia	30.0	25.0	1.200000	D	
7	2199-6067	acrocephalus	9.0	15.0	0.600000	C	
8	1846-0453	acta adriatica	28.0	37.0	0.756757	NaN	
9	1854-1941	acta agriculturae slovenica	71.0	97.0	0.731959	C	

Dealing with missing values

Learn

Check how many values are missing for each column.

The **isnull()** command returns **True** for each cell of the dataset that is missing a value.

In [7]:
```
df_journals.isnull().head(10)
```

Out[7]:

	issn	journal_name	citation_count_sum	paper_count_sum	avg_cites_per_paper	ranking	pr
0	False	False	False	False	False	False	F
1	False	False	False	False	False	False	F
2	False	False	False	False	False	False	F
3	False	False	False	False	False	True	F
4	False	False	False	False	False	False	F
5	False	False	False	False	False	False	F
6	False	False	False	False	False	False	F
7	False	False	False	False	False	False	F
8	False	False	False	False	False	True	F
9	False	False	False	False	False	False	F

Is it broken?

This visualization is not practical for big datasets. You can try to sum all rows for each column. As all the values above are booleans, if you sum by column (feature), you will have the amount of **true** values--the number of missing values for each feature.

> ## Question 2
>
> ### Fix
>
> Apply the **.isnull()** function to your dataset as above, but concatenate the result with a **.sum()** function to show the number of missing values for each feature.

> `isnull` (documentation)
> `sum` (documentation)

In [8]:
```
# Enter your code here
df_journals.isnull().sum()
```

Out[8]:
```
issn                    0
journal_name            0
citation_count_sum     12
paper_count_sum        12
avg_cites_per_paper    12
ranking               633
proj_ai                12
dtype: int64
```

Learn

You observed that there are missing values in the dataset.

Missing values are an important issue. Most models won't deal well with missing values.

You can remove the missing values or impute values for them. Each choice has pros and cons, depending on the importance of the particular feature for your training job, if you can afford to remove those missing values, etc.

The following command filters only the rows with `any` (documentation) missing value. The first 10 rows display.

In [9]:
```
df_journals_null_data = df_journals[df_journals.isnull().any(axis=1)]
df_journals_null_data.head(10)
```

Out[9]:

	issn	journal_name	citation_count_sum	paper_count_sum	avg_cites_per_paper	ranking
3	1545-7230	academic psychiatry	537.0	490.0	1.095918	NaN
8	1846-0453	acta adriatica	28.0	37.0	0.756757	NaN
18	1614-7065	acta chimica sinica	619.0	537.0	1.152700	NaN
25	1958-5454	acta endoscopica	31.0	70.0	0.442857	NaN
38	0386-300X	acta medica okayama	257.0	228.0	1.127193	NaN
46	1745-3674	acta orthopaedica	2364.0	611.0	3.869067	NaN
60	0303-464X	acta reumatologica portuguesa	213.0	205.0	1.039024	NaN
70	1940-0640	addiction science & clinical practice	294.0	133.0	2.210526	NaN
91	1687-711X	advances in fuzzy systems	128.0	107.0	1.196262	NaN
95	1687-7365	advances in high energy physics	791.0	373.0	2.120643	NaN

Dealing with missing values

Fix

Let's suppose you have decided to remove the rows with missing values.

Remove the missing values by applying the `dropna` function (documentation) to your dataset. Save the result in a new dataset named **df_journals_no_miss**. Use the `shape` function (documentation) after that to confirm that your dataset has fewer rows.

Learn

How many rows are left?

In [10]:
```
df_journals_no_miss = df_journals.dropna()
df_journals_no_miss.shape
```

Out[10]:
```
(2972, 7)
```

Learn

Confirm that you have removed all missing values.

In [11]:
```
df_journals_no_miss.isna().any()
```

Out[11]:
```
issn                   False
journal_name           False
citation_count_sum     False
paper_count_sum        False
avg_cites_per_paper    False
ranking                False
proj_ai                False
dtype: bool
```

Now, suppose that you cannot afford to remove the rows with missing values. Maybe you don't want to reduce your already small dataset.

Imputing numerical values

Learn

One way to impute numerical values is to consider the mean of the feature (column) value. The following command calculates the mean of all numerical features in your dataset.

