Part-03-EDA-&-Feature-Scaling

March 9, 2021

[1]:
```
# magic function
%matplotlib inline

# Importing libraries
import os
import pandas as pd
import numpy as np

import matplotlib.pyplot as plt
from matplotlib.colors import ListedColormap
import seaborn as sns

from scipy import sparse
from sklearn import decomposition
from sklearn.preprocessing import Normalizer, MinMaxScaler, OrdinalEncoder

# Hiding warnings during display of plots
import warnings
warnings.filterwarnings('ignore')
```

[2]:
```
data = pd.read_csv("df_mature_mirna_sequences_features.csv")
data.head()
```

[2]:

	A	C	G	U	AA	AC	AG	AU	CA	CC	…	UUGU	UUUA	UUUC	UUUG	UUUU	\
0	5	0	8	9	0	0	4	1	0	0	…	1	0	0	0	0	
1	5	6	1	9	1	2	0	2	1	0	…	0	0	1	0	0	
2	3	9	3	7	0	1	2	0	1	3	…	0	0	1	0	0	
3	3	0	10	9	0	0	3	0	0	0	…	1	0	0	0	0	
4	5	10	1	6	1	3	0	1	1	4	…	0	0	0	0	0	

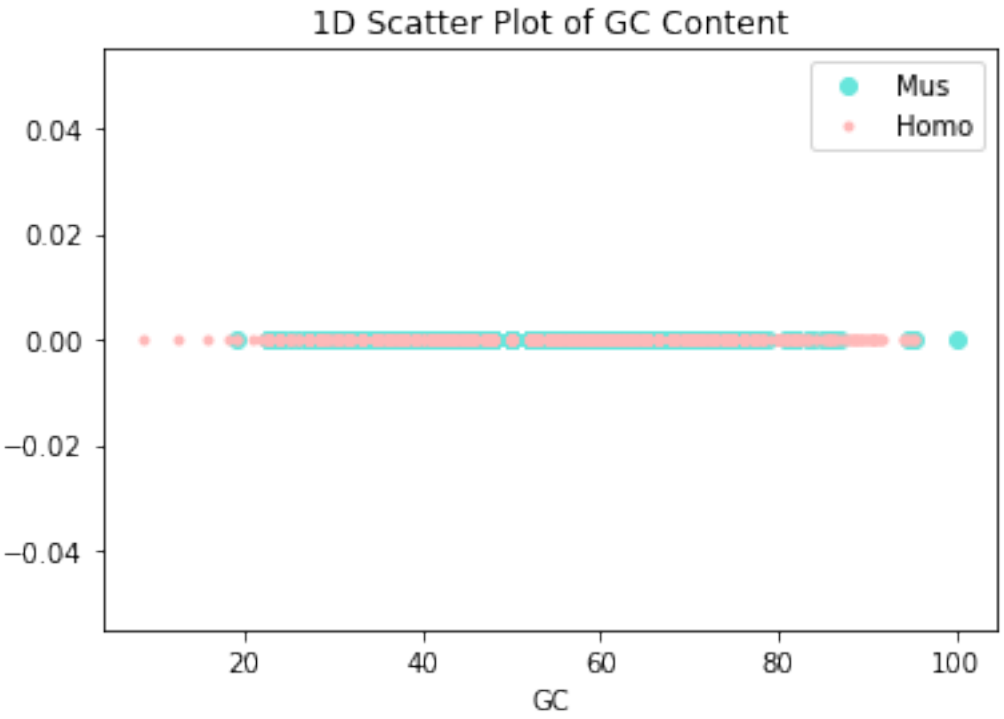
	x_axis	y_axis	z_axis	gc_content	Species
0	4	-12	6	36.363636	Homo sapiens
1	-9	1	7	33.333333	Homo sapiens
2	-10	2	-2	54.545455	Homo sapiens
3	4	-16	2	45.454545	Homo sapiens
4	-10	8	0	50.000000	Homo sapiens

[5 rows x 345 columns]

