Project_2_CemKazan

February 28, 2023

1 Structural Discovery of Macromolecules

author: Cem Kazan date: 02/28/2023

2 Structural Discovery of Macromolecules

The main question in structural discovery field is how macro molecules behave in their natural forms and natural environments and how macromolecules stray away from natural behavior.

3 Setup for Data Analysis

Loading Libraries and the Data Frame

[1]:
```
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import numpy as np
from sklearn.cluster import DBSCAN
from sklearn.cluster import KMeans
from sklearn.cluster import AgglomerativeClustering
from sklearn.preprocessing import StandardScaler
from sklearn.decomposition import PCA
sns.set_context('talk')
```

[2]:
```
import tensorflow as tf
from tensorflow import keras
from tensorflow.keras import layers
from keras.wrappers.scikit_learn import KerasClassifier
```

- For data visualization, I use **matplotlib** or **seaborn** to uncover patterns and relationships in my data.
- For data manipulation, I use **pandas** to filter, summarize, and transform my data.
- For clustering analysis, I use **scikit-learn** and its **DBSCAN** algorithm to identify clusters within large datasets.
- For deep learning, I use **TensorFlow** to build and train neural networks
- For dimensionality reduction, I use **scikit-learn** and its **PCA** algorithm to reduce the number of features in my data while retaining as much information as possible

```
[2]:
```

3.1 Data Summary

```
[3]: df_input = pd.read_csv('./pdb_data_no_dups.csv')
     display(df_input)
     df_input.describe(include='all')
```

```
       structureId                           classification  \
0             100D                          DNA-RNA HYBRID
1             101D                                     DNA
2             101M                        OXYGEN TRANSPORT
3             102D                                     DNA
4             102L                      HYDROLASE(O-GLYCOSYL)
…              …                                        …
141396        9RUB                     LYASE(CARBON-CARBON)
141397        9TNA                                   T-RNA
141398        9WGA                      LECTIN (AGGLUTININ)
141399        9XIA  ISOMERASE(INTRAMOLECULAR OXIDOREDUCTASE)
141400        9XIM  ISOMERASE(INTRAMOLECULAR OXIDOREDUCTASE)

       experimentalTechnique macromoleculeType  residueCount  resolution  \
0          X-RAY DIFFRACTION    DNA/RNA Hybrid            20        1.90
1          X-RAY DIFFRACTION               DNA            24        2.25
2          X-RAY DIFFRACTION           Protein           154        2.07
3          X-RAY DIFFRACTION               DNA            24        2.20
4          X-RAY DIFFRACTION           Protein           165        1.74
…                        …                 …             …           …
141396     X-RAY DIFFRACTION           Protein           932        2.60
141397     X-RAY DIFFRACTION               NaN             0         NaN
141398     X-RAY DIFFRACTION           Protein           342        1.80
141399     X-RAY DIFFRACTION           Protein           388        1.90
141400     X-RAY DIFFRACTION           Protein          1572        2.40

        structureMolecularWeight          crystallizationMethod  \
0                        6360.30  VAPOR DIFFUSION, HANGING DROP
1                        7939.35                            NaN
2                       18112.80                            NaN
3                        7637.17  VAPOR DIFFUSION, SITTING DROP
4                       18926.61                            NaN
…                            …                             …
141396                 101838.68                            NaN
141397                  24244.34                            NaN
141398                  34270.22                            NaN
141399                  43542.29                            NaN
141400                 174722.12                            NaN
```

```
        crystallizationTempK  densityMatthews  densityPercentSol  \
0                        NaN             1.78              30.89
1                        NaN             2.00              38.45
2                        NaN             3.09              60.20
3                      277.0             2.28              46.06
4                        NaN             2.75              55.28
…                        …               …                 …
141396                   NaN             2.38              48.29
141397                   NaN             3.17              61.18
141398                   NaN             2.50              50.76
141399                   NaN             2.79              55.93
141400                   NaN             3.96              68.92

                                               pdbxDetails  phValue  \
0                  pH 7.00, VAPOR DIFFUSION, HANGING DROP      7.0
1                                                      NaN      NaN
2        3.0 M AMMONIUM SULFATE, 20 MM TRIS, 1MM EDTA, …      9.0
3        pH 7.00, VAPOR DIFFUSION, SITTING DROP, temper…      7.0
4                                                      NaN      NaN
…                                                    …      …
141396                                                 NaN      NaN
141397                                                 NaN      NaN
141398                                                 NaN      NaN
141399                                                 NaN      NaN
141400                                                 NaN      NaN

        publicationYear
0                1994.0
1                1995.0
2                1999.0
3                1995.0
4                1993.0
…                 …
141396           1991.0
141397           1986.0
141398           1990.0
141399           1989.0
141400           1992.0

[141401 rows x 14 columns]
```

[3]:
```
       structureId classification experimentalTechnique macromoleculeType  \
count       141401         141399                141401            137636
unique      140911           5050                    33                13
top           2FYM      HYDROLASE     X-RAY DIFFRACTION           Protein
freq             4          20915                126432            127798
mean           NaN            NaN                   NaN               NaN
```

```
std             NaN            NaN                    NaN                NaN
min             NaN            NaN                    NaN                NaN
25%             NaN            NaN                    NaN                NaN
50%             NaN            NaN                    NaN                NaN
75%             NaN            NaN                    NaN                NaN
max             NaN            NaN                    NaN                NaN

         residueCount     resolution  structureMolecularWeight  \
count   141401.000000  128589.000000              1.414010e+05
unique            NaN            NaN                       NaN
top               NaN            NaN                       NaN
freq              NaN            NaN                       NaN
mean       825.374849       2.263807              1.120790e+05
std       2136.461080       1.410878              5.690152e+05
min          0.000000       0.480000              3.143800e+02
25%        226.000000       1.800000              2.612856e+04
50%        414.000000       2.100000              4.747779e+04
75%        820.000000       2.500000              9.408484e+04
max     313236.000000      70.000000              9.773054e+07

               crystallizationMethod  crystallizationTempK  densityMatthews  \
count                          96242          97039.000000    124724.000000
unique                           549                   NaN              NaN
top     VAPOR DIFFUSION, HANGING DROP                   NaN              NaN
freq                           53870                   NaN              NaN
mean                             NaN            290.967713         2.670267
std                              NaN              9.541080         0.783740
min                              NaN              4.000000         0.000000
25%                              NaN            290.000000         2.210000
50%                              NaN            293.000000         2.490000
75%                              NaN            295.000000         2.910000
max                              NaN            398.000000        99.000000

        densityPercentSol pdbxDetails        phValue  publicationYear
count       124749.000000      118534  105110.000000    117602.000000
unique                NaN       91025            NaN              NaN
top                   NaN      pH 7.5            NaN              NaN
freq                  NaN         361            NaN              NaN
mean            51.353163         NaN       6.788685      2008.922365
std             10.104561         NaN       2.556819         8.459286
min              0.000000         NaN       0.000000       201.000000
25%             44.370000         NaN       6.000000      2005.000000
50%             50.500000         NaN       7.000000      2010.000000
75%             57.710000         NaN       7.500000      2014.000000
max             92.000000         NaN     724.000000      2018.000000
```

[4]:
```
col_names = df_input.columns.tolist()
col_names_str = ', '.join(col_names)
```

The Structural Protein Sequences data [@structur] frame comprises 14 columns, as indicated by structureId, classification, experimentalTechnique, macromoleculeType, residueCount, resolution, structureMolecularWeight, crystallizationMethod, crystallizationTempK, densityMatthews, densityPercentSol, pdbxDetails, phValue, publicationYear. An examination of the summary statistics revealed the presence of NA and empty values that must be addressed. Additionally, columns deemed irrelevant to our analysis have been removed.

[5]:
```
df_clean = df_input.dropna()
df_clean = df_clean.drop(columns=['publicationYear', 'pdbxDetails'])
df_clean
```

[5]:
```
       structureId classification experimentalTechnique macromoleculeType  \
3             102D            DNA      X-RAY DIFFRACTION               DNA
27            110D            DNA      X-RAY DIFFRACTION               DNA
30            111D            DNA      X-RAY DIFFRACTION               DNA
36            113D            DNA      X-RAY DIFFRACTION               DNA
44            117D            DNA      X-RAY DIFFRACTION               DNA
…              …             …                    …                 …
141064        6F6S  VIRAL PROTEIN      X-RAY DIFFRACTION           Protein
141066        6F73   FLAVOPROTEIN      X-RAY DIFFRACTION           Protein
141068        6F8P  VIRAL PROTEIN      X-RAY DIFFRACTION           Protein
141077        6FAH   FLAVOPROTEIN      X-RAY DIFFRACTION           Protein
141172        7BNA            DNA      X-RAY DIFFRACTION               DNA

        residueCount  resolution  structureMolecularWeight  \
3                 24        2.20                   7637.17
27                 6        1.90                   2337.73
30                24        2.25                   7374.83
36                24        2.50                   7356.81
44                12        2.55                   3663.39
…                …          …                        …
141064           497        2.29                  58337.03
141066          1148        2.22                 128053.03
141068           316        1.60                  34958.86
141077          2074        3.13                 231360.91
141172            24        1.90                   7326.78

                crystallizationMethod  crystallizationTempK  densityMatthews  \
3       VAPOR DIFFUSION, SITTING DROP                277.00             2.28
27      VAPOR DIFFUSION, SITTING DROP                277.00             2.90
30      VAPOR DIFFUSION, SITTING DROP                277.00             2.29
36      VAPOR DIFFUSION, SITTING DROP                281.00             2.35
44                    VAPOR DIFFUSION                277.00             3.01
…                               …                    …               …
```

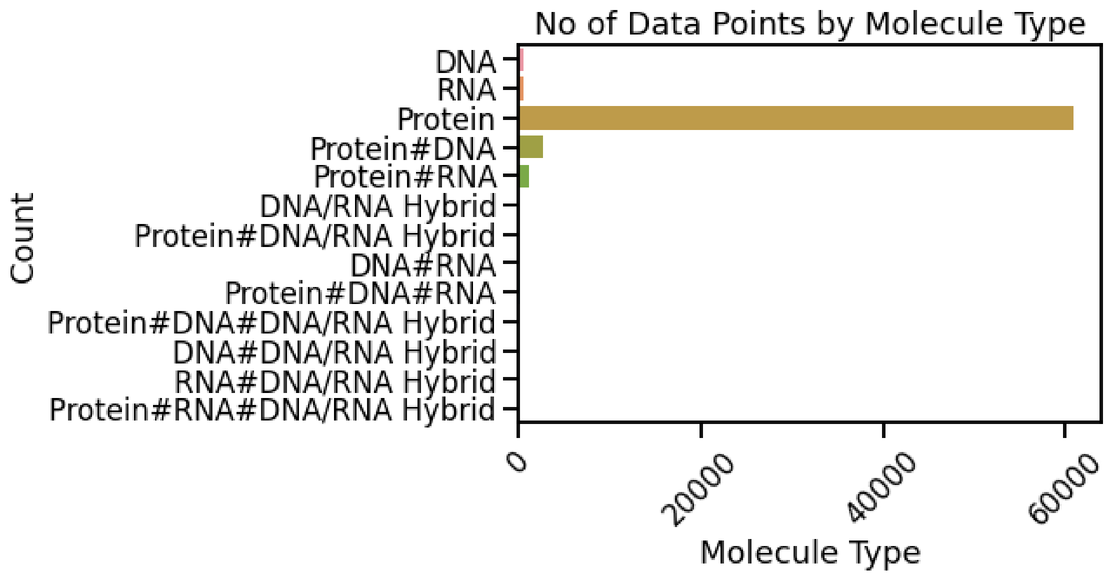
```
141064  VAPOR DIFFUSION, SITTING DROP                293.00              3.83
141066  VAPOR DIFFUSION, HANGING DROP                294.00              2.90
141068  VAPOR DIFFUSION, SITTING DROP                298.00              2.47
141077  VAPOR DIFFUSION, SITTING DROP                293.15              3.49
141172                VAPOR DIFFUSION                290.00              2.27

        densityPercentSol  phValue
3                   46.06      7.0
27                  57.63      6.6
30                  46.25      6.6
36                  47.59      7.4
44                  59.09      6.5
…                     …       …
141064              67.89      5.2
141066              57.00      5.0
141068              50.15      7.0
141077              64.73      8.5
141172              45.79      7.5

[65886 rows x 12 columns]
```

4 Data Analysis

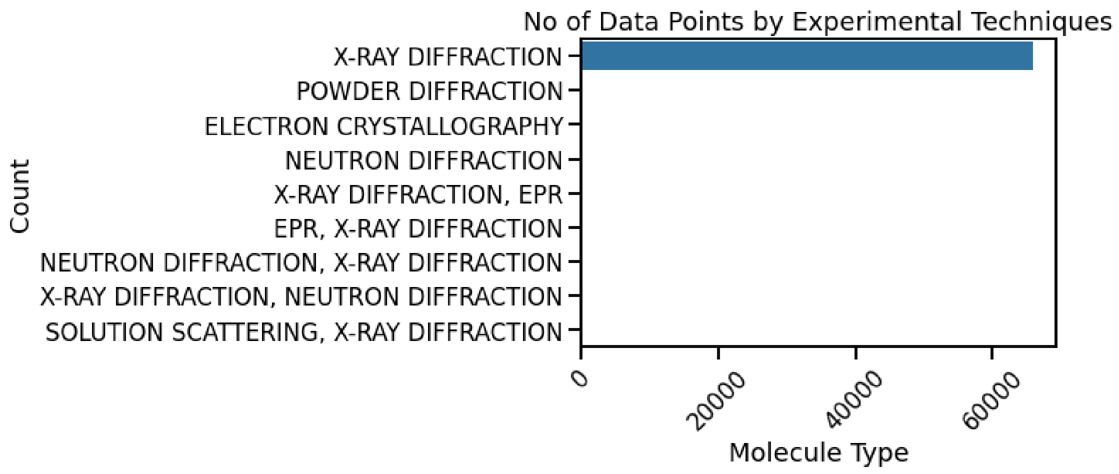
4.1 Molecule Type and Experiment Technique

First thing that need to be considered are the molecule types and the technique used for the experiment to choose ideal data for examination.