In [12]:
```
citation_count_sum_MEAN = df_journals["citation_count_sum"].mean()
paper_count_sum_MEAN = df_journals["paper_count_sum"].mean()
avg_cites_per_paper_MEAN = df_journals["avg_cites_per_paper"].mean()
proj_ai_MEAN = df_journals["proj_ai"].mean()
print("citation_count_sum_MEAN: {}".format(citation_count_sum_MEAN))
print("paper_count_sum_MEAN: {}".format(paper_count_sum_MEAN))
print("avg_cites_per_paper_MEAN: {}".format(avg_cites_per_paper_MEAN))
print("proj_ai_MEAN: {}".format(proj_ai_MEAN))
```

```
citation_count_sum_MEAN: 1446.713849569803
paper_count_sum_MEAN: 509.67110741049123
avg_cites_per_paper_MEAN: 2.118970176206788
proj_ai_MEAN: 0.5165542603386067
```

The following command updates each missing value with the calculated mean for the feature.

Note: The `inplace` clause (documentation) means that the update acts on the original dataset, so you don't need to attribute the result on a new dataset.

In [13]:
```
df_journals["citation_count_sum"].fillna(citation_count_sum_MEAN, inplace=True)
df_journals["paper_count_sum"].fillna(paper_count_sum_MEAN, inplace=True)
```

```
df_journals["avg_cites_per_paper"].fillna(avg_cites_per_paper_MEAN, inplace=True
df_journals["proj_ai"].fillna(proj_ai_MEAN, inplace=True)
```

Learn

Confirm that you have imputed for all of the numerical values. You will deal with categorical values next.

In [14]:
```
df_journals.isna().any()
```

Out[14]:
```
issn                   False
journal_name           False
citation_count_sum     False
paper_count_sum        False
avg_cites_per_paper    False
ranking                 True
proj_ai                False
dtype: bool
```

Imputing categorical values

Learn

For categorical value imputation, a common approach is to use the most frequent value (the mode).

Try

Check the possible values for the "ranking" feature.

Pandas has an interesting command that prints the frequency for categoricals: `value_counts` (documentation).

Apply this command to the feature in your dataset to see the categoricals distribution of "ranking".

In [15]:
```
df_journals["ranking"].value_counts()
```

Out[15]:
```
D    1222
B     590
A     589
C     581
Name: ranking, dtype: int64
```

Now, check for the most frequent value for the categorical feature. Use the `mode` function (documentation).

Note: You can access the feature using `df_journals["ranking"]` or `df_journals.ranking`.

In [16]:
```
df_journals.ranking.mode()[0]
```

Out[16]:
```
'D'
```

Learn

The command returned **D** as the most frequent value (the mode).

Use the same command that you used to impute the numerical features to impute the most frequent ranking **D**.

```
In [17]: df_journals["ranking"].fillna('D', inplace=True)
```

Learn

Now, run the following command to see if you have any null values left. You should only have **False** values now.

```
In [18]: df_journals.isna().any()
```

```
Out[18]: issn                  False
         journal_name          False
         citation_count_sum    False
         paper_count_sum       False
         avg_cites_per_paper   False
         ranking               False
         proj_ai               False
         dtype: bool
```

Learn

To make sure the missing values turned into D, the **value_counts()** command should reflect that the new count for the categorical value **D** is the sum of the original one and the number of null values.

```
In [19]: df_journals["ranking"].value_counts()
```

```
Out[19]: D    1855
         B     590
         A     589
         C     581
         Name: ranking, dtype: int64
```

Is it broken?

Unbalanced labels occur when the distribution between the labels presents some of them with much higher frequency than the others. For this dataset, it is not the case.

Basic statistics for numerical values

Exploring distributions

Try

Calculate the min value, max value, mean, standard deviation, and the 25% and 75% percentiles for each column. Use the `describe` command (documentation).

In [20]:
```
df_journals.describe()
```

Out[20]:

	citation_count_sum	paper_count_sum	avg_cites_per_paper	proj_ai
count	3615.000000	3615.000000	3615.000000	3615.000000
mean	1446.713850	509.671107	2.118970	0.516554
std	7983.573195	1920.708341	1.685032	0.571603
min	0.000000	1.000000	0.000000	0.000000
25%	151.000000	107.000000	1.056067	0.199000
50%	424.000000	240.000000	1.722628	0.368000
75%	1113.500000	520.500000	2.705021	0.649500
max	426949.000000	104705.000000	26.318824	11.367000