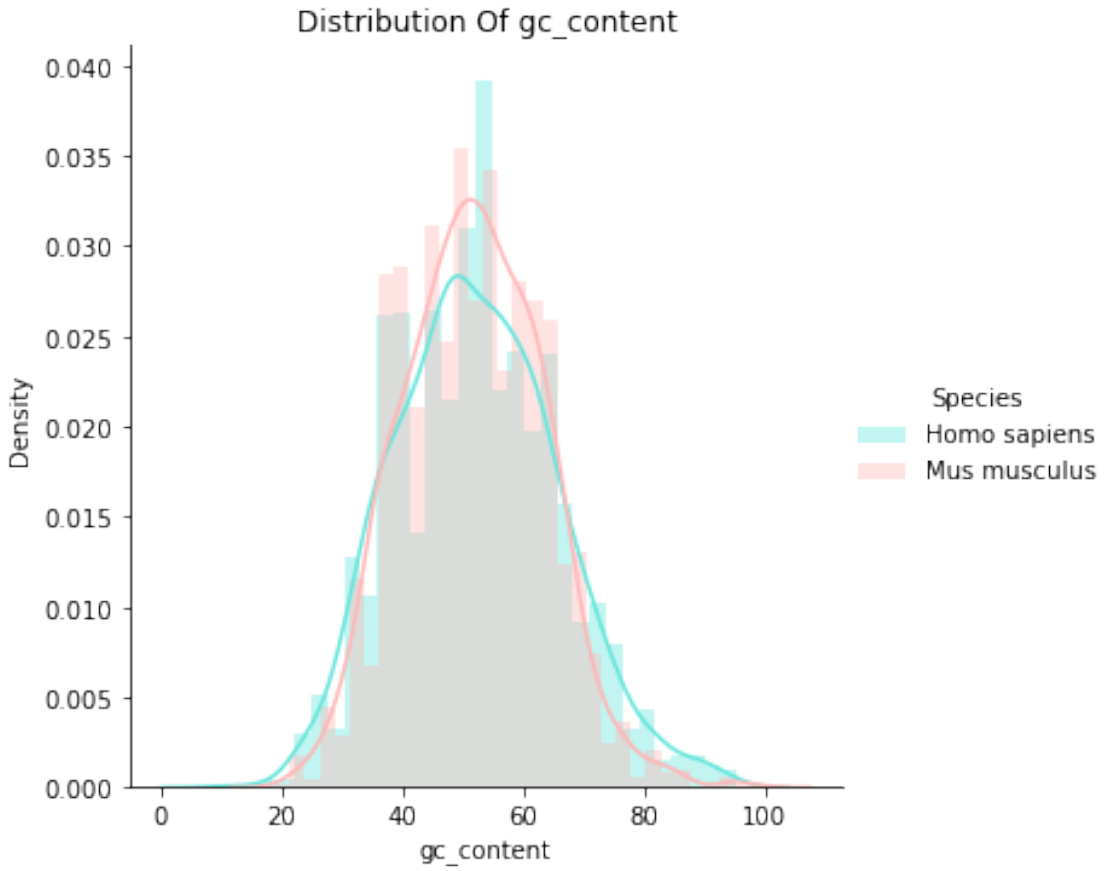
1 Exploratory Data Analysis

1.1 GC Content

[3]:
```
mus = data[data['Species'] == 'Mus musculus']
homo = data[data['Species'] == 'Homo sapiens']

gc_content = data.gc_content

plt.plot(mus['gc_content'],
         np.zeros_like(mus['gc_content']),'o',
         color='#67e6dc',
         label="Mus", markersize=6)
plt.plot(homo['gc_content'],
         np.zeros_like(homo['gc_content']),'o',
         color='#ffb8b8',
         label="Homo", markersize=3)

plt.legend()
plt.title('1D Scatter Plot of GC Content')
plt.xlabel('GC')
plt.show()
```