[6]:
```
sns.countplot(y='macromoleculeType', data=df_clean)
plt.title("No of Data Points by Molecule Type")
plt.xlabel("Molecule Type")
plt.ylabel("Count")
plt.xticks(rotation=45)
plt.show()
```



[7]:
```
sns.countplot(y='experimentalTechnique', data=df_clean)
plt.title("No of Data Points by Experimental Techniques")
plt.xlabel("Molecule Type")
plt.ylabel("Count")
plt.xticks(rotation=45)
plt.show()
```



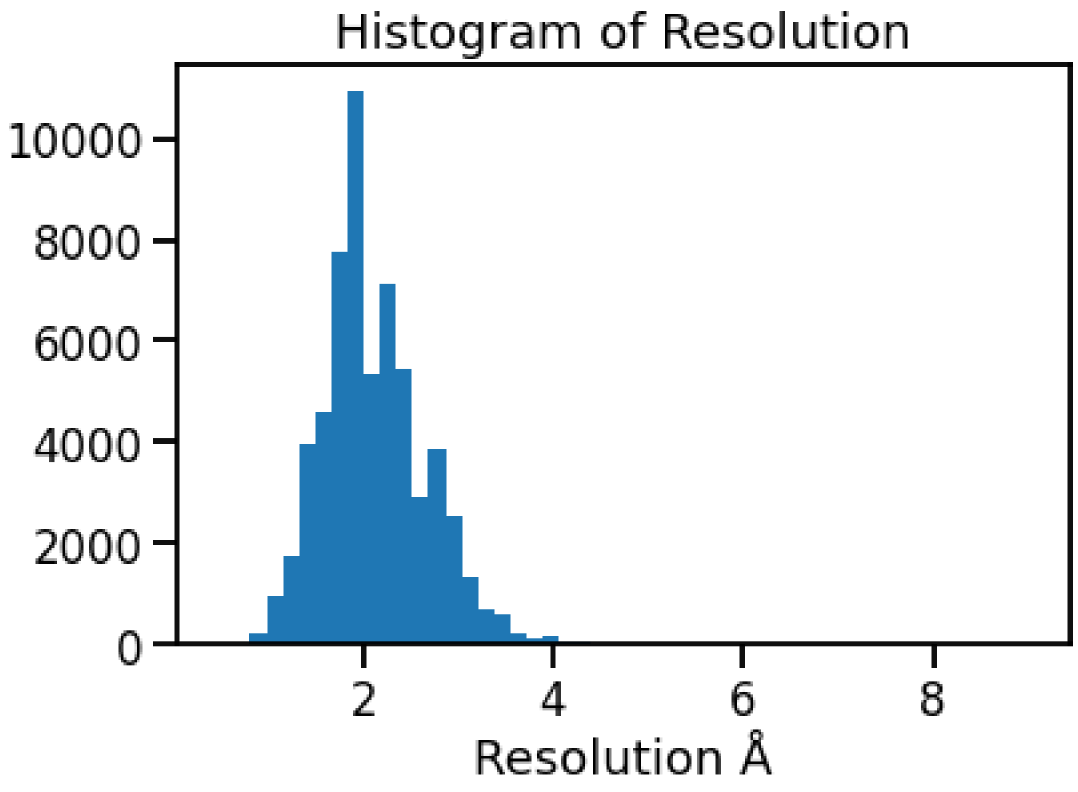
[8]:
```
df_select_1 = df_clean[
    (
        df_clean['macromoleculeType'] == 'Protein'
    ) & (
        df_clean['experimentalTechnique'] == 'X-RAY DIFFRACTION'
    )
].copy()
```

Due to the large amount of data available for proteins, it was selected as the subject of further analysis. Given the majority of the results are obtained through x-ray diffraction, my focus was specifically directed towards proteins that have been studied using this technique.

4.2 Effect of Resolution

Majority of the protein structural discoveries uses the x-ray diffraction and one major achievement in discovery is obtaining a resolution (in angstrom units) as close to one as possible.[@warren1990; @whittig1986] This is limited by the physics behind it. To understand this one dimensional data I used histogram to see how it is distributed.

[9]:
```
plt.hist(df_select_1['resolution'], bins=50)
plt.title("Histogram of Resolution")
plt.xlabel("Resolution Å")
plt.show()
```



The histogram of resolution shows that majority of the experiments can resolve structures with a resolution around 2. (As there are more then 60000 data points in my set, the number of bins is selected as 50 to get the details about the distribution more precisely). Investigation of structures with resolution below 2 would give much deeper understanding of the structural features and the underlying physics/chemistry.

```
[10]: df_select_2 = df_select_1[
          (
              df_select_1['resolution'] < 2
          )
      ]
```

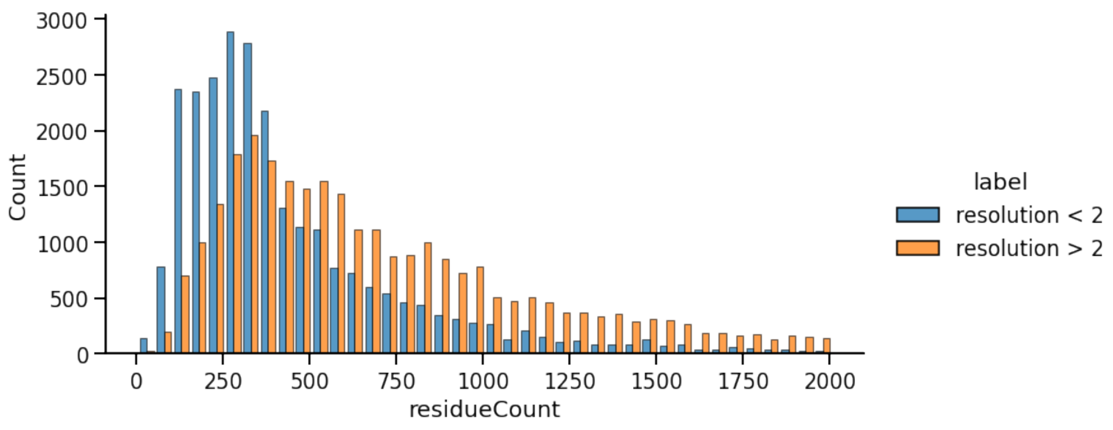
The number of protein structures with a resolution below two are 26248.

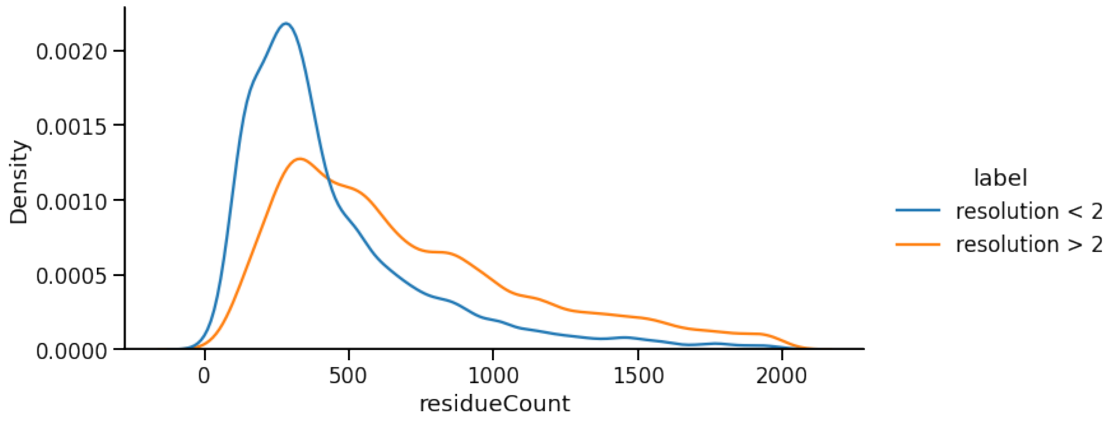
4.3 Effect of Residue Count

Next I wanted to understand how residue count (the number of residue in macromolecules) affects the resolution of the discovered structure.

```
[11]: df_protein1 = df_select_1[(df_select_1['resolution'] < 2) &␣
       ↪(df_select_1['residueCount'] < 2000)].copy()
      df_protein2 = df_select_1[(df_select_1['resolution'] > 2) &␣
       ↪(df_select_1['residueCount'] < 2000)].copy()
      df_protein1['label'] = 'resolution < 2'
      df_protein2['label'] = 'resolution > 2'

      df_plot = pd.concat([df_protein1, df_protein2])


      sns.displot(
          data=df_plot,
          x='residueCount',
          hue='label',
          kind='hist',
          common_norm=False,
          binwidth=50,
          multiple='dodge',
          shrink=0.8,
          aspect=2,
      )
      sns.displot(
          data=df_plot,
          x='residueCount',
          hue='label',
          kind='kde',
          common_norm=False,
          aspect=2,
      )
```

```
[11]: <seaborn.axisgrid.FacetGrid at 0x7f646b965f10>
```





The relation between resolution and number of residues is intriguing. The plot shows that number of residues in a protein is a factor in determining the protein resolution. There is a negative correlation between the number of residues and resolution. The lesser the number of residues better the resolution (close to 1). Most of the high resolution structures have less than 500 residues. Thus, I investigated that set.

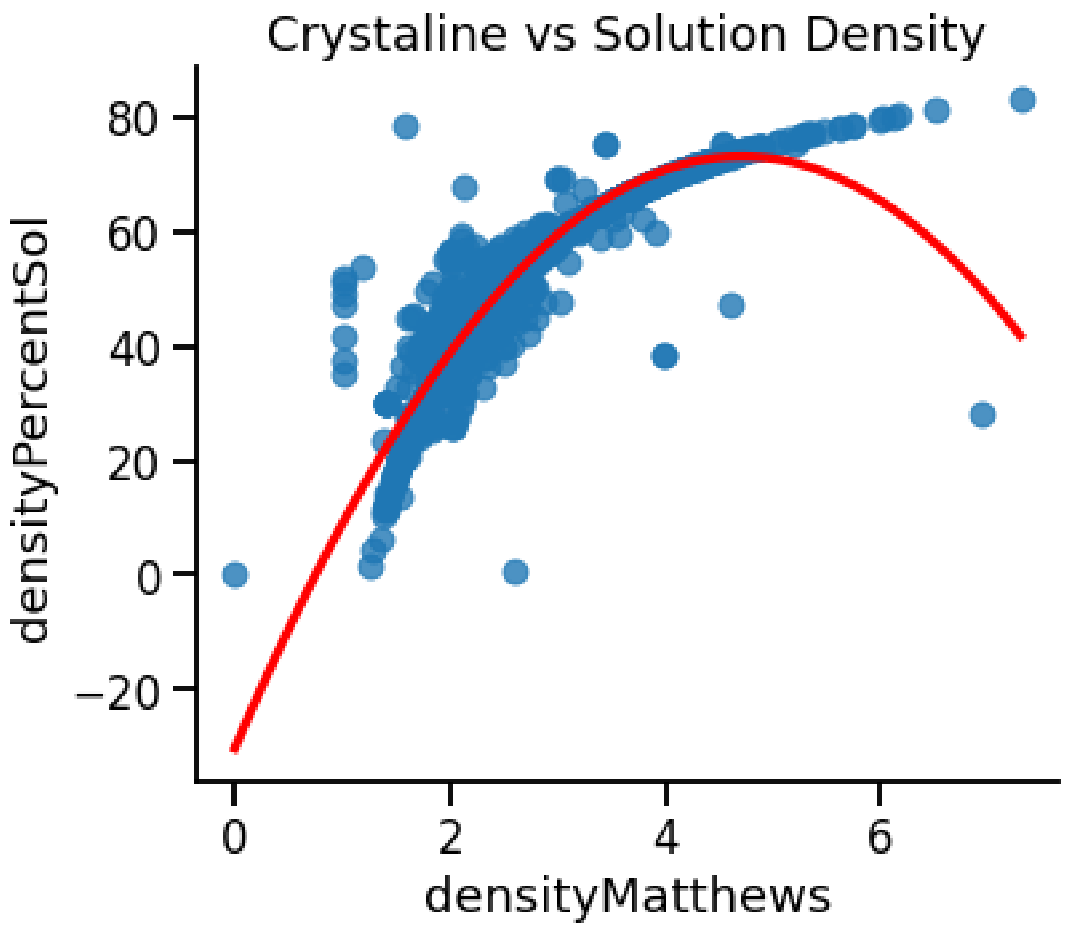
```
[12]: df_select_residu = df_select_2[(df_select_2['residueCount'] < 500)]
```

4.4 Exploring Discrepancies in the Density of Proteins in Crystalline and Soluble Forms

Proteins in solution has shown to display features that are being missed in structural discovery. One of the parameters that has been trusted in protein studies in solution is solution density calculation. On the other side structural discovery utilizes a metric depending on the protein crystals. Now the question is how do proteins act in solution (normal conditions) versus in a crystal lattice (restricted environment) ? Thus I investigated two features from both calculations.

```
[13]: sns.lmplot(
          data = df_select_residu,
          x='densityMatthews',
          y='densityPercentSol',
          order = 2,
          ci = 0,
          line_kws={'color': 'red'},
          aspect=1.2,
          legend = True
      )
      plt.title("Crystaline vs Solution Density")
```

```
[13]: Text(0.5, 1.0, 'Crystaline vs Solution Density')
```



The spread of the data in the plot resembles a second degree polynomial fit, hence I added a second degree polynomial fit to capture the underlying principle that correlates these two metrics. However because of the outliers the fit does not recapitulate the data.Thus the outliers needs to be removed.

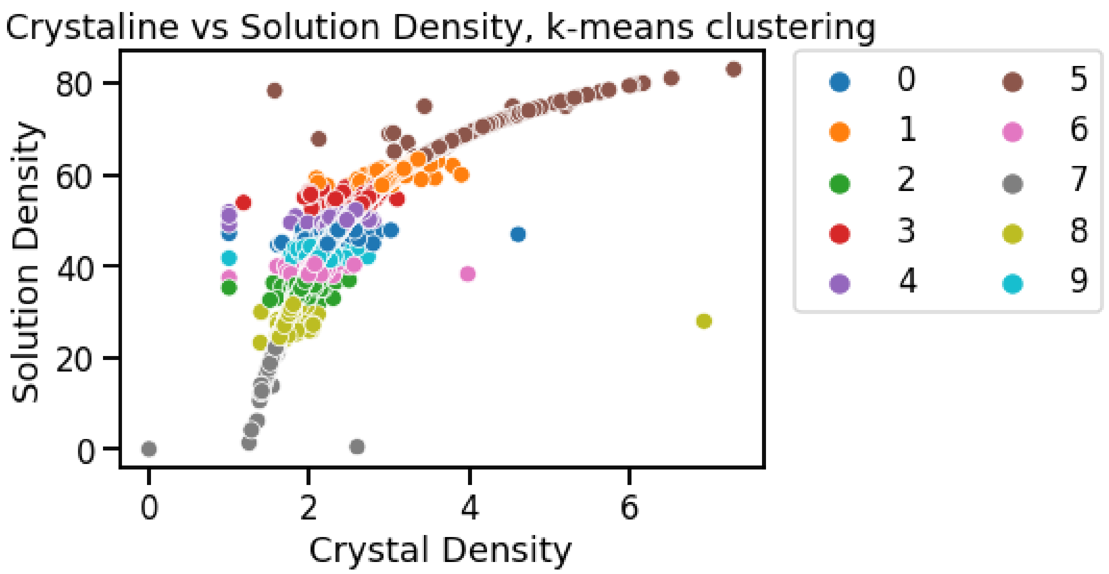
4.4.1 K-means clustering

I used K-means clustering to discover similar data points in the clusters within the two feature space. It can reveal hidden patterns and trends such that it can cluster and separate the data points that don't follow the correct trend.There are thousands of data points in my system therefore I selected k value as 20 to be able to generate unique clusters.

```
[14]: df_density = df_select_residu[['densityMatthews', 'densityPercentSol']].copy()
      kmeans_fit = KMeans(n_clusters=10, max_iter=20, n_init=2).fit(df_density)
      df_density['clusters'] = kmeans_fit.labels_
```

```
[15]: sns.scatterplot(
          data = df_density,
          x='densityMatthews',
          y='densityPercentSol',
          legend = True,
          hue='clusters',
          palette = sns.color_palette('tab10')
      )
      plt.xlabel('Crystal Density')
      plt.ylabel('Solution Density')
      plt.title('Crystaline vs Solution Density, k-means clustering')
      plt.legend(bbox_to_anchor=(1.05, 1), loc=2, borderaxespad=0., ncol=2)
```

```
[15]: <matplotlib.legend.Legend at 0x7f646b502be0>
```