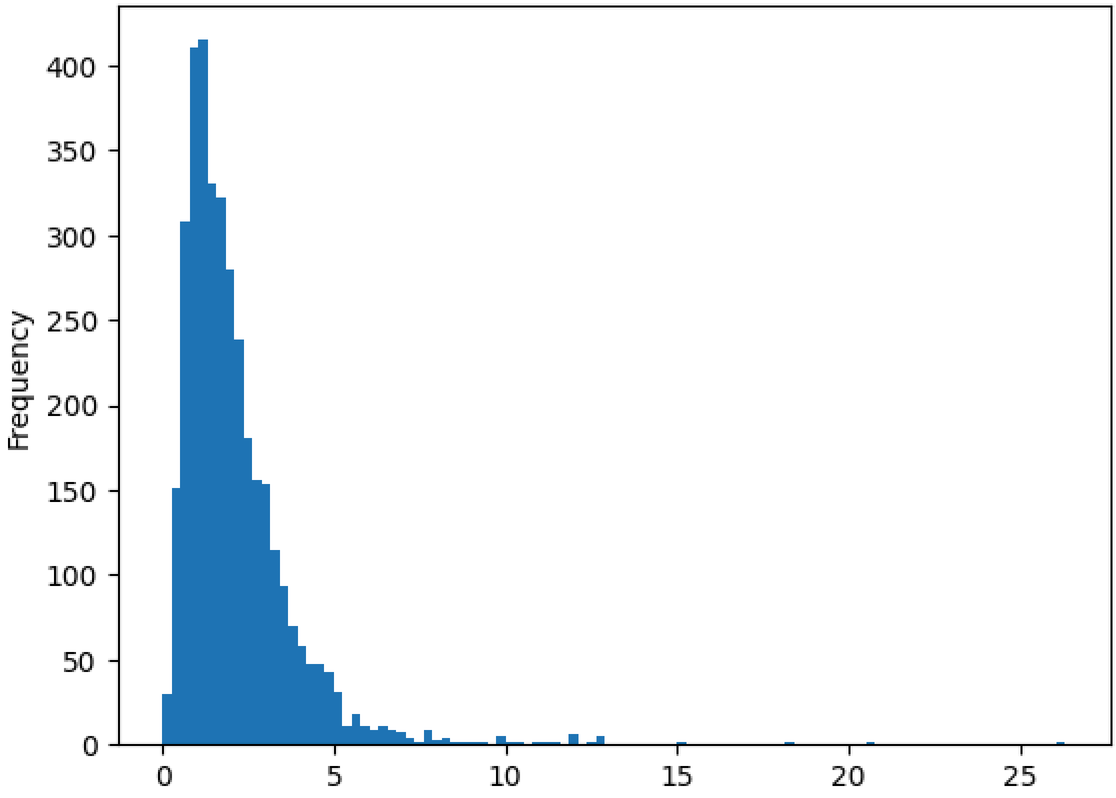
> ## Question 3

Plot the distribution of the "avg_cites_per_paper" feature. Use the `.plot.hist(bins=100)` function from matplotlib to plot the distribution of each feature.

> `hist` (documentation)

In [21]:
```
# Enter your code here
df_journals["avg_cites_per_paper"].plot.hist(bins=100)
```