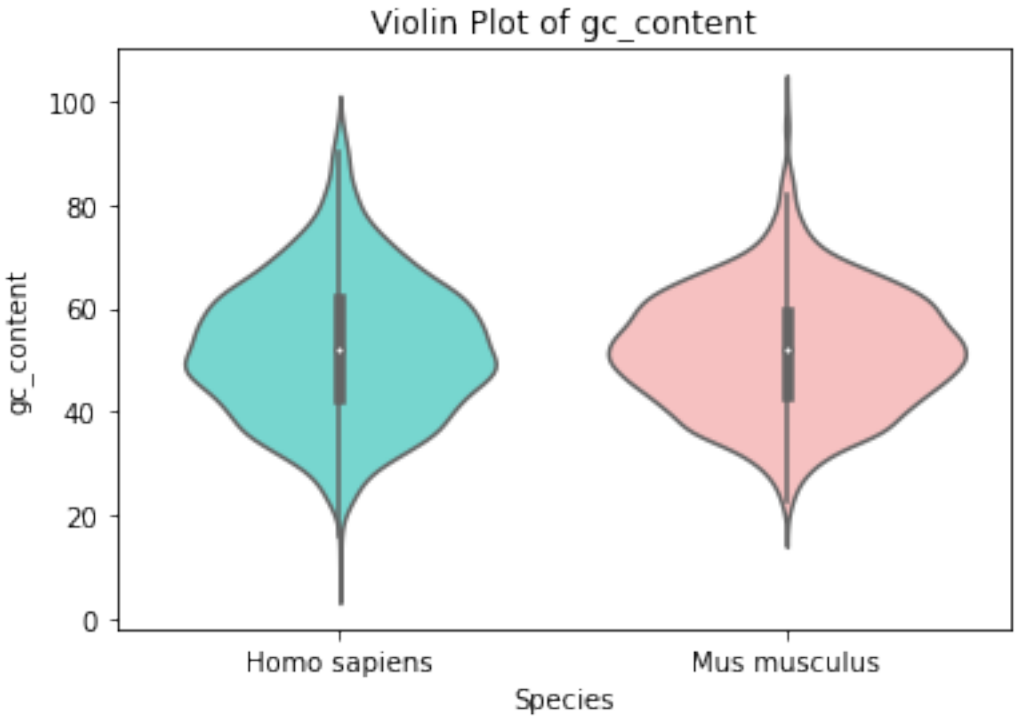


[4]:
```
sns.FacetGrid(data, hue="Species",
              palette=['#67e6dc', '#ffb8b8'],
              size=5) \
   .map(sns.distplot, "gc_content") \
   .add_legend()

plt.title("Distribution Of gc_content")
plt.xlabel("gc_content")
plt.ylabel("Density")
plt.show()
```



[5]:
```
ax = sns.violinplot(x="Species", y="gc_content",
                    data=data,
                    palette=['#67e6dc', '#ffb8b8'],
                    scale="area")

plt.title("Violin Plot of gc_content")
plt.xlabel("Species")
plt.ylabel("gc_content")
```

```
plt.show()
```