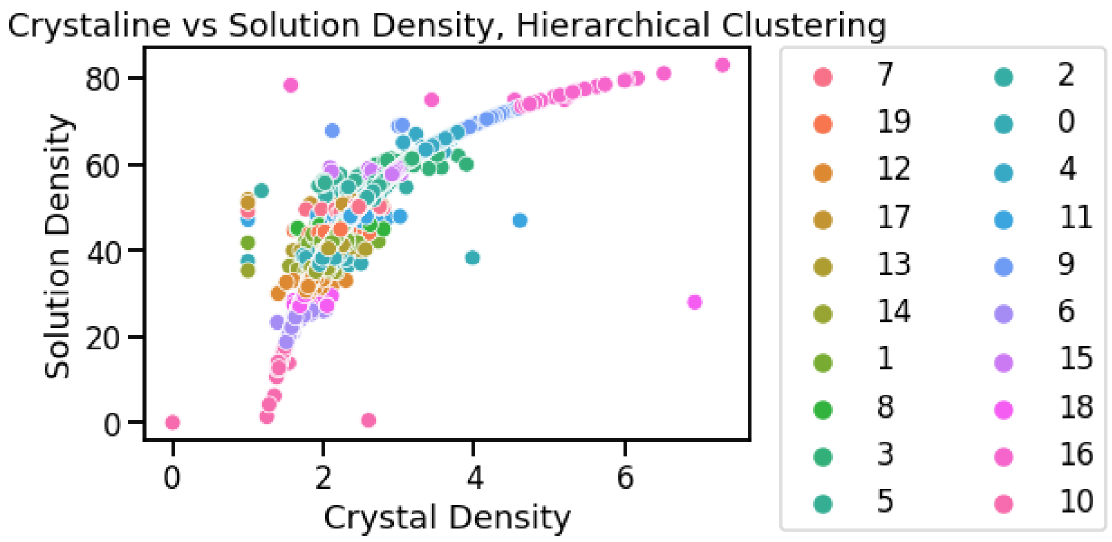
The K-means clustering failed to identify the correct clusters, therefore I used Hierarchical clustering that can identify clusters using agglomerative method which does not require a prior specification of the number of clusters.

4.4.2 Hierarchical clustering

[16]:
```
df_density_2 = df_select_residu[['densityMatthews', 'densityPercentSol']].copy()
hierarchical_cluster = AgglomerativeClustering(n_clusters=20,␣
  ↪affinity='euclidean', linkage='ward')
labels = hierarchical_cluster.fit_predict(df_density_2)
df_density_2['cluster'] = labels
df_density_2['cluster'] = df_density_2['cluster'].astype(str)
```

[17]:
```
sns.scatterplot(
    data = df_density_2,
    x='densityMatthews',
    y='densityPercentSol',
    legend = True,
    hue='cluster',
)
plt.xlabel('Crystal Density')
plt.ylabel('Solution Density')
plt.title('Crystaline vs Solution Density, Hierarchical Clustering')
plt.legend(bbox_to_anchor=(1.05, 1), loc=2, borderaxespad=0., ncol=2)
```

[17]:
```
<matplotlib.legend.Legend at 0x7f646d452940>
```



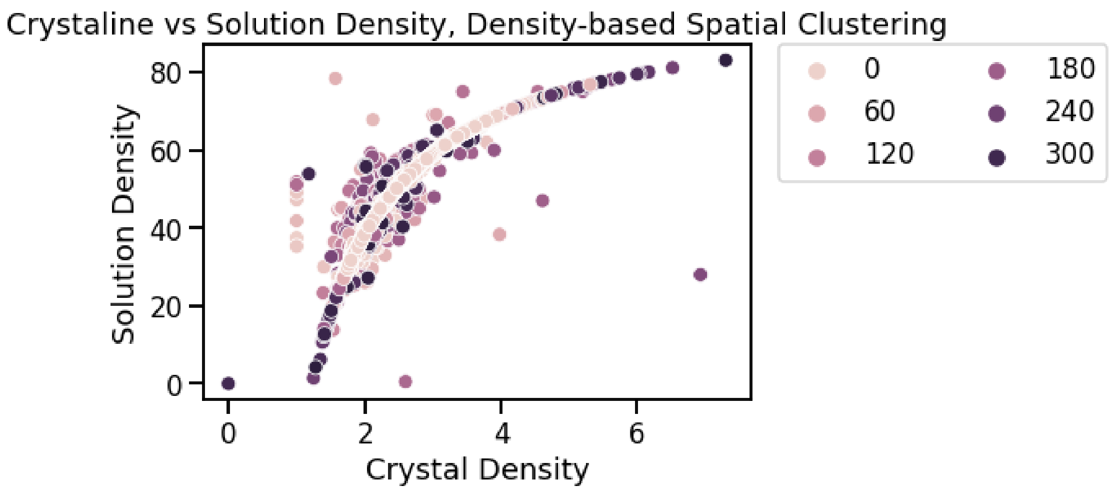
The figures indicate that kmeans and hierarchical clustering was not the best approach to identify the main overlapping points versus the outliers in the data. This data show dense regions around several data points. Therefore a density based clustering approach would be more useful in understanding this data. To achieve that I used dbscan function. DBscan is a density-based clustering algorithm that groups together data points that are close in space and separates points that are far apart. Dbscan is useful because it can find clusters of arbitrary shapes and sizes, unlike k-means and hierarchical clustering which tend to find circular clusters.

4.4.3 Density Based Clustering

[18]:
```
df_density_3 = df_select_residu[['densityMatthews', 'densityPercentSol']].copy()
dbscan = DBSCAN(eps=0.1, min_samples=1)
result = dbscan.fit_predict(df_density_3)
df_density_3['cluster'] = result
# print(df_density_3['cluster'].value_counts())
```

[19]:
```
sns.scatterplot(
    data = df_density_3,
    x='densityMatthews',
    y='densityPercentSol',
    legend = True,
    hue='cluster',
)
plt.xlabel('Crystal Density')
plt.ylabel('Solution Density')
plt.title('Crystaline vs Solution Density, Density-based Spatial Clustering')
plt.legend(bbox_to_anchor=(1.05, 1), loc=2, borderaxespad=0., ncol=2)
```

[19]:
```
<matplotlib.legend.Legend at 0x7f646ab86b50>
```

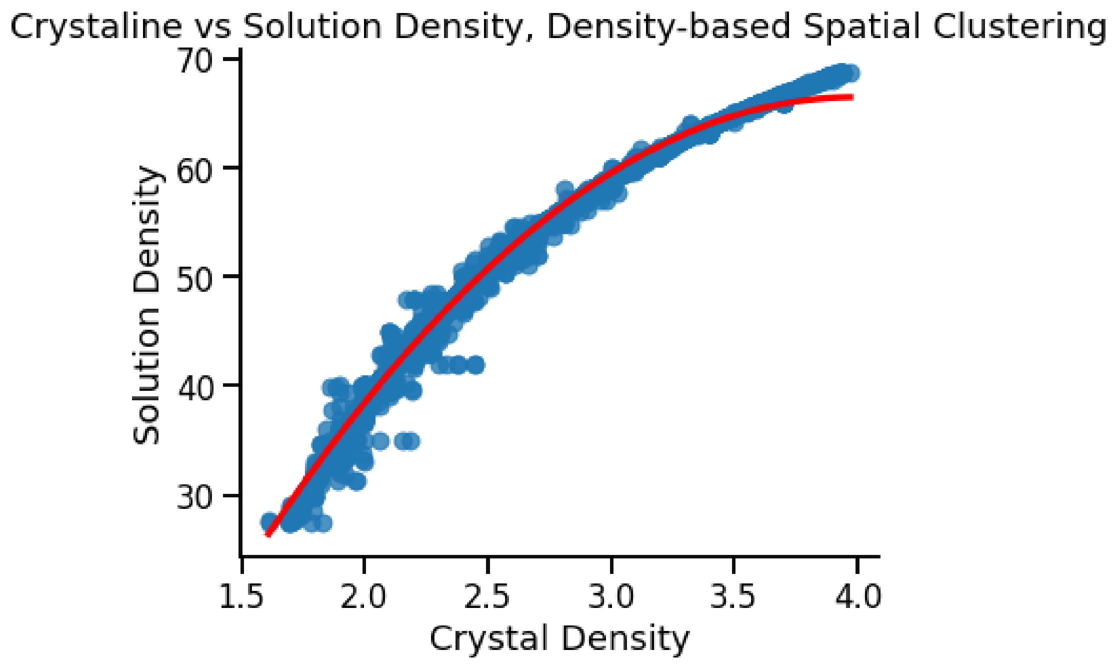


Looking at the plot we can clearly see the outliers in our data set. To focus more clearly on the data I choose main cluster and re-plot the data. I added a second degree polynomial fit once again to discover the underlying relation. The polynomial fit now captures more than 95% of the data as shown in the plot below.

[20]:
```
df_density_4 = df_density_3[df_density_3['cluster'] == 0]
```

```
sns.lmplot(
    data = df_density_4,
    x='densityMatthews',
    y='densityPercentSol',
    order = 2,
    ci = 0,
    line_kws={'color': 'red'},
    aspect=1.2,

)
plt.title("Crystaline vs Solution Density")
plt.xlabel('Crystal Density')
plt.ylabel('Solution Density')
plt.title('Crystaline vs Solution Density, Density-based Spatial Clustering')
```

```
[20]: Text(0.5, 1.0, 'Crystaline vs Solution Density, Density-based Spatial
      Clustering')
```



The results of this analysis demonstrate that through the utilization of various machine learning techniques, it is possible to identify and decipher fundamental relationships within a data set. This study highlights the challenges of achieving results that resemble natural phenomena using these techniques, with only 26% of the data points, equivalent to only 26% of the experiments, resulting in naturally occurring behavior that captures the correct underlying fundamentals.

So far focused on only several features from the dataset and filtering based on physics based principals I was able to distinguish different protein structures from each other. However, the dataset contains vast number of features that could be understood in a cohesive manner. In example for every protein 5 features could be analyzed at the same time to achive higher clarity in its natural behaviour relative with other proteins in the set. Several mathematical approaches could be utilized to achieve this. In the next chapters I will apply several diffrent methods to analyze the data. This will hopefully provide a better understanding of the data and potentially be able to distinguish proteins with similar characteristics from the ones that behave differently.

5 Principal Component Analysis

PCA is a technique that helps us understand complex datasets by simplifying them into a smaller number of variables (dimension reduction). The most significant links and patterns in the data are found, and new variables are then created to capture those relationships and patterns. These new variables, referred to as principle components, are simpler to use and can provide us with new perspectives on the underlying structure of the data.

First I will define a python function that takes a dataframe with several features and outputs its principal components.

```
[21]: def pca_df(df):
        # first we need to scale the values to avoid bias
          x = StandardScaler(with_mean=True, with_std=False).fit_transform(df.values)
          # now we do pca model and fit
          pca = PCA()
          principal_components = pca.fit_transform(x)
          print(pca.singular_values_)
          principal_df = pd.DataFrame(
              data=principal_components,
              index=df.index,
              columns=['PC{}'.format(a) for a in range(1, principal_components.
       ↪shape[1] + 1)]
          )
          return principal_df
```

```
[22]: df_clean
```

```
[22]:        structureId classification experimentalTechnique macromoleculeType  \
      3             102D            DNA      X-RAY DIFFRACTION               DNA
      27            110D            DNA      X-RAY DIFFRACTION               DNA
      30            111D            DNA      X-RAY DIFFRACTION               DNA
      36            113D            DNA      X-RAY DIFFRACTION               DNA
      44            117D            DNA      X-RAY DIFFRACTION               DNA
      …                …              …                    …                 …
      141064        6F6S  VIRAL PROTEIN      X-RAY DIFFRACTION           Protein
      141066        6F73   FLAVOPROTEIN      X-RAY DIFFRACTION           Protein
      141068        6F8P  VIRAL PROTEIN      X-RAY DIFFRACTION           Protein
      141077        6FAH   FLAVOPROTEIN      X-RAY DIFFRACTION           Protein
      141172        7BNA            DNA      X-RAY DIFFRACTION               DNA
```

```
        residueCount  resolution  structureMolecularWeight  \
3                 24        2.20                   7637.17
27                 6        1.90                   2337.73
30                24        2.25                   7374.83
36                24        2.50                   7356.81
44                12        2.55                   3663.39
…                …          …                         …
141064           497        2.29                  58337.03
141066          1148        2.22                 128053.03
141068           316        1.60                  34958.86
141077          2074        3.13                 231360.91
141172            24        1.90                   7326.78

                crystallizationMethod  crystallizationTempK  densityMatthews  \
3       VAPOR DIFFUSION, SITTING DROP                277.00             2.28
27      VAPOR DIFFUSION, SITTING DROP                277.00             2.90
30      VAPOR DIFFUSION, SITTING DROP                277.00             2.29
36      VAPOR DIFFUSION, SITTING DROP                281.00             2.35
44                    VAPOR DIFFUSION                277.00             3.01
…                                 …                   …               …
141064  VAPOR DIFFUSION, SITTING DROP                293.00             3.83
141066  VAPOR DIFFUSION, HANGING DROP                294.00             2.90
141068  VAPOR DIFFUSION, SITTING DROP                298.00             2.47
141077  VAPOR DIFFUSION, SITTING DROP                293.15             3.49
141172                VAPOR DIFFUSION                290.00             2.27

        densityPercentSol  phValue
3                   46.06      7.0
27                  57.63      6.6
30                  46.25      6.6
36                  47.59      7.4
44                  59.09      6.5
…                     …      …
141064              67.89      5.2
141066              57.00      5.0
141068              50.15      7.0
141077              64.73      8.5
141172              45.79      7.5

[65886 rows x 12 columns]
```

[23]:
```
df_PCA_input= df_clean[[
    'structureId',
    'residueCount','resolution','structureMolecularWeight',
    'crystallizationTempK','densityMatthews','densityPercentSol','phValue'
]]
```

```
df_PCA_input.set_index('structureId', inplace=True)
display(df_PCA_input)
```

```
            residueCount  resolution  structureMolecularWeight  \
structureId
102D                  24        2.20                   7637.17
110D                   6        1.90                   2337.73
111D                  24        2.25                   7374.83
113D                  24        2.50                   7356.81
117D                  12        2.55                   3663.39
…                    …         …                       …
6F6S                 497        2.29                  58337.03
6F73                1148        2.22                 128053.03
6F8P                 316        1.60                  34958.86
6FAH                2074        3.13                 231360.91
7BNA                  24        1.90                   7326.78

            crystallizationTempK  densityMatthews  densityPercentSol  phValue
structureId
102D                      277.00             2.28              46.06      7.0
110D                      277.00             2.90              57.63      6.6
111D                      277.00             2.29              46.25      6.6
113D                      281.00             2.35              47.59      7.4
117D                      277.00             3.01              59.09      6.5
…                          …               …                 …       …
6F6S                      293.00             3.83              67.89      5.2
6F73                      294.00             2.90              57.00      5.0
6F8P                      298.00             2.47              50.15      7.0
6FAH                      293.15             3.49              64.73      8.5
7BNA                      290.00             2.27              45.79      7.5

[65886 rows x 7 columns]
```