Out[21]:
```
<Axes: ylabel='Frequency'>
```



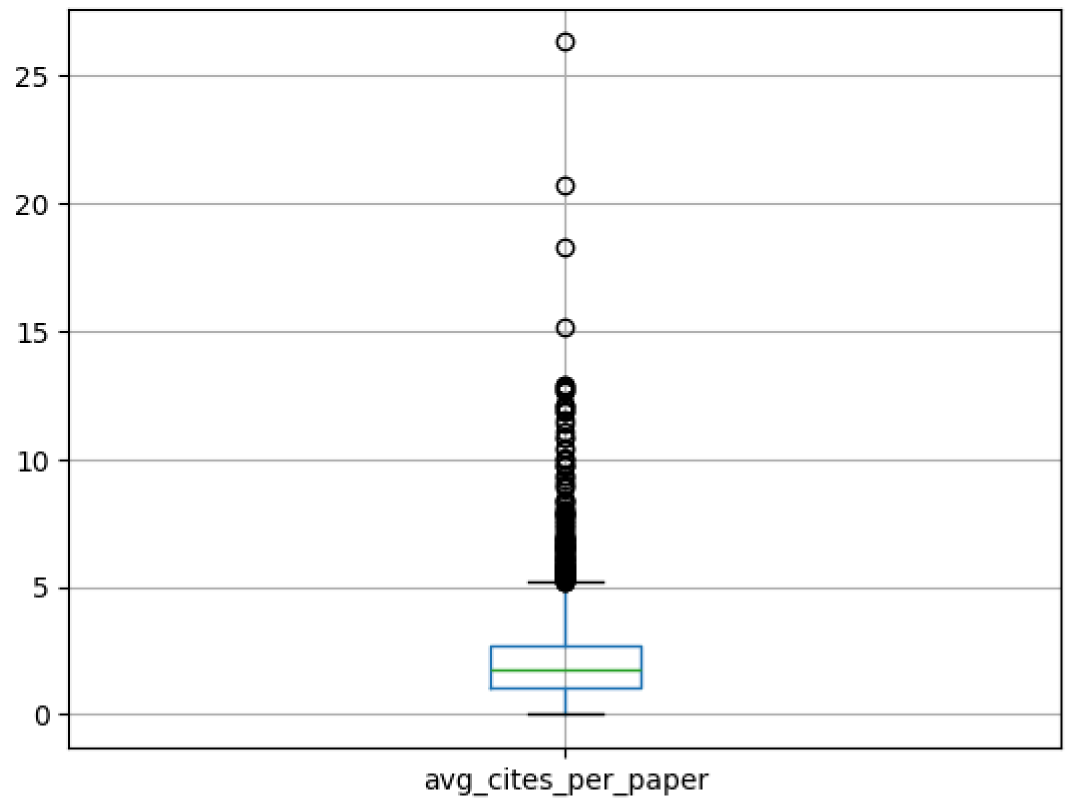
Box and whisker plots

Box and whisker plots are great for spoting outliers. Let's explore using a box and whisker plot.

> ### Question 4
>
> #### Try
>
> The same way you've plotted the distribution, now make a box and whisker plot using the `boxplot` function (documentation) for the numerical feature "avg_cites_per_paper".

In [22]:
```
# Enter your code here
df_journals.boxplot(["avg_cites_per_paper"])
```

Out[22]:
```
<Axes: >
```



Learn

Notice that the box and whisker plot helps to spot outliers.

Learn

Now, let's use a more interesting technique to remove outliers using the percentiles.

To print the percentiles of the dataset's numerical values, use the **.describe()** command.

```
In [23]: df_journals.describe()
```

Out[23]:

	citation_count_sum	paper_count_sum	avg_cites_per_paper	proj_ai
count	3615.000000	3615.000000	3615.000000	3615.000000
mean	1446.713850	509.671107	2.118970	0.516554
std	7983.573195	1920.708341	1.685032	0.571603
min	0.000000	1.000000	0.000000	0.000000
25%	151.000000	107.000000	1.056067	0.199000
50%	424.000000	240.000000	1.722628	0.368000
75%	1113.500000	520.500000	2.705021	0.649500
max	426949.000000	104705.000000	26.318824	11.367000

You will use the 25%, 50%, and 75% percentiles (or quartiles) as a guideline to remove the outliers.

For each feature, you will remove all data points outside the interquartile range (IQR), where:

$$IQR = 75\%\ quartile - 25\%\ quartile$$

$$Lower\ Threshold = 50\%\ percentile - 1.5 * IQR$$

$$Upper\ Threshold = 50\%\ percentile + 1.5 * IQR$$

The NumPy package has the `percentile` function (documentation) that can help you to get the threshold values.

> ## Question 5 (Optional)
>
> Try
>
> **This question is optional and will not be graded**, but it is a nice way to exercise your curious side!

> Implement the following algorithm using the NumPy **percentile** function.

Fix

Do the following for the "citation_count_sum" feature:

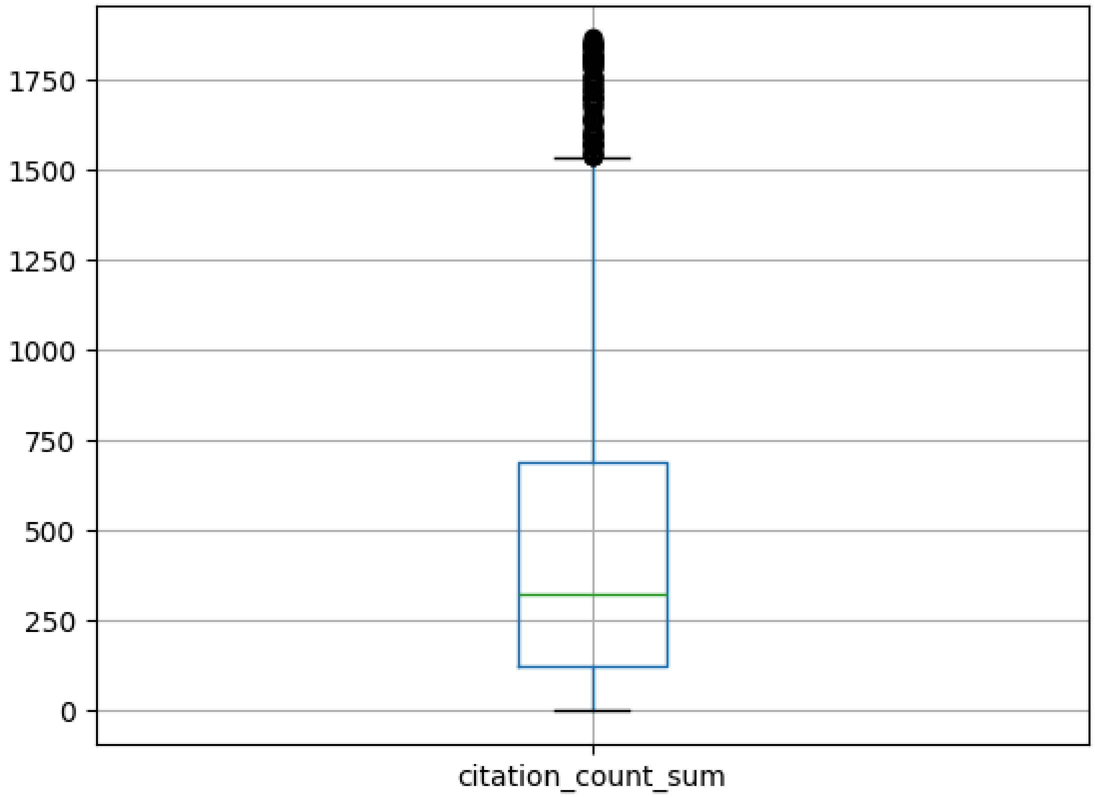
- Use the guidelines and **percentile** function above to calculate the thresholds for each feature.
- Remove the outliers outside this range for each feature.
- Plot the box and whisker plot again to see the results.
- Use the **shape** command before and after removal to see how many rows were removed.

```
In [24]: # Enter your code here
         print("Number of samples before: {}".format(df_journals.shape[0]))
         # Save the quartiles
         citation_count_sum_25 = np.percentile(df_journals['citation_count_sum'], 25)
         citation_count_sum_50 = np.percentile(df_journals['citation_count_sum'], 50)
         citation_count_sum_75 = np.percentile(df_journals['citation_count_sum'], 75)

         # Calculate the thresholds
         IQR_citation_count_sum = citation_count_sum_75 - citation_count_sum_25
         Lower_Limit = citation_count_sum_50 - IQR_citation_count_sum * 1.5
         Upper_Limit = citation_count_sum_50 + IQR_citation_count_sum * 1.5

         # Remove the outliers
         df_journals = df_journals.loc[(df_journals['citation_count_sum'] > Lower_Limit)
                                       (df_journals['citation_count_sum'] < Upper_Limit)]
         df_journals.boxplot(["citation_count_sum"])
         print("Number of samples after: {}".format(df_journals.shape[0]))
```

```
Number of samples before: 3615
Number of samples after: 3066
```