[24]:
```
principal_df = pca_df(df_PCA_input)
print(principal_df)

df_PCA_output = pd.concat([df_PCA_input, principal_df], axis=1)
print(df_PCA_output)
```

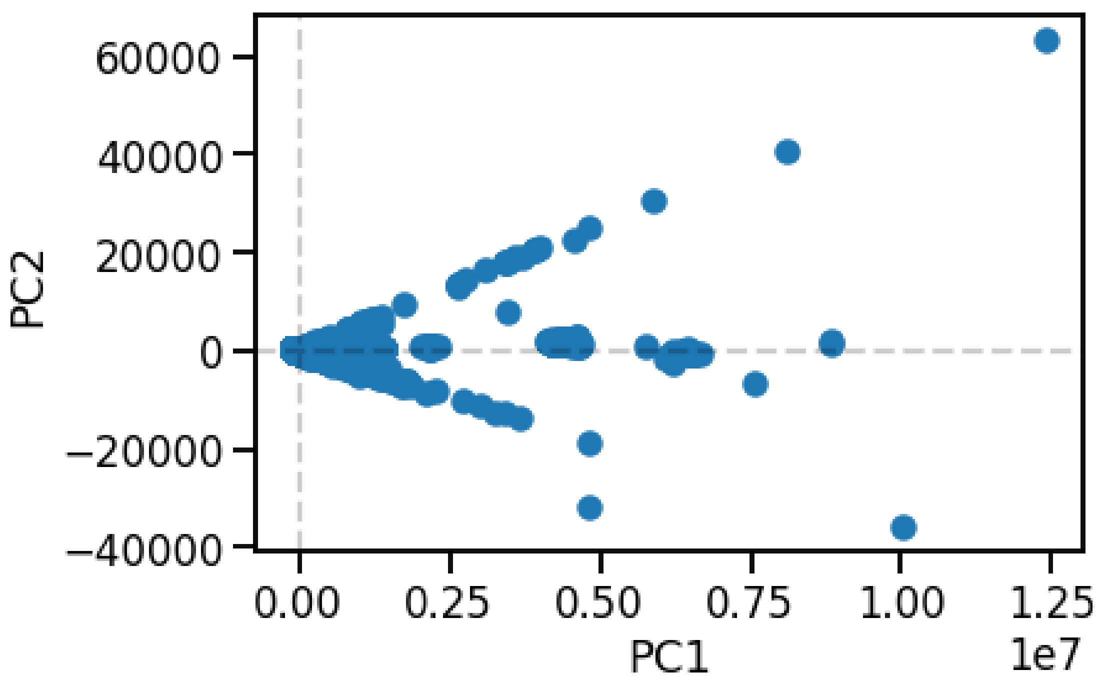
```
[7.41476344e+07 1.63878371e+05 2.56273553e+03 2.29696160e+03
 3.31008249e+02 1.27457167e+02 6.82179473e+01]
                      PC1         PC2        PC3        PC4       PC5  \
structureId
102D        -92952.188408  302.324139   1.442777  14.778515  0.219619
110D        -98251.650145  292.661844  12.073082  10.172944 -0.197828
111D        -93214.524838  300.955409   1.617215  14.702583 -0.179696
113D        -93232.544587  300.858965   1.262695  10.496945  0.626207
117D        -96925.976875  293.574242  13.425705   9.584843 -0.288906
```

```
…                    …          …          …          …         …
6F6S         -42250.550792   93.752619  14.588273  -8.368569 -1.597463
6F73          27467.896436 -193.569594   3.390525  -4.616139 -1.794568
6F8P         -65629.346967  152.835223  -3.529095  -5.956155  0.218748
6FAH         130779.201212 -580.698352   9.772903  -6.473497  1.696199
7BNA         -93262.574191  300.705058  -3.983118   2.962916  0.725861

                  PC6       PC7
structureId
102D         0.270970 -0.071607
110D        -0.330770 -0.149403
111D         0.322020 -0.079975
113D         0.513798 -0.125839
117D         0.280719 -0.198232
…                 …         …
6F6S        -0.226797  0.102477
6F73        -0.094823 -0.120307
6F8P        -0.499678 -0.064418
6FAH         0.482994 -0.080599
7BNA        -0.049173 -0.028479

[65886 rows x 7 columns]
             residueCount  resolution  structureMolecularWeight  \
structureId
102D                   24        2.20                   7637.17
110D                    6        1.90                   2337.73
111D                   24        2.25                   7374.83
113D                   24        2.50                   7356.81
117D                   12        2.55                   3663.39
…                     …           …                       …
6F6S                  497        2.29                  58337.03
6F73                 1148        2.22                 128053.03
6F8P                  316        1.60                  34958.86
6FAH                 2074        3.13                 231360.91
7BNA                   24        1.90                   7326.78

             crystallizationTempK  densityMatthews  densityPercentSol  \
structureId
102D                       277.00             2.28              46.06
110D                       277.00             2.90              57.63
111D                       277.00             2.29              46.25
113D                       281.00             2.35              47.59
117D                       277.00             3.01              59.09
…                           …             …                  …
6F6S                       293.00             3.83              67.89
6F73                       294.00             2.90              57.00
6F8P                       298.00             2.47              50.15
6FAH                       293.15             3.49              64.73
```

```
7BNA                          290.00              2.27              45.79

             phValue            PC1         PC2        PC3        PC4  \
structureId
102D             7.0  -92952.188408  302.324139   1.442777  14.778515
110D             6.6  -98251.650145  292.661844  12.073082  10.172944
111D             6.6  -93214.524838  300.955409   1.617215  14.702583
113D             7.4  -93232.544587  300.858965   1.262695  10.496945
117D             6.5  -96925.976875  293.574242  13.425705   9.584843
…                …              …           …          …          …
6F6S             5.2  -42250.550792   93.752619  14.588273  -8.368569
6F73             5.0   27467.896436 -193.569594   3.390525  -4.616139
6F8P             7.0  -65629.346967  152.835223  -3.529095  -5.956155
6FAH             8.5  130779.201212 -580.698352   9.772903  -6.473497
7BNA             7.5  -93262.574191  300.705058  -3.983118   2.962916

                  PC5       PC6       PC7
structureId
102D         0.219619  0.270970 -0.071607
110D        -0.197828 -0.330770 -0.149403
111D        -0.179696  0.322020 -0.079975
113D         0.626207  0.513798 -0.125839
117D        -0.288906  0.280719 -0.198232
…                 …         …         …
6F6S        -1.597463 -0.226797  0.102477
6F73        -1.794568 -0.094823 -0.120307
6F8P         0.218748 -0.499678 -0.064418
6FAH         1.696199  0.482994 -0.080599
7BNA         0.725861 -0.049173 -0.028479

[65886 rows x 14 columns]
```

The first two principal components in PCA are often the most important because they capture the largest amount of variation in the original dataset. This means that they contain the most information about the underlying patterns and relationships in the data. By analyzing these components, we can gain a better understanding of the key factors that are driving the variation in the dataset, and use this information to make better decisions or predictions. Essentially, the first two components give us a high-level overview of the data and provide a foundation for deeper analysis.

[25]:
```python
plt.scatter(
    x= df_PCA_output['PC1'],
    y= df_PCA_output['PC2'],
)
plt.axhline(y=0, color='k', linestyle='--', alpha=0.2)
plt.axvline(x=0, color='k', linestyle='--', alpha=0.2)
plt.xlabel('PC1')
plt.ylabel('PC2')
plt.show()
```



By plotting the first two principal components using matplotlib scatter plot we can identify data points that are most deviant and the ones that are similar to eachother. Here intriguingly PC2 identifies and seperates outliers very clearly. Thus first I will investigate the differences between these clusters.

[26]:
```
df_PC2_1 = df_PCA_output [ (df_PCA_output['PC2'] > 0)]
df_PC2_2 = df_PCA_output [ (df_PCA_output['PC2'] < 0)]
```

[27]:
```
df_PC2_1.mean()
```

[27]:
```
residueCount                  435.409737
resolution                      2.030232
structureMolecularWeight    60391.695490
crystallizationTempK          291.161979
densityMatthews                 2.604698
densityPercentSol              50.299365
phValue                         6.773873
PC1                        -40196.234610
PC2                           166.088967
PC3                            -0.758308
PC4                             0.285095
PC5                            -0.008981
PC6                            -0.056183
PC7                             0.013720
dtype: float64
```

```
[28]: df_PC2_2.mean()
```

```
[28]: residueCount                   1637.439114
      resolution                        2.429300
      structureMolecularWeight     188973.750474
      crystallizationTempK            291.013852
      densityMatthews                   2.836193
      densityPercentSol                54.425100
      phValue                           6.818693
      PC1                           88390.341108
      PC2                            -365.224768
      PC3                               1.667497
      PC4                              -0.626916
      PC5                               0.019749
      PC6                               0.123545
      PC7                              -0.030170
      dtype: float64
```

By looking at the mean values of each feature in two clusters separated by PC2, we observe a marginal difference in the number of residues of a protein (residueCount). The first cluster have an average residue count of 435, while the second cluster has an average of 1637. Following, the molecular weights of the protein (structureMolecularWeight) shows a similar trend. One of the most important components in structural discovery , resolution , shows distinction in these two clusters. We have previously seen the effect of residue count on resolution in this study and PCA was able to identify this difference robustly. The first cluster with an average less number of residues shows an average resolution of 2 angstrom, while the second cluster containing proteins with a large number of residues has an average of 2.4 angstrom. On the other hand the second principal component was not able to distinguish the difference of densities of proteins.

```
[29]: df_PC1_1 = df_PCA_output [ (df_PCA_output['PC1'] > 0)]
      df_PC1_2 = df_PCA_output [ (df_PCA_output['PC1'] < 0)]
      print(df_PC1_1.mean())
```

```
residueCount                   2133.092425
resolution                        2.520103
structureMolecularWeight     276029.527503
crystallizationTempK            291.091253
densityMatthews                   2.904525
densityPercentSol                55.344906
phValue                           6.818821
PC1                          175447.519219
PC2                            -406.775345
PC3                               1.998317
PC4                              -0.883510
PC5                               0.010809
PC6                               0.154124
PC7                              -0.024116
dtype: float64
```

[30]:
```
print(df_PC1_2.mean())
```

```
residueCount                   399.138125
resolution                       2.041178
structureMolecularWeight     45903.344035
crystallizationTempK           291.123286
densityMatthews                  2.606167
densityPercentSol               50.418430
phValue                          6.778241
PC1                         -54684.578158
PC2                            126.786279
PC3                             -0.622848
PC4                              0.275378
PC5                             -0.003369
PC6                             -0.048038
PC7                              0.007517
dtype: float64
```

By investigating the first principal component we again see a similar trend as PC2. Thus I looked into the third principal component.

[31]:
```
df_PC3_1 = df_PCA_output [ (df_PCA_output['PC3'] > 0)]
df_PC3_2 = df_PCA_output [ (df_PCA_output['PC3'] < 0)]
print(df_PC3_1.mean())
```

```
residueCount                   848.059225
resolution                       2.357352
structureMolecularWeight    103099.207839
crystallizationTempK           288.626577
densityMatthews                  3.170135
densityPercentSol               59.624731
phValue                          6.791331
PC1                           2512.849230
PC2                            -23.800663
PC3                              8.330472
PC4                             -0.898369
PC5                             -0.004923
PC6                             -0.007954
PC7                             -0.032932
dtype: float64
```

[32]:
```
print(df_PC3_2.mean())
```

```
residueCount                  779.146510
resolution                      1.979356
structureMolecularWeight    98405.916627
crystallizationTempK          293.275799
densityMatthews                 2.249158
```

```
densityPercentSol           44.615448
phValue                      6.784893
PC1                      -2180.737672
PC2                         20.655040
PC3                         -7.229472
PC4                          0.779636
PC5                          0.004272
PC6                          0.006902
PC7                          0.028579
dtype: float64
```

The average of the features when separating the data by its third principal componant shows that the density of a protein in solution (densityPercentSol) is different in two clusters. Following, the density of a protein in crystal (densityMatthews) shows a similar trend. We have previously shown the correlation between the densities in solution and crystal, and we are observing the same distinction with PC3 clustering of the data. The crystal and solution densities for the first and second cluster of PC3 is 3.1, 59.6, and 2.2, 44.6, respectively.

By utilizing PCA, we observe that the features residue count, resolution and molecular weight are tied together within the second and first principal component, while density related features are tied to the third principal component. This implies that one can harness the power of dimensionality reduction techniques to identify the physical characteristics of proteins and distinguish, and potentially predict behaviours of new proteins by looking into several of their features.

6 Non-Linear Data Analyses with Artificial Neural Network Treatment

Previous analyses have shown great promise in deciphering the structural data of proteins. However, using all the features of the data together most of the methods uses functions in a linear fashion and this challenges and restricts the possible highly accurate understanding and predictions of the data. Hence, I wanted to follow a more non linear approach which are Artificial Neural Networks. In this study I want to explore the data and try to pin down the underlying physics to be able to classify proteins by their structural data. One interesting way to achieve this is using unsupervised learning. Unsupervised learning is useful when we do not already have the defining labels for the data and trying to learn the representations of the data which will provide us with the classification of the proteins in this study. Autoencoders, which are a type of neural networks, are often used for unsupervised learning tasks, meaning that the data used to train the autoencoder does not have any labels. Instead, the autoencoder tries to learn the underlying structure of the data without any guidance from an outside source or predefined criteria. Once the autoencoder is trained, it can be used for various classifications of proteins. It is composed of two parts: an encoder and a decoder. The encoder takes the input data and compresses it into a lower-dimensional representation, and the decoder takes this compressed representation and reconstructs the data as closely to the original as possible. This systematic algorithm learns the most important parts of the data and uses it to reconstruct it. Here I apply a simple autoencoder to understand the structural data from structural discovery.

[33]:
```
# this function separates data as features and labels.
# This is not required in the current case as it is unsupervised but
# the function splitting the data requries labels, hence
# I used dummy data as labels to use it later on splitting.
def prepare_xy(dataset, x_label_list, y_label_list):
  x = dataset.loc[:, x_label_list]
  y = dataset.loc[:, y_label_list]
  print('x: {}'.format(x.shape))
  print('y: {}'.format(y.shape))
  return x, y
```

[34]:
```
# the data going into a neural network needs to be renormalized for it to be
# functioning better, meaning a data distributed evenly between negative and
# positive values with a mean around zero, would make multiplying and summing
# up the weights and values much easire, leading to shorter convergance of
# neural network training and easier learning.
def scaler_1(x):
  from sklearn.preprocessing import StandardScaler
  sc = StandardScaler()
  sc.fit(x)
  xs = sc.transform(x)
  return sc, xs
```

[35]:
```
# This function is used to split the data into training and testing.
# This is an important step as I am training the model with part of my data,
# and testing the ability of my model in capturing correct featrues with
# previously unseen data for the neural network.
# I am using 90% training, 10% testing splitting.
# 85% to 15% is also a common way to split, but as I have thousands of data
# points, I would already have enough data points to test the neural network␣
 ↪with.
def splitter_1(x, y, test_size=0.1):
  from sklearn.model_selection import train_test_split
  display(y.apply(pd.value_counts))
  x_train, x_test, y_train, y_test = train_test_split(x, y, test_size =␣
 ↪test_size)
  print('x_train: {}'.format(x_train.shape))
  display(x_train)
  print('x_test: {}'.format(x_test.shape))
  display(x_test)
  print('y_train: {}'.format(y_train.shape))
  display(y_train)
  display(y_train.apply(pd.value_counts))
  print('y_test: {}'.format(y_test.shape))
  display(y_test)
  display(y_test.apply(pd.value_counts))
  return x_train, x_test, y_train, y_test
```

[36]:
```
# Here I build the architecture of my neural net
def build_keras_model(input_dim, output_dim):
  classifier = tf.keras.Sequential()
  # Input layer takes the input data and passes it to hidden layers
  classifier.add(layers.Dense(
      units=(0.6 * input_dim),
      kernel_initializer=tf.initializers.he_uniform(),
      activation=tf.keras.activations.relu,
      input_dim = input_dim
      )
  )
  classifier.add(layers.Dense(
      units=(0.2 * input_dim),
      kernel_initializer=tf.initializers.he_uniform(),
      activation=tf.keras.activations.relu
      )
  )
# The number of nodes in each layer decreases initially and then increases.
# this is to reduce the dimensions as much as possible and try to
# recapitulate the inital data values later
  classifier.add(layers.Dense(
      units=(0.6 * input_dim),
      kernel_initializer=tf.initializers.he_uniform(),
      activation=tf.keras.activations.relu
      )
  )
#  The final layer is the output layer which has a sigmoid function.
# Sigmoid is important here as it give a distribution of values between 0 and 1,
# and these values can be translated back into real values later.
  classifier.add(layers.Dense(
      units=output_dim,
      kernel_initializer=tf.initializers.glorot_uniform(),
      activation=tf.keras.activations.sigmoid
      )
  )
# the last part is the seelction of minimizer and loss function. Adam is a
# common minimizer and MSE is a robust function to check how much the system is
# closer to the original data
  classifier.compile(
      optimizer=tf.keras.optimizers.Adam(),
      loss=tf.keras.losses.MeanSquaredError(),
      metrics=[
              tf.keras.metrics.Accuracy(),
              tf.keras.metrics.BinaryAccuracy(),
              tf.keras.metrics.AUC(),
              tf.keras.metrics.TruePositives(),
              tf.keras.metrics.TrueNegatives(),
              tf.keras.metrics.FalsePositives(),
              tf.keras.metrics.FalseNegatives()
              ]
  )
  return classifier
```

[37]:
```
# this function is to do the fitting of the data on to the model which is the
# neural network architecture built here.
def train_classifier(x_train, x_test, y_train, y_test, keras_model,␣
 ↪train_num=10):
  for count1 in range(0, 10):
    keras_model.fit(x_train, y_train, batch_size = 10, epochs=(train_num - 1),␣
 ↪verbose=0)
    keras_model.fit(x_train, y_train, batch_size = 10, epochs=1,␣
 ↪validation_data=(x_test, y_test), verbose=2)
```

[38]:
```
# this function is used to make predictions on the test data set.
def predict_1(keras_model, x_test):
  y_pred = keras_model.predict(x_test)
  return y_pred
```

[39]:
```
# Here we are preparing the input data and splitting it into train and test
x1, y1 = prepare_xy(
    df_PCA_output,
    [
    'residueCount','resolution','structureMolecularWeight',
    'crystallizationTempK','densityMatthews','densityPercentSol','phValue'
    ],
    ['PC1']
    )
sc, x1s = scaler_1(x1)
x1s = pd.DataFrame(index=x1.index, columns=x1.columns, data=x1s)
x1_train, x1_test, y1_train, y1_test = splitter_1(x1s, y1, 0.1)
```

```
x: (65886, 7)
y: (65886, 1)

               PC1
-69696.566349    9
-40586.367926    7
-86536.188918    6
-86537.168902    5
-86554.198676    4
…             …
-79200.268356    1
-78995.971125    1
-83953.497492    1
-84714.907141    1
```

```
-93262.574191    1

[65705 rows x 1 columns]

x_train: (59297, 7)
             residueCount  resolution  structureMolecularWeight  \
structureId
1LL7            -0.016600   -0.265744                 -0.045554
1FV2            -0.207255    0.591600                 -0.154751
5GSU             0.285271    1.620412                  0.346139
4DFI            -0.417465   -0.608681                 -0.300258
3REH             0.277938    0.591600                  0.339800
…                   …          …                      …
3L5H            -0.135759    2.477755                 -0.101584
4JVR            -0.319693   -0.780150                 -0.227082
2G75             0.064062    0.214368                 -0.010429
5UDV             0.552922    0.797362                  0.315303
4O9C             1.425536   -0.265744                  0.778229

             crystallizationTempK  densityMatthews  densityPercentSol  \
structureId
1LL7                     0.754795        -0.633587          -0.675803
1FV2                     0.206597        -0.165904           0.041208
5GSU                     0.206597         0.018334           0.753205
4DFI                    -0.012683        -1.129614          -1.699674
3REH                    -0.231962        -0.010010           0.238762
…                           …               …                  …
3L5H                     0.754795         4.170789           2.661558
4JVR                    -1.547638        -0.704448          -0.809177
2G75                     0.206597        -0.463521          -0.393009
5UDV                     0.332682        -0.364315          -0.246599
4O9C                     0.425876         0.230917           0.517544

              phValue
structureId
1LL7         0.552108
1FV2         1.327414
5GSU        -0.610851
4DFI         1.327414
3REH        -0.610851
…               …
3L5H        -0.610851
4JVR        -1.386157
2G75         1.327414
5UDV        -0.223198
4O9C         0.552108

[59297 rows x 7 columns]
```

```
x_test: (6589, 7)

             residueCount  resolution  structureMolecularWeight  \
structureId
1Y7A             0.053063   -0.660122                 -0.019047
4V9D            12.294720    1.448943                 14.615002
3EII             0.012732    0.162928                 -0.026963
2Q67            -0.356357    0.248662                 -0.259335
3MJ3            -0.469406    1.620412                 -0.298657
…                    …          …                        …
1RK5            -0.192589   -0.608681                 -0.162419
3RL7            -0.063041    0.248662                 -0.076680
1Q7Q             0.196054    1.620412                  0.092361
1HZT            -0.379578   -1.208822                 -0.273429
4J1G             0.106226    1.088859                  0.063445

             crystallizationTempK  densityMatthews  densityPercentSol  \
structureId
1Y7A                     0.206597         0.755289           0.622840
4V9D                    -0.012683         0.882838           1.116223
3EII                     0.754795        -0.265110          -0.103197
2Q67                     0.754795         3.150391           2.335643
3MJ3                     0.206597         0.726944           0.982849
…                           …                …                  …
1RK5                     0.425876         0.641911           0.884574
3RL7                    -0.451241        -0.831998          -1.054866
1Q7Q                    -1.547638         3.802312           2.552251
1HZT                     0.206597        -0.803653          -1.002719
4J1G                    -0.231962        -0.619415          -0.662766

              phValue
structureId
1Y7A         2.102720
4V9D        -0.223198
3EII        -0.223198
2Q67         0.939761
3MJ3         0.552108
…               …
1RK5        -0.920974
3RL7         0.552108
1Q7Q        -0.843443
1HZT        -0.998504
4J1G         0.164455

[6589 rows x 7 columns]

y_train: (59297, 1)

                       PC1
```

```
structureId
1LL7          -13158.819632
1FV2          -44703.197913
5GSU           99988.557954
4DFI          -86736.370547
3REH           98157.400246
…                     …
3L5H          -29344.776423
4JVR          -65597.913477
2G75           -3011.869117
5UDV           91083.513759
4O9C          224812.153269

[59297 rows x 1 columns]

                PC1
-69696.566349     9
-40586.367926     7
-86536.188918     6
-86537.168902     5
 241431.298559    4
…             …
-14268.240232     1
-382.630995       1
-63564.094675     1
-77513.224733     1
 224812.153269    1

[59144 rows x 1 columns]

y_test: (6589, 1)

                      PC1
structureId
1Y7A         -5.501349e+03
4V9D          4.221809e+06
3EII         -7.788452e+03
2Q67         -7.491483e+04
3MJ3         -8.627429e+04
…                    …
1RK5         -4.691825e+04
3RL7         -2.215034e+04
1Q7Q          2.668109e+04
1HZT         -7.898630e+04
4J1G          1.832764e+04

[6589 rows x 1 columns]

                PC1
-66774.258365     2
```

```
-86554.198676     2
-5501.349088      1
 93348.899293     1
-83709.287793     1
…               …
-2890.129007      1
-44485.310474     1
-83900.786425     1
 132753.140476    1
 18327.640479     1

[6587 rows x 1 columns]
```

[40]:
```
# Summary of the neural net architecture with the number of nodes
# scaled based on the number of input features
keras_model_1 = build_keras_model(x1s.shape[1], x1s.shape[1])
keras_model_1.summary()
```

```
Model: "sequential"
_________________________________________________________________
 Layer (type)                Output Shape              Param #
=================================================================
 dense (Dense)               (None, 4)                 32

 dense_1 (Dense)             (None, 1)                 5

 dense_2 (Dense)             (None, 4)                 8

 dense_3 (Dense)             (None, 7)                 35

=================================================================
Total params: 80
Trainable params: 80
Non-trainable params: 0
_________________________________________________________________
```

[41]:
```
# Training the model, This takes time.
# In the training the loss function value is an important paramater to follow
# as it gives an idea about how close the final representation is to
# the original data. The loss should decrease over multiple iterations (epochs)
train_classifier(
    x1_train, x1_test,
    x1_train, x1_test,
    keras_model_1, train_num=10,
    )
```

```
5930/5930 - 14s - loss: 0.7948 - accuracy: 0.0000e+00 - binary_accuracy:
0.0000e+00 - auc: 0.0000e+00 - true_positives: 52065.0000 - true_negatives:
```

```
0.0000e+00 - false_positives: 0.0000e+00 - false_negatives: 363014.0000 -
val_loss: 0.7329 - val_accuracy: 0.0000e+00 - val_binary_accuracy: 0.0000e+00 -
val_auc: 0.0000e+00 - val_true_positives: 5946.0000 - val_true_negatives:
0.0000e+00 - val_false_positives: 0.0000e+00 - val_false_negatives: 40177.0000 -
14s/epoch - 2ms/step
5930/5930 - 15s - loss: 0.7923 - accuracy: 0.0000e+00 - binary_accuracy:
0.0000e+00 - auc: 0.0000e+00 - true_positives: 51471.0000 - true_negatives:
0.0000e+00 - false_positives: 0.0000e+00 - false_negatives: 363608.0000 -
val_loss: 0.7310 - val_accuracy: 0.0000e+00 - val_binary_accuracy: 0.0000e+00 -
val_auc: 0.0000e+00 - val_true_positives: 5763.0000 - val_true_negatives:
0.0000e+00 - val_false_positives: 0.0000e+00 - val_false_negatives: 40360.0000 -
15s/epoch - 3ms/step
5930/5930 - 14s - loss: 0.7911 - accuracy: 0.0000e+00 - binary_accuracy:
0.0000e+00 - auc: 0.0000e+00 - true_positives: 50301.0000 - true_negatives:
0.0000e+00 - false_positives: 0.0000e+00 - false_negatives: 364778.0000 -
val_loss: 0.7295 - val_accuracy: 0.0000e+00 - val_binary_accuracy: 0.0000e+00 -
val_auc: 0.0000e+00 - val_true_positives: 5870.0000 - val_true_negatives:
0.0000e+00 - val_false_positives: 0.0000e+00 - val_false_negatives: 40253.0000 -
14s/epoch - 2ms/step
5930/5930 - 14s - loss: 0.7905 - accuracy: 0.0000e+00 - binary_accuracy:
0.0000e+00 - auc: 0.0000e+00 - true_positives: 53594.0000 - true_negatives:
0.0000e+00 - false_positives: 0.0000e+00 - false_negatives: 361485.0000 -
val_loss: 0.7284 - val_accuracy: 0.0000e+00 - val_binary_accuracy: 0.0000e+00 -
val_auc: 0.0000e+00 - val_true_positives: 5874.0000 - val_true_negatives:
0.0000e+00 - val_false_positives: 0.0000e+00 - val_false_negatives: 40249.0000 -
14s/epoch - 2ms/step
5930/5930 - 14s - loss: 0.7904 - accuracy: 0.0000e+00 - binary_accuracy:
0.0000e+00 - auc: 0.0000e+00 - true_positives: 53667.0000 - true_negatives:
0.0000e+00 - false_positives: 0.0000e+00 - false_negatives: 361412.0000 -
val_loss: 0.7280 - val_accuracy: 0.0000e+00 - val_binary_accuracy: 0.0000e+00 -
val_auc: 0.0000e+00 - val_true_positives: 6186.0000 - val_true_negatives:
0.0000e+00 - val_false_positives: 0.0000e+00 - val_false_negatives: 39937.0000 -
14s/epoch - 2ms/step
5930/5930 - 14s - loss: 0.7902 - accuracy: 0.0000e+00 - binary_accuracy:
0.0000e+00 - auc: 0.0000e+00 - true_positives: 53915.0000 - true_negatives:
0.0000e+00 - false_positives: 0.0000e+00 - false_negatives: 361164.0000 -
val_loss: 0.7285 - val_accuracy: 0.0000e+00 - val_binary_accuracy: 0.0000e+00 -
val_auc: 0.0000e+00 - val_true_positives: 5853.0000 - val_true_negatives:
0.0000e+00 - val_false_positives: 0.0000e+00 - val_false_negatives: 40270.0000 -
14s/epoch - 2ms/step
5930/5930 - 14s - loss: 0.7900 - accuracy: 0.0000e+00 - binary_accuracy:
0.0000e+00 - auc: 0.0000e+00 - true_positives: 53333.0000 - true_negatives:
0.0000e+00 - false_positives: 0.0000e+00 - false_negatives: 361746.0000 -
val_loss: 0.7275 - val_accuracy: 0.0000e+00 - val_binary_accuracy: 0.0000e+00 -
val_auc: 0.0000e+00 - val_true_positives: 6107.0000 - val_true_negatives:
0.0000e+00 - val_false_positives: 0.0000e+00 - val_false_negatives: 40016.0000 -
14s/epoch - 2ms/step
5930/5930 - 15s - loss: 0.7908 - accuracy: 0.0000e+00 - binary_accuracy:
```

```
0.0000e+00 - auc: 0.0000e+00 - true_positives: 52491.0000 - true_negatives:
0.0000e+00 - false_positives: 0.0000e+00 - false_negatives: 362588.0000 -
val_loss: 0.7289 - val_accuracy: 0.0000e+00 - val_binary_accuracy: 0.0000e+00 -
val_auc: 0.0000e+00 - val_true_positives: 5805.0000 - val_true_negatives:
0.0000e+00 - val_false_positives: 0.0000e+00 - val_false_negatives: 40318.0000 -
15s/epoch - 3ms/step
5930/5930 - 13s - loss: 0.7898 - accuracy: 0.0000e+00 - binary_accuracy:
0.0000e+00 - auc: 0.0000e+00 - true_positives: 54053.0000 - true_negatives:
0.0000e+00 - false_positives: 0.0000e+00 - false_negatives: 361026.0000 -
val_loss: 0.7275 - val_accuracy: 0.0000e+00 - val_binary_accuracy: 0.0000e+00 -
val_auc: 0.0000e+00 - val_true_positives: 6159.0000 - val_true_negatives:
0.0000e+00 - val_false_positives: 0.0000e+00 - val_false_negatives: 39964.0000 -
13s/epoch - 2ms/step
5930/5930 - 13s - loss: 0.7900 - accuracy: 0.0000e+00 - binary_accuracy:
0.0000e+00 - auc: 0.0000e+00 - true_positives: 53496.0000 - true_negatives:
0.0000e+00 - false_positives: 0.0000e+00 - false_negatives: 361583.0000 -
val_loss: 0.7274 - val_accuracy: 0.0000e+00 - val_binary_accuracy: 0.0000e+00 -
val_auc: 0.0000e+00 - val_true_positives: 6186.0000 - val_true_negatives:
0.0000e+00 - val_false_positives: 0.0000e+00 - val_false_negatives: 39937.0000 -
13s/epoch - 2ms/step
```