Learn

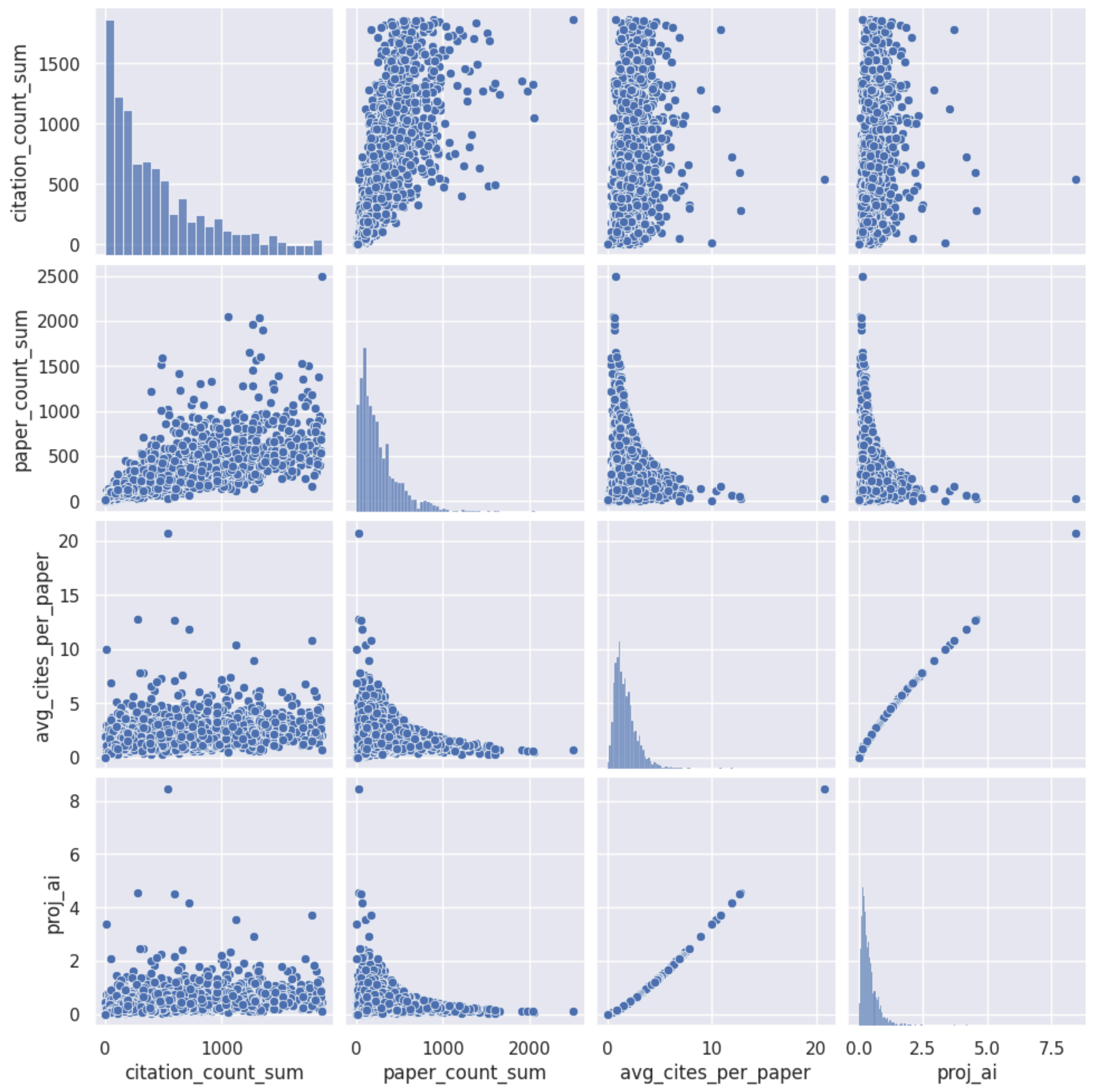
Nice! You were successful in removing the outliers.

Correlations: Multivariate statistics

Try

Use a correlation matrix for all features, plotting a scatter plot for each combination of numerical features in your dataset.

```
In [25]: numerical_df = df_journals[["citation_count_sum", "paper_count_sum","avg_cites_p
         sns.set()
         grid = sns.pairplot(numerical_df)
```



Is it broken?

There is one highly correlated feature.