[42]:
```
# After the model is trained we can make predictions. Here the predictions are␣
 ↪on training set
# meaining the neural network already learned this data and should be very good␣
 ↪at predciting it again.
x1_train_pred = predict_1(keras_model_1, x1_train)
x1_train_pred = pd.DataFrame(index=x1_train.index, columns=x1_train.columns,␣
 ↪data=x1_train_pred)
display(x1_train_pred)
```

```
1854/1854 [==============================] - 3s 2ms/step

             residueCount    resolution  structureMolecularWeight  \
structureId
1LL7         0.000000e+00  0.000000e+00              0.000000e+00
1FV2         0.000000e+00  0.000000e+00              0.000000e+00
5GSU         1.604278e-02  9.999959e-01              4.211403e-03
4DFI         0.000000e+00  0.000000e+00              0.000000e+00
3REH         0.000000e+00  2.045232e-15              0.000000e+00
…                     …             …                         …
3L5H         6.441210e-08  9.997588e-01              3.130737e-10
4JVR         0.000000e+00  0.000000e+00              0.000000e+00
2G75         0.000000e+00  0.000000e+00              0.000000e+00
5UDV         0.000000e+00  0.000000e+00              0.000000e+00
4O9C         0.000000e+00  5.548220e-13              0.000000e+00

             crystallizationTempK  densityMatthews  densityPercentSol  \
structureId
```

```
1LL7                0.000000e+00        0.000000          0.000000
1FV2                0.000000e+00        0.000000          0.000000
5GSU                2.202764e-26        0.999997          0.999996
4DFI                0.000000e+00        0.000000          0.000000
3REH                0.000000e+00        0.040100          0.208307
…                            …             …                 …
3L5H                5.168652e-31        0.999988          0.999988
4JVR                0.000000e+00        0.000000          0.000000
2G75                0.000000e+00        0.000000          0.000000
5UDV                0.000000e+00        0.000000          0.000000
4O9C                0.000000e+00        0.223872          0.585437

                  phValue
structureId
1LL7         0.000000e+00
1FV2         0.000000e+00
5GSU         5.847347e-01
4DFI         0.000000e+00
3REH         3.931682e-24
…                       …
3L5H         1.164974e-02
4JVR         0.000000e+00
2G75         0.000000e+00
5UDV         0.000000e+00
4O9C         2.814206e-21

[59297 rows x 7 columns]
```

[43]:
```
# prediction using test data subset.
x1_test_pred = predict_1(keras_model_1, x1_test)
x1_test_pred = pd.DataFrame(index=x1_test.index, columns=x1_test.columns,␣
 ↪data=x1_test_pred)
display(x1_test_pred)
```

```
206/206 [==============================] - 1s 2ms/step

             residueCount   resolution  structureMolecularWeight  \
structureId
1Y7A         0.000000e+00  3.027744e-13              0.000000e+00
4V9D         9.999892e-01  9.999960e-01              9.997815e-01
3EII         0.000000e+00  0.000000e+00              0.000000e+00
2Q67         8.911152e-04  9.999894e-01              9.137367e-05
3MJ3         6.960497e-07  9.998894e-01              7.240248e-09
…                       …             …                     …
1RK5         0.000000e+00  7.112930e-11              0.000000e+00
3RL7         0.000000e+00  0.000000e+00              0.000000e+00
1Q7Q         1.230201e-05  9.999568e-01              3.205005e-07
1HZT         0.000000e+00  0.000000e+00              0.000000e+00
```

```
4J1G         0.000000e+00  0.000000e+00            0.000000e+00

             crystallizationTempK  densityMatthews  densityPercentSol  \
structureId
1Y7A                 0.000000e+00         0.189679           0.540786
4V9D                 2.726076e-02         0.999985           0.999977
3EII                 0.000000e+00         0.000000           0.000000
2Q67                 1.826831e-27         0.999996           0.999995
3MJ3                 3.972193e-30         0.999991           0.999990
…                             …              …                  …
1RK5                 0.000000e+00         0.605994           0.858229
3RL7                 0.000000e+00         0.000000           0.000000
1Q7Q                 4.653240e-29         0.999994           0.999993
1HZT                 0.000000e+00         0.000000           0.000000
4J1G                 0.000000e+00         0.000000           0.000000

                  phValue
structureId
1Y7A         1.382845e-21
4V9D         2.406809e-01
3EII         0.000000e+00
2Q67         3.154294e-01
3MJ3         2.858829e-02
…                     …
1RK5         8.360880e-19
3RL7         0.000000e+00
1Q7Q         8.153911e-02
1HZT         0.000000e+00
4J1G         0.000000e+00

[6589 rows x 7 columns]
```

[44]:
```
# obtaining real values, or observables by using the final representation
# calculated by the neural network.
x1_train_inverse = pd.DataFrame(index=x1_train.index, columns=x1_train.columns,␣
 ↪data=sc.inverse_transform(x1_train))
x1_train_pred_inverse = pd.DataFrame(index=x1_train_pred.index,␣
 ↪columns=x1_train_pred.columns, data=sc.inverse_transform(x1_train_pred))
x1_test_inverse = pd.DataFrame(index=x1_test.index, columns=x1_test.columns,␣
 ↪data=sc.inverse_transform(x1_test))
x1_test_pred_inverse = pd.DataFrame(index=x1_test_pred.index,␣
 ↪columns=x1_test_pred.columns, data=sc.inverse_transform(x1_test_pred))
```

[45]:
```
# displaying the newly calcualted features.
display(x1_train_inverse)
display(x1_train_pred_inverse)
display(x1_test_inverse)
display(x1_test_pred_inverse)
```

```
             residueCount  resolution  structureMolecularWeight  \
structureId
1LL7                784.0        2.00                  87427.66
1FV2                472.0        2.50                  55884.48
5GSU               1278.0        3.10                 200574.00
4DFI                128.0        1.80                  13852.53
3REH               1266.0        2.50                 198742.88
…                     …           …                       …
3L5H                589.0        3.60                  71242.50
4JVR                288.0        1.70                  34990.44
2G75                916.0        2.28                  97574.06
5UDV               1716.0        2.62                 191666.55
4O9C               3144.0        2.00                 325389.56

             crystallizationTempK  densityMatthews  densityPercentSol  phValue
structureId
1LL7                       298.00             2.23              44.85      7.5
1FV2                       293.00             2.56              52.00      8.5
5GSU                       293.00             2.69              59.10      6.0
4DFI                       291.00             1.88              34.64      8.5
3REH                       289.00             2.67              53.97      6.0
…                             …                …                   …        …
3L5H                       298.00             5.62              78.13      6.0
4JVR                       277.00             2.18              43.52      5.0
2G75                       293.00             2.35              47.67      8.5
5UDV                       294.15             2.42              49.13      6.5
4O9C                       295.00             2.84              56.75      7.5

[59297 rows x 7 columns]

             residueCount  resolution  structureMolecularWeight  \
structureId
1LL7           811.164795    2.154981             100586.515625
1FV2           811.164795    2.154981             100586.515625
5GSU           837.418152    2.738175             101803.046875
4DFI           811.164795    2.154981             100586.515625
3REH           811.164795    2.154981             100586.515625
…                     …           …                       …
3L5H           811.164917    2.738037             100586.515625
4JVR           811.164795    2.154981             100586.515625
2G75           811.164795    2.154981             100586.515625
5UDV           811.164795    2.154981             100586.515625
4O9C           811.164795    2.154981             100586.515625

             crystallizationTempK  densityMatthews  densityPercentSol  \
structureId
```

```
1LL7                   291.115662         2.677063          51.589073
1FV2                   291.115662         2.677063          51.589073
5GSU                   291.115662         3.382668          61.560989
4DFI                   291.115662         2.677063          51.589073
3REH                   291.115662         2.705358          53.666302
…                           …              …                 …
3L5H                   291.115662         3.382662          61.560902
4JVR                   291.115662         2.677063          51.589073
2G75                   291.115662         2.677063          51.589073
5UDV                   291.115662         2.677063          51.589073
4O9C                   291.115662         2.835029          57.427021

              phValue
structureId
1LL7         6.787884
1FV2         6.787884
5GSU         7.542082
4DFI         6.787884
3REH         6.787884
…               …
3L5H         6.802910
4JVR         6.787884
2G75         6.787884
5UDV         6.787884
4O9C         6.787884

[59297 rows x 7 columns]
             residueCount  resolution  structureMolecularWeight  \
structureId
1Y7A                898.0        1.77                  95084.64
4V9D              20931.0        3.00                4322348.00
3EII                832.0        2.25                  92797.85
2Q67                228.0        2.30                  25673.71
3MJ3                 43.0        3.10                  14315.06
…                     …         …                       …
1RK5                496.0        1.80                  53669.27
3RL7                708.0        2.30                  78436.41
1Q7Q               1132.0        3.10                 127266.30
1HZT                190.0        1.45                  21602.38
4J1G                985.0        2.79                 118913.50

             crystallizationTempK  densityMatthews  densityPercentSol  phValue
structureId
1Y7A                        293.0             3.21              57.80      9.5
4V9D                        291.0             3.30              62.72      6.5
3EII                        298.0             2.49              50.56      6.5
2Q67                        298.0             4.90              74.88      8.0
```

```
3MJ3                        293.0            3.19              61.39      7.5
…                           …             …                 …      …
1RK5                        295.0            3.13              60.41      5.6
3RL7                        287.0            2.09              41.07      7.5
1Q7Q                        277.0            5.36              77.04      5.7
1HZT                        293.0            2.11              41.59      5.5
4J1G                        289.0            2.24              44.98      7.0

[6589 rows x 7 columns]
             residueCount  resolution  structureMolecularWeight  \
structureId
1Y7A           811.164795    2.154981             100586.515625
4V9D          2447.608398    2.738176             389388.375000
3EII           811.164795    2.154981             100586.515625
2Q67           812.623047    2.738172             100612.914062
3MJ3           811.165894    2.738113             100586.515625
…                   …          …                      …
1RK5           811.164795    2.154981             100586.515625
3RL7           811.164795    2.154981             100586.515625
1Q7Q           811.184937    2.738153             100586.609375
1HZT           811.164795    2.154981             100586.515625
4J1G           811.164795    2.154981             100586.515625

             crystallizationTempK  densityMatthews  densityPercentSol  \
structureId
1Y7A                   291.115662         2.810902          56.981762
4V9D                   291.364319         3.382659          61.560799
3EII                   291.115662         2.677063          51.589073
2Q67                   291.115662         3.382667          61.560978
3MJ3                   291.115662         3.382664          61.560928
…                           …             …                 …
1RK5                   291.115662         3.104656          60.147289
3RL7                   291.115662         2.677063          51.589073
1Q7Q                   291.115662         3.382665          61.560951
1HZT                   291.115662         2.677063          51.589073
4J1G                   291.115662         2.677063          51.589073

              phValue
structureId
1Y7A         6.787884
4V9D         7.098317
3EII         6.787884
2Q67         7.194729
3MJ3         6.824757
…               …
1RK5         6.787884
3RL7         6.787884
```

```
1Q7Q         6.893054
1HZT         6.787884
4J1G         6.787884

[6589 rows x 7 columns]
```

```
[46]: # reindexing and relabeling for analyses in the next part
x1_train_inverse.reset_index(inplace=True)
x1_train_inverse['label'] = 'train'
x1_train_pred_inverse.reset_index(inplace=True)
x1_train_pred_inverse['label'] = 'train_pred'
x1_test_inverse.reset_index(inplace=True)
x1_test_inverse['label'] = 'test'
x1_test_pred_inverse.reset_index(inplace=True)
x1_test_pred_inverse['label'] = 'test_pred'
```

```
[47]: df_train_final = pd.concat([x1_train_inverse, x1_train_pred_inverse])
df_train_final.reset_index(inplace=True)
df_test_final = pd.concat([x1_test_inverse, x1_test_pred_inverse])
df_test_final.reset_index(inplace=True)
```

```
[48]: display(df_train_final)
display(df_test_final)
```

```
        index structureId  residueCount  resolution  structureMolecularWeight  \
0           0        1LL7    784.000000    2.000000              87427.660000
1           1        1FV2    472.000000    2.500000              55884.480000
2           2        5GSU   1278.000000    3.100000             200574.000000
3           3        4DFI    128.000000    1.800000              13852.530000
4           4        3REH   1266.000000    2.500000             198742.880000
…           …           …             …           …                         …
118589  59292        3L5H    811.164917    2.738037             100586.515625
118590  59293        4JVR    811.164795    2.154981             100586.515625
118591  59294        2G75    811.164795    2.154981             100586.515625
118592  59295        5UDV    811.164795    2.154981             100586.515625
118593  59296        4O9C    811.164795    2.154981             100586.515625

        crystallizationTempK  densityMatthews  densityPercentSol   phValue  \
0                 298.000000         2.230000          44.850000  7.500000
1                 293.000000         2.560000          52.000000  8.500000
2                 293.000000         2.690000          59.100000  6.000000
3                 291.000000         1.880000          34.640000  8.500000
4                 289.000000         2.670000          53.970000  6.000000
…                          …                …                  …         …
118589            291.115662         3.382662          61.560902  6.802910
118590            291.115662         2.677063          51.589073  6.787884
118591            291.115662         2.677063          51.589073  6.787884
118592            291.115662         2.677063          51.589073  6.787884
```

```
118593           291.115662         2.835029          57.427021  6.787884

             label
0            train
1            train
2            train
3            train
4            train
…            …
118589  train_pred
118590  train_pred
118591  train_pred
118592  train_pred
118593  train_pred

[118594 rows x 10 columns]
       index structureId  residueCount  resolution  structureMolecularWeight  \
0          0        1Y7A    898.000000    1.770000              9.508464e+04
1          1        4V9D  20931.000000    3.000000              4.322348e+06
2          2        3EII    832.000000    2.250000              9.279785e+04
3          3        2Q67    228.000000    2.300000              2.567371e+04
4          4        3MJ3     43.000000    3.100000              1.431506e+04
…        …          …             …          …                         …
13173   6584        1RK5    811.164795    2.154981              1.005865e+05
13174   6585        3RL7    811.164795    2.154981              1.005865e+05
13175   6586        1Q7Q    811.184937    2.738153              1.005866e+05
13176   6587        1HZT    811.164795    2.154981              1.005865e+05
13177   6588        4J1G    811.164795    2.154981              1.005865e+05

       crystallizationTempK  densityMatthews  densityPercentSol   phValue  \
0                293.000000         3.210000          57.800000  9.500000
1                291.000000         3.300000          62.720000  6.500000
2                298.000000         2.490000          50.560000  6.500000
3                298.000000         4.900000          74.880000  8.000000
4                293.000000         3.190000          61.390000  7.500000
…                       …              …                  …        …
13173            291.115662         3.104656          60.147289  6.787884
13174            291.115662         2.677063          51.589073  6.787884
13175            291.115662         3.382665          61.560951  6.893054
13176            291.115662         2.677063          51.589073  6.787884
13177            291.115662         2.677063          51.589073  6.787884

           label
0           test
1           test
2           test
3           test
```

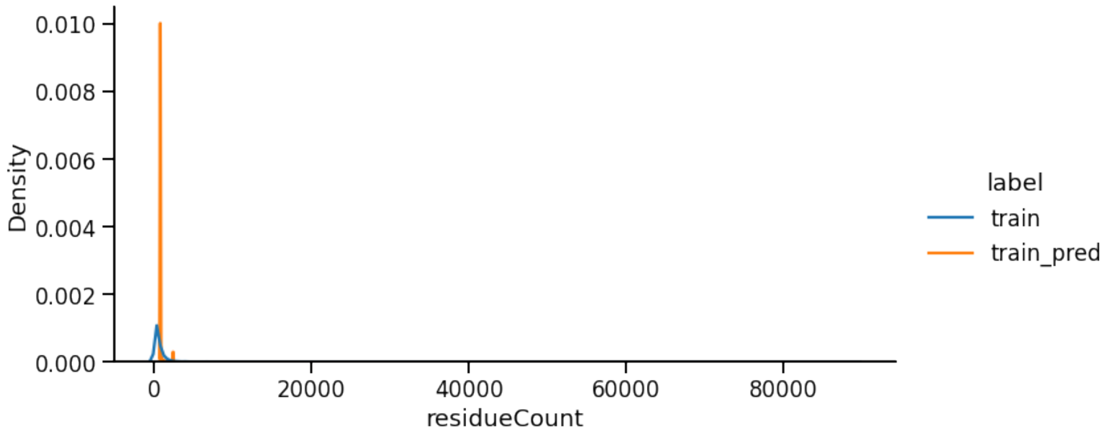
```
4           test
…           …
13173   test_pred
13174   test_pred
13175   test_pred
13176   test_pred
13177   test_pred

[13178 rows x 10 columns]
```

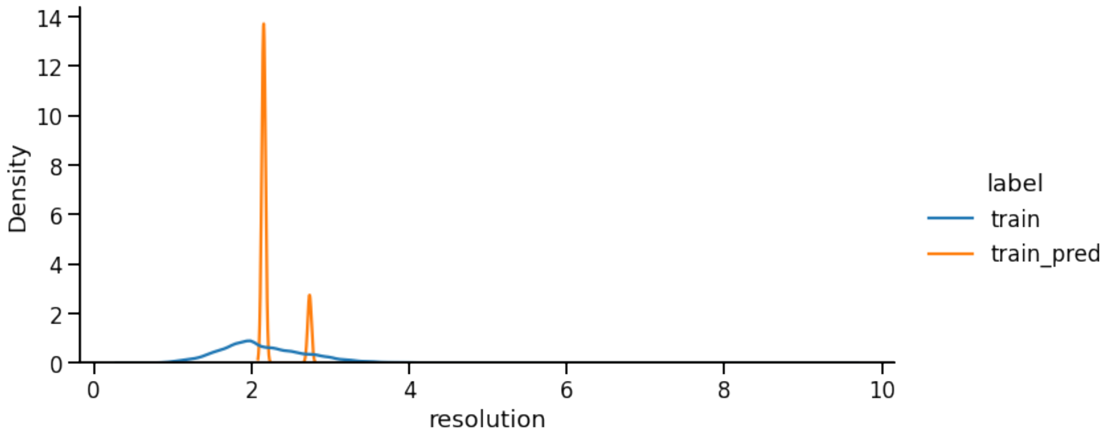
After the training of the neural net is completed, I looked at the predictions of the network based on the training data subset and compared it to the original values. I do it by plotting their distributions and also comparing the means of the data (original vs prediction). The mean values show that the neural network can learn the hidden features of the data well enough to make predictions very close to original values. However, when the distributions of each feature is inspected we can recognize that neural network learned important features that are already closer to the mean values of the original data (peak of the distributions of blue curves), meaning the orange curve (distribution of predictions) have peak or peaks that are closer to the peaks of the original data. This is an interesting observation as the neural network show more than one peak for most of the features, implying that there might be two separate clusters of proteins in the data set.

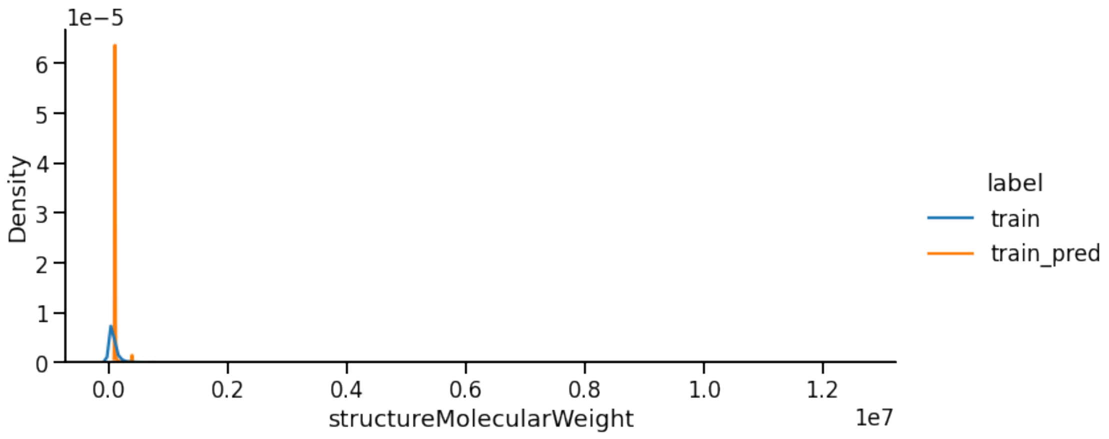
[49]:
```python
for feature in [
    'residueCount','resolution','structureMolecularWeight',
    'crystallizationTempK','densityMatthews','densityPercentSol','phValue'
    ]:
  sns.displot(
      data=df_train_final,
      x=feature,
      hue='label',
      kind='kde',
      common_norm=False,
      aspect=2,
    )
  print(
      '{} means for training data, original:{:.2f} <-> prediction:{:.2f}'.
 ↪format(
          feature,
          df_train_final[df_train_final['label'] == 'train'][feature].mean(),
          df_train_final[df_train_final['label'] == 'train_pred'][feature].
 ↪mean()
      )
  )
```

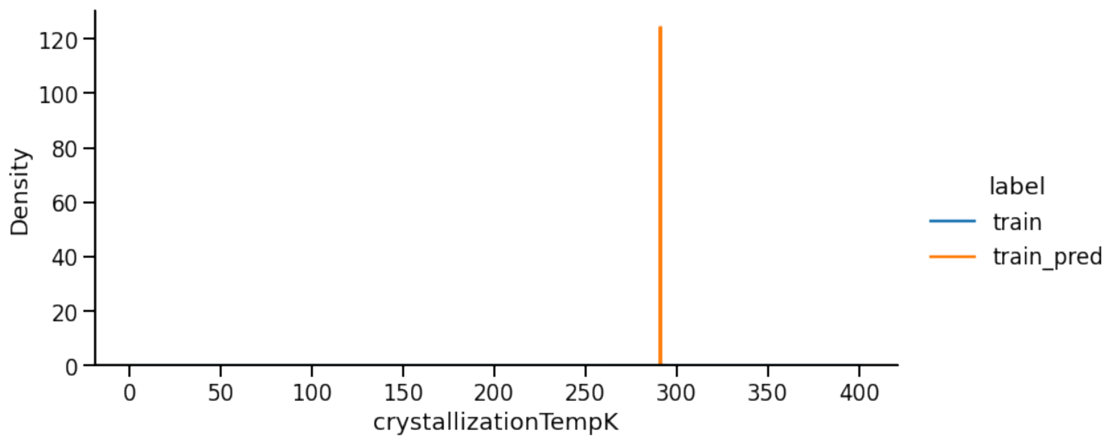
```
residueCount means for training data, original:812.90 <-> prediction:896.42
resolution means for training data, original:2.16 <-> prediction:2.25
structureMolecularWeight means for training data, original:100858.02 <->
prediction:112630.61
crystallizationTempK means for training data, original:291.09 <->
```

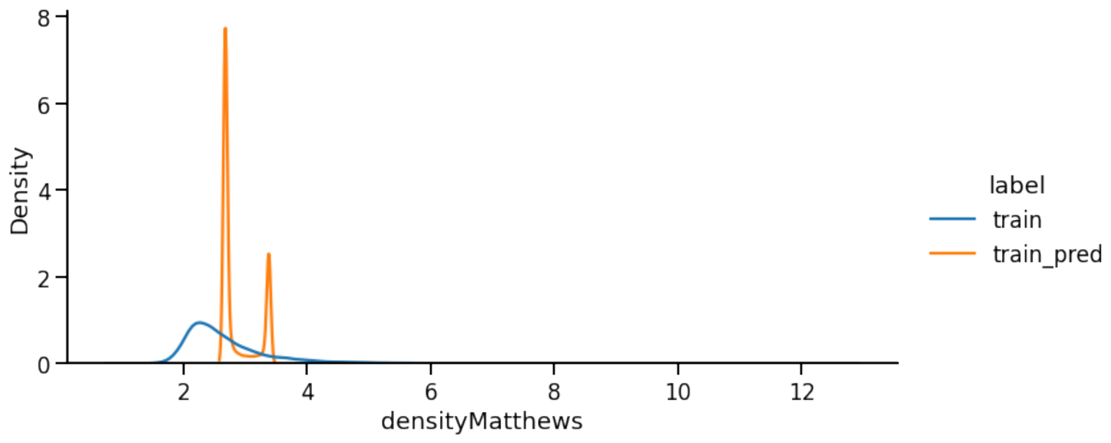
```
prediction:291.12
densityMatthews means for training data, original:2.68 <-> prediction:2.87
densityPercentSol means for training data, original:51.58 <-> prediction:54.79
phValue means for training data, original:6.79 <-> prediction:6.87
```