Learn

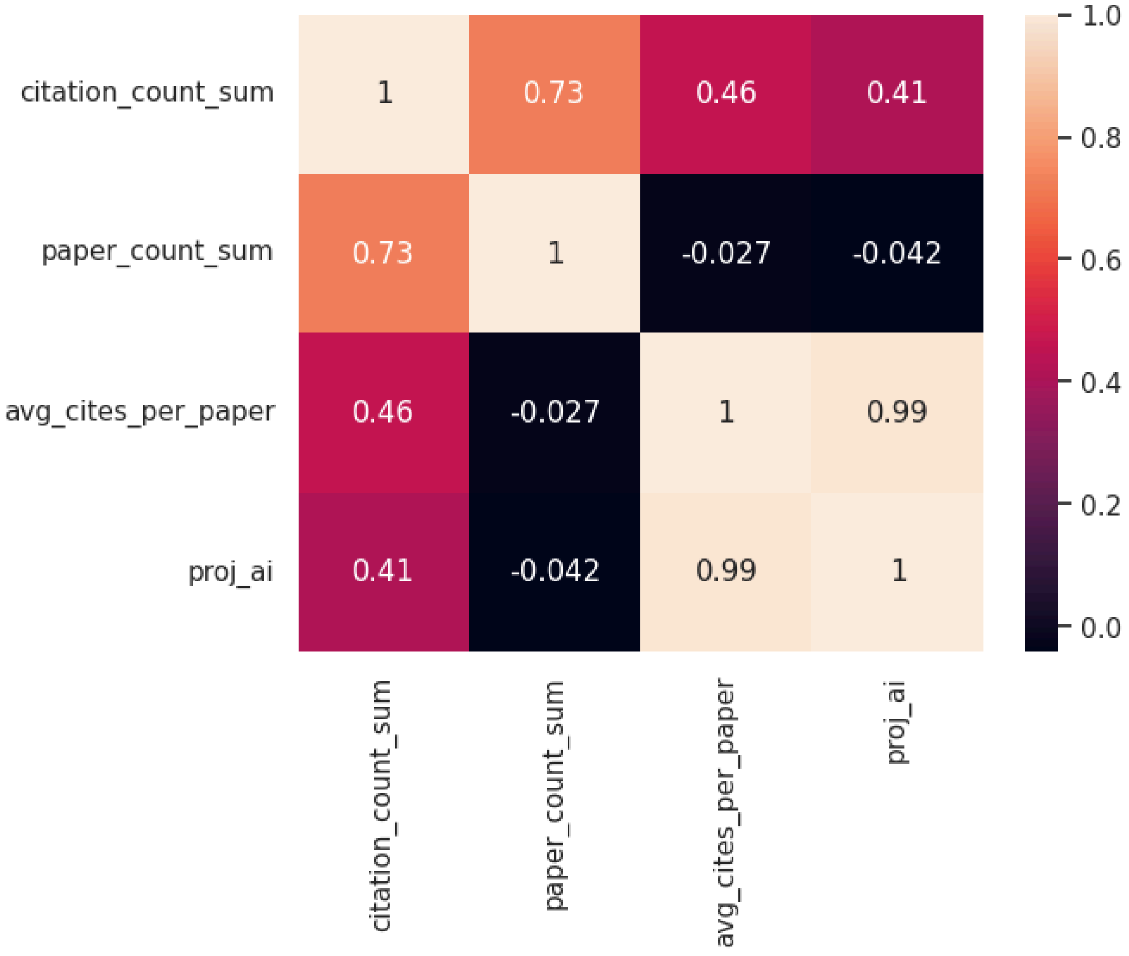
There is a strong nonlinear correlation between proj_ai x avg_cites_per_paper. There is also some correlation between other variables here. But we need numbers to make a decision whether to remove some highly correlated feature. For this, a heat map with values is useful.

Use a `heatmap` (documentation) to confirm the correlation between the variables and the target, after removing the correlation.

> ## Question 6
>
> **Try**

> Use the `corr` function (documentation) in the df_journal dataframe to print the correlations.

In [26]:
```python
# Enter your code here
corr = numerical_df.corr()
ax = sns.heatmap(corr, annot=True)
```



Learn

Notice that the diagonal is always 1 (one), because it represents the variable against itself.

Is it broken?

The **proj_ai** and **avg_cites_per_paper** variables are highly correlated (over 99%).