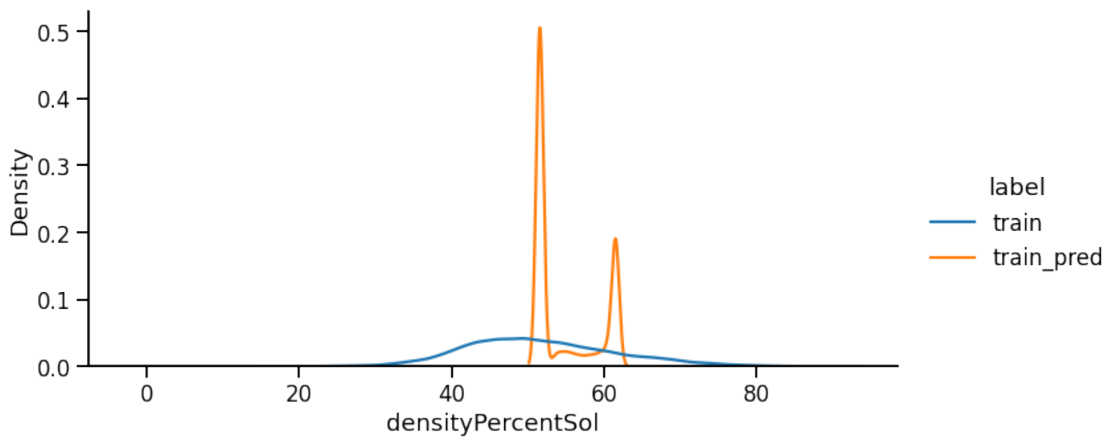


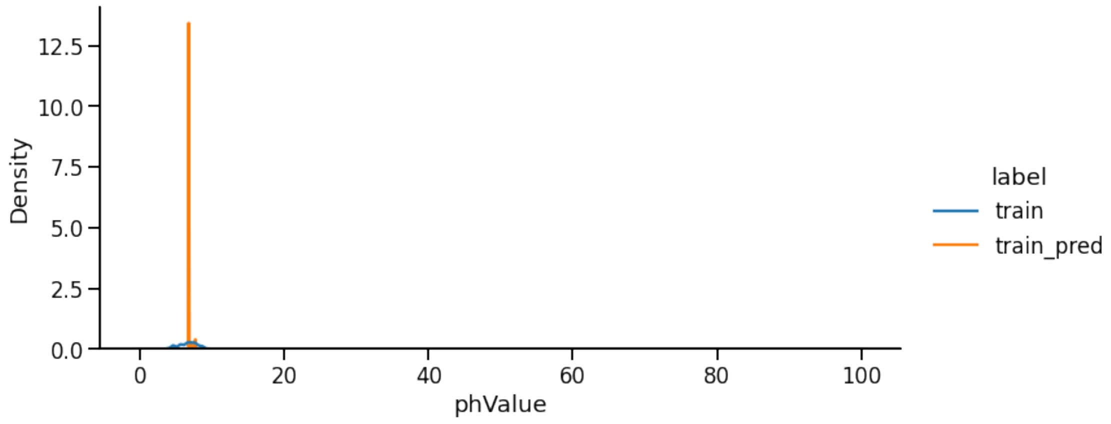





Density
crystallizationTempK
label
train
train_pred


Density
densityMatthews
label
train
train_pred

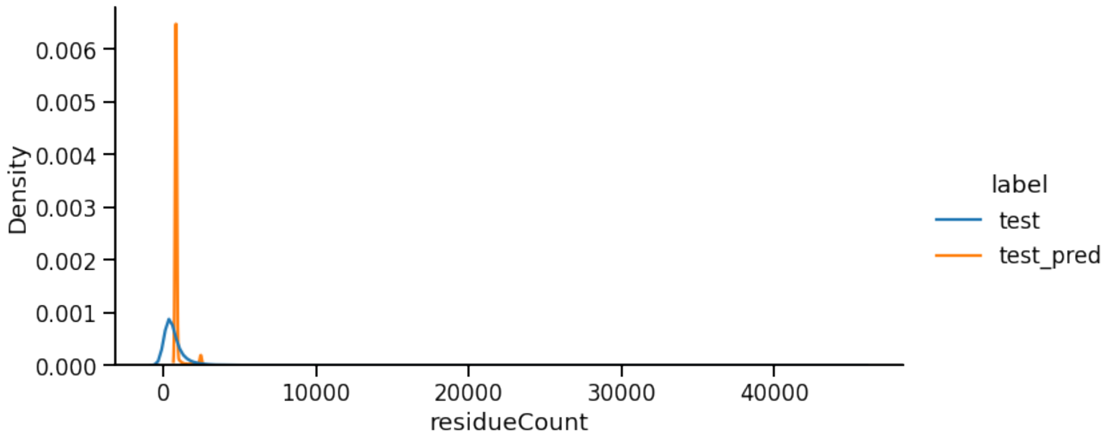

Density
densityPercentSol
label
train
train_pred

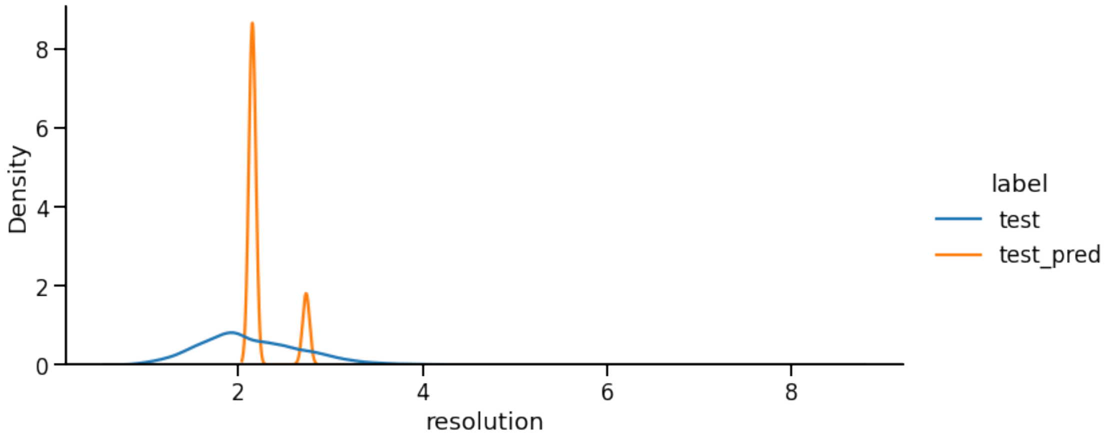


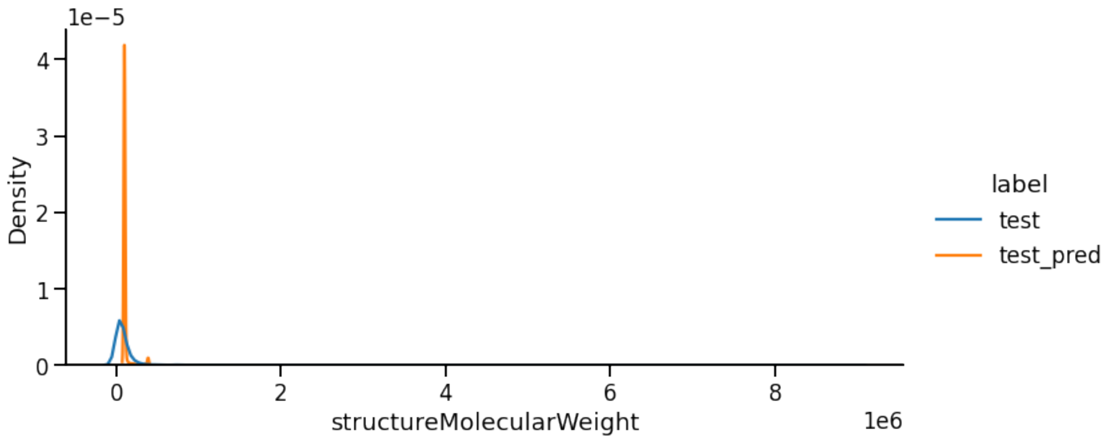
The same analyses applied on training data is subjected on the testing subset. This is very curcial as this is data which is completely new to the neural network (unseen) data. The results show that, we still observe a similar trend seen with the training set as the predictions are close to the original values within ~5% deviation.

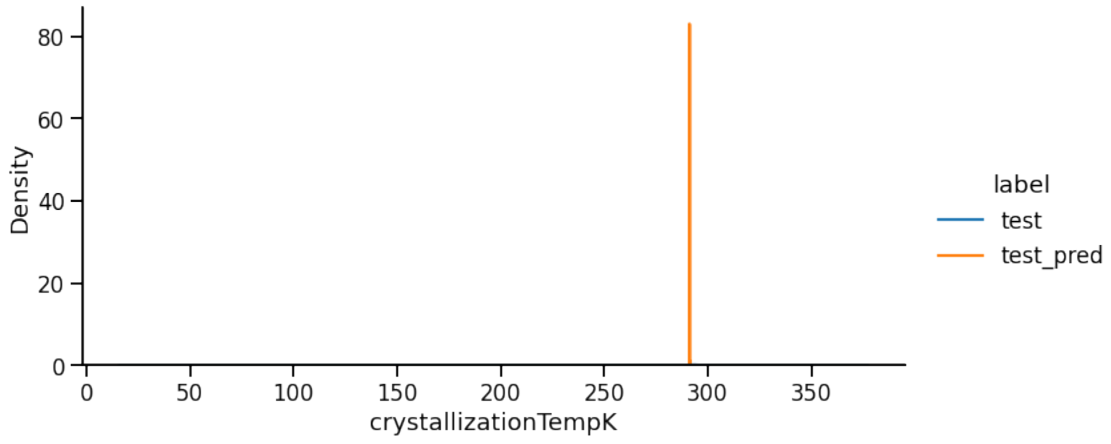
[50]:
```python
for feature in [
    'residueCount','resolution','structureMolecularWeight',
    'crystallizationTempK','densityMatthews','densityPercentSol','phValue'
    ]:
  sns.displot(
      data=df_test_final,
      x=feature,
      hue='label',
      kind='kde',
      common_norm=False,
      aspect=2,
    )
  print(
      '{} means for test data, original:{:.2f} <-> prediction:{:.2f}'.format(
          feature,
          df_test_final[df_test_final['label'] == 'test'][feature].mean(),
          df_test_final[df_test_final['label'] == 'test_pred'][feature].mean()
      )
    )
```

```
residueCount means for test data, original:795.59 <-> prediction:897.36
resolution means for test data, original:2.15 <-> prediction:2.26
structureMolecularWeight means for test data, original:98143.13 <->
prediction:112591.51
crystallizationTempK means for test data, original:291.31 <-> prediction:291.12
densityMatthews means for test data, original:2.68 <-> prediction:2.88
densityPercentSol means for test data, original:51.65 <-> prediction:54.89
phValue means for test data, original:6.80 <-> prediction:6.87
```

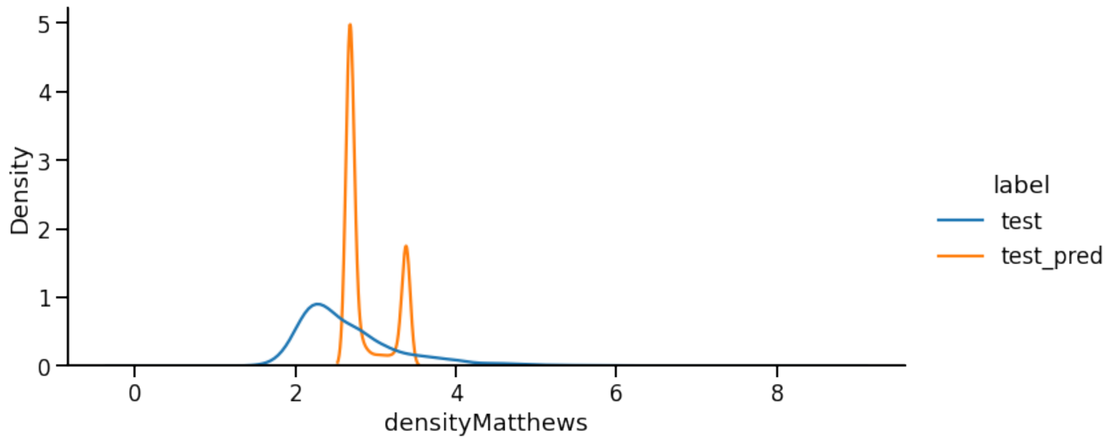

0.006
0.005
0.004
0.003
0.002
0.001
0.000
Density
0
10000
20000
30000
40000
residueCount
label
test
test_pred


8
6
4
2
0
Density
2
4
6
8
resolution
label
test
test_pred

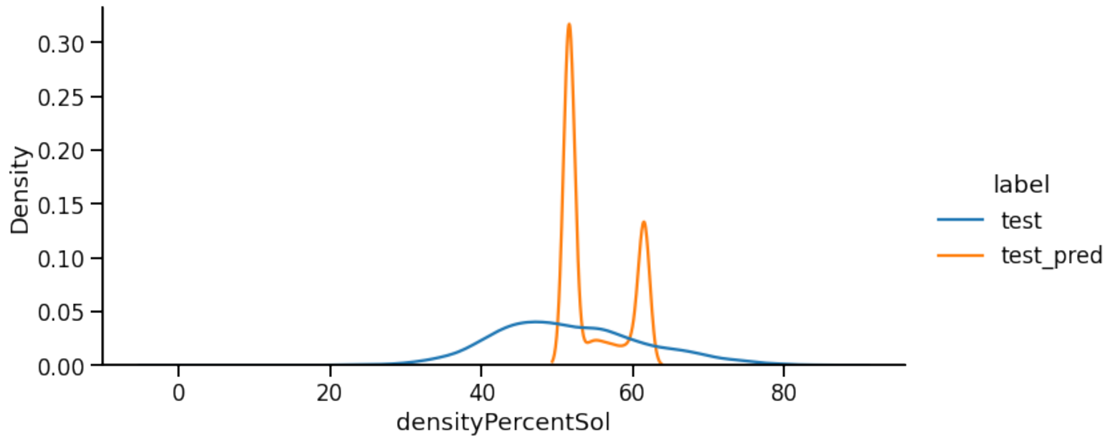

1e−5
4
3
2
1
0
Density
0
2
4
6
8
structureMolecularWeight
1e6
label
test
test_pred



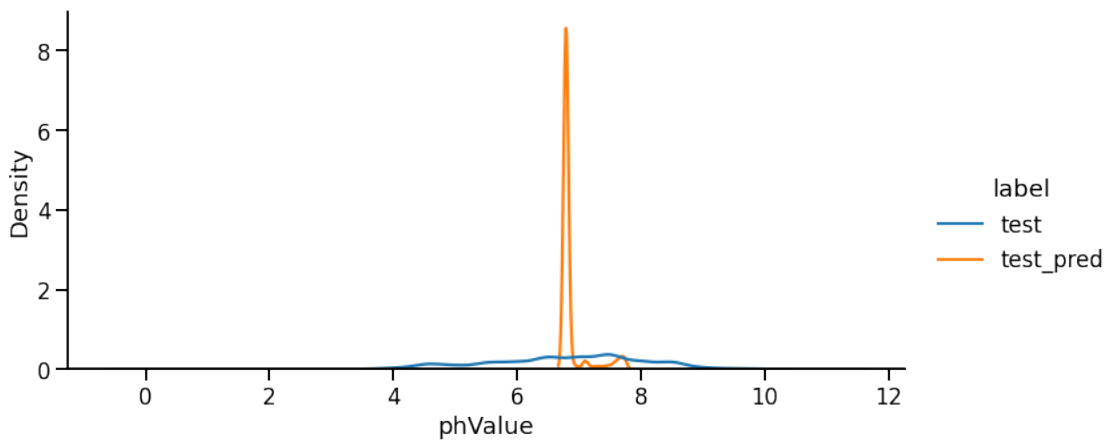
Density
80
60
40
20
0
0
50
100
150
200
250
300
350
crystallizationTempK
label
test
test_pred



Density
5
4
3
2
1
0
0
2
4
6
8
densityMatthews
label
test
test_pred



Density
0.30
0.25
0.20
0.15
0.10
0.05
0.00
0
20
40
60
80
densityPercentSol
label
test
test_pred



Overall the neural network treatment was successful and it captured the essence of the structural protein features strong enough to make predictions not so far from the originals. However one drawback seen from distributions is that predictions are not as diverse as the original data, meaning predictions are mostly centered on one or two regions whereas original data points are distributed across multiple values for each feature. Besides the drawback neural network was able to identify multiple classes which can not be easily comprehended from the distribution of original values. This is the strongest achievement of the autoencoder as it captures the fundamental details that are missed by human (by human observation). On the other hand, when the computational cost is considered the overall enhancement in classification compared to PCA is minimal. While for the current data set this might be true but, considering only 7 features in structural protein data, when the number of features are increased several fold, the power of autoencoders will shine more as the first two components of PCA could become very convoluted and several more components should be considered and additional techniques should be incorporated to further understand the data.

7 Conclusion

Through my analysis of structural discovery protein data, we were able to utilize both machine learning, PCA and neural network techniques to gain new insights into several properties of the proteins. This study highlights the challenges of achieving results that resemble natural phenomena by comparing solution densities to crystal densities. By using machine learning techniques (k-means clustering, hierarchical clustering, DBSCAN) these results obtained show that only 26% of the experimental data points display naturally occurring behavior that captures the correct underlying biological fundamentals. Thus, I used PCA technique to better understand the data. PCA allowed me to identify key factors driving variation in the dataset and provided a simplified view of the underlying patterns and relationships. PCA analyses showed that the first three principal components can distinguish key protein features from each other and enabled me to cluster the protein labels based on these differences.

In addition, by using a non-linear approach like neural network, I was able to accurately distinguish input features, highlighting its potential for learning complex patterns in protein structural discovery data. The results showed that the autoencoder learned the hidden characteristics of protein structural features and was able to reconstruct the features accurately. When compared to the distributions and the means of the original data, the features that were reconstructed from the autoencoder showed high overlap and indicated the existence of two separate clusters (multiple peaks in the distribution) of proteins in the dataset. This observation is intriguing as for future investigations to determine if there are indeed distinct groups of proteins provided their structural features. Overall, the results demonstrate the potential of both PCA and neural networks in analyzing complex protein data, and the insights gained from these techniques can provide valuable information for further research in the field.

8 References

- "Structural Protein Sequences." n.d. https://www.kaggle.com/datasets/shahir/protein-data-set.
- Warren, Bertram Eugene. 1990. X-Ray Diffraction. Courier Corporation.
- Whittig, L. D., and W. R. Allardice. 1986. "X-Ray Diffraction Techniques." Methods of Soil Analysis: Part 1 Physical and Mineralogical Methods 5: 331362.
- Fausett, L. V. (2006). Fundamentals of neural networks: architectures, algorithms and applications. Pearson Education India.
- Haykin, S. (2009). Neural networks and learning machines, 3/E. Pearson Education India.
- SKLEARN.DECOMPOSITION.PCA. scikit. (n.d.). Retrieved February 28, 2023, from https://scikit-learn.org/stable/modules/generated/sklearn.decomposition.PCA.html