Fix

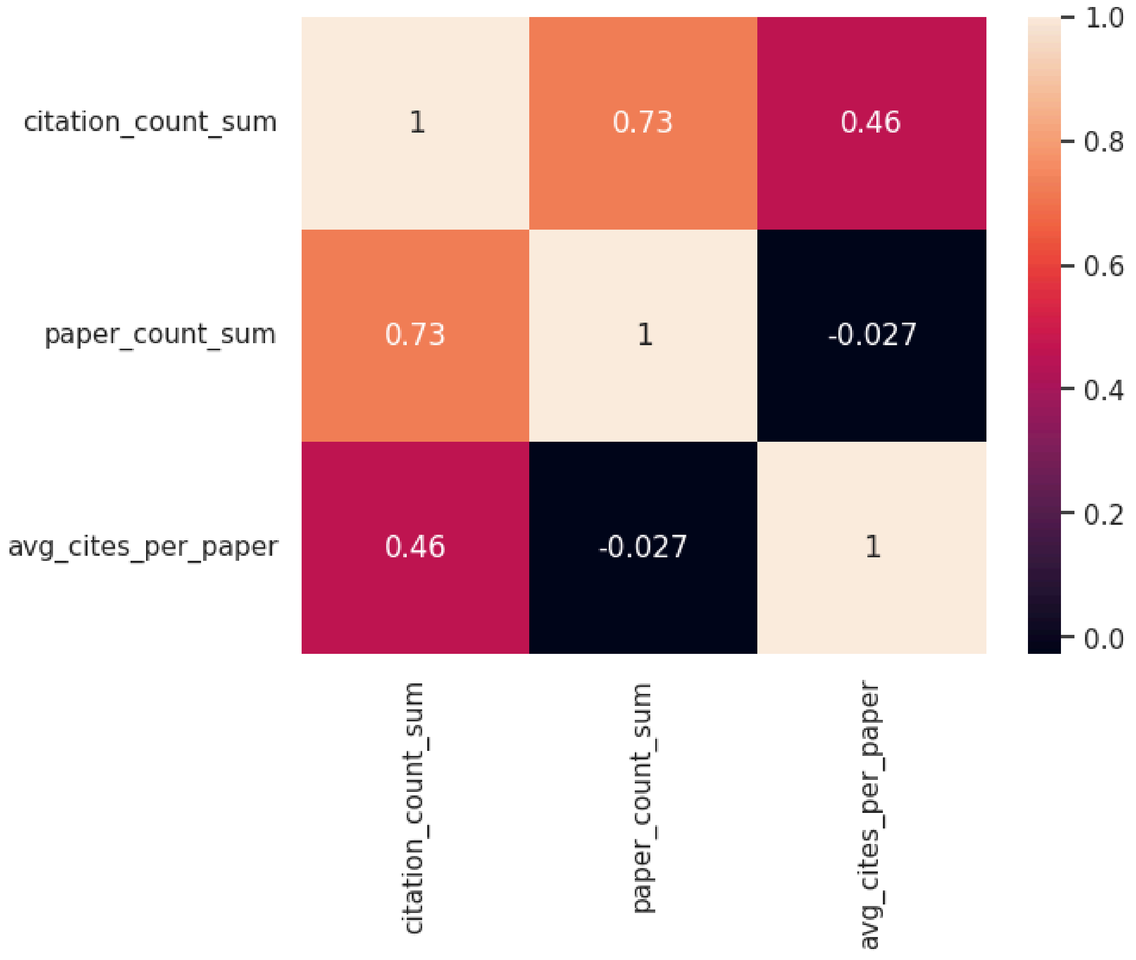
Let's try removing one of them. You will remove the **proj_ai** feature from the dataset.

In [27]:
```python
del numerical_df["proj_ai"]
```

Learn

Use another `heatmap` to confirm the correlation between the variables and the target, after removing the correlation.

```
In [28]: corr = numerical_df.corr()
         ax = sns.heatmap(corr, annot=True,)
```



Conclusion

In this exercise, you practiced different ways to know your data.

You explored your data over several dimensions and views to bring your raw data to a state of processed data, ready to be used for your model.

You needed to understand a short business scenario and corresponding dataset. You analyzed the data using descriptive statistics to better understand it.

You used visualization tools, including box and whisker plots and histograms, to support this analysis and understand the distribution of your data. You applied multivariate statistics with the help of scatter plots to spot correlations between features.

In **question 1**, you discovered the importance of a first glance at your data. You looked at how many features there were and how many samples. You looked at the first lines to see if anything caught your attention, such as missing values.

In **question 2**, you learned and practiced how to decide whether to remove or impute missing values. In the case of imputation, you practiced how to handle numerical or categorical imputation.

Questions 3 gave you an understanding of basic statistics that you can apply to your data. You practiced plotting the distribution of features.

For **question 4**, you practiced with another important plot for numerical features: the box and whisker plot. This is a great tool for spotting outliers.

Question 5 showed you an interesting guideline for removing outliers using percentiles. You were challenged to implement the algorithm.

Finally, in **question 6** you learned and practiced using multivariate techniques, such as a correlation matrix and scatter plot, to spot correlations between features and how to deal with that.

Good work!

Now you have a dataset cleaned and ready to pass to the modeling step.