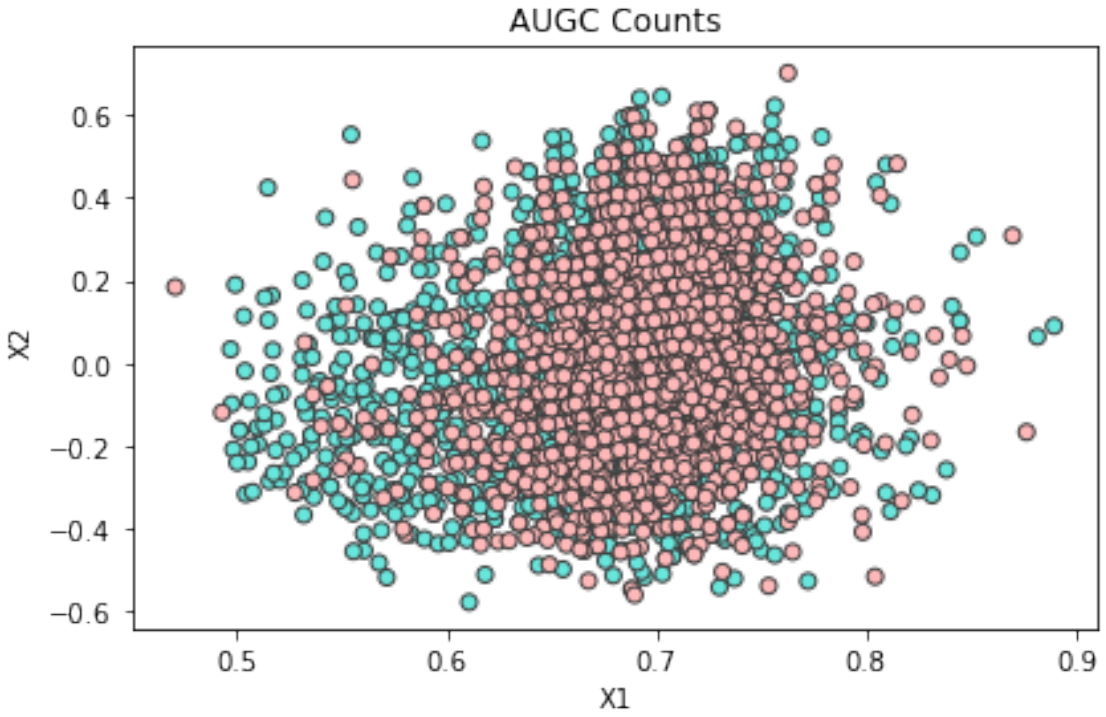


[6]:
```
y = np.array(data['Species'])
y = (OrdinalEncoder().fit_transform(y.reshape(-1, 1)))
y.shape

X = data.drop(['Species'], axis=1)
X = MinMaxScaler().fit_transform(X)
```

1.2 AUGC - Monomers

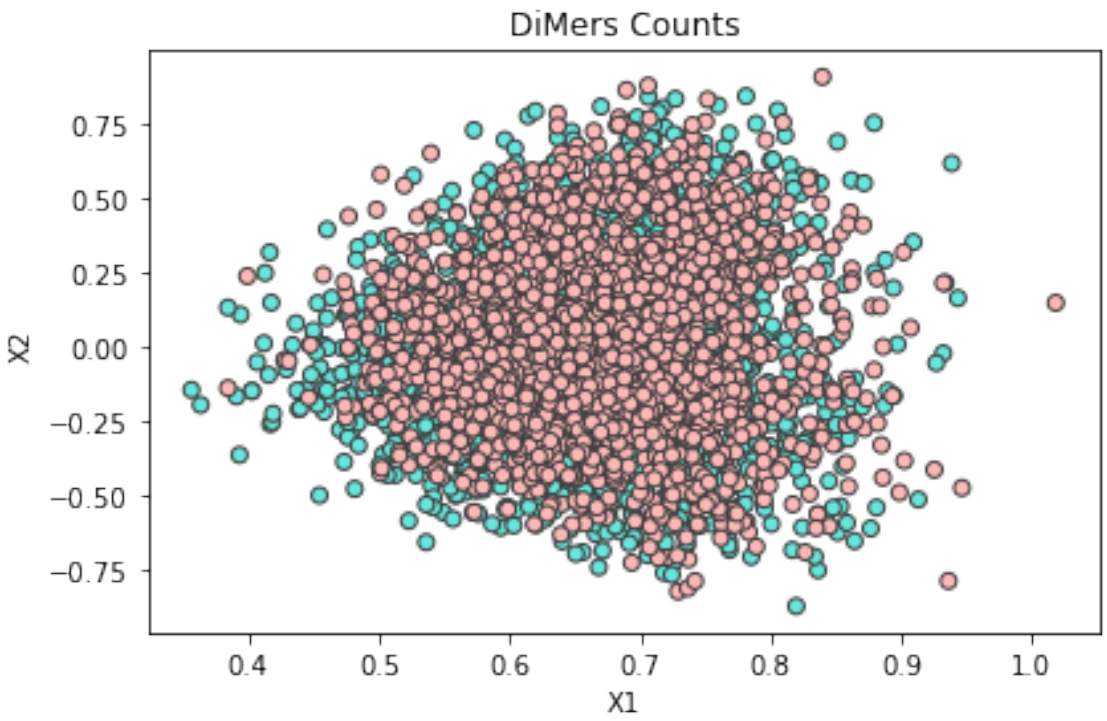
[7]:
```
atgc_count = X[:, 0:4]

atgc_count = decomposition.TruncatedSVD(n_components=2).
 ↪fit_transform(atgc_count)

binaryThemeDark = ListedColormap(['#67e6dc', '#ffb8b8'])
plt.scatter(atgc_count[:,0], atgc_count[:,1],
            c=y, cmap=binaryThemeDark,
            edgecolor='#3d3d3d', linewidth=1)
plt.xlabel('X1')
plt.ylabel('X2')
plt.title('AUGC Counts')
```

```
plt.tight_layout()
plt.savefig("AUGC-Counts",dpi=300)
plt.show()
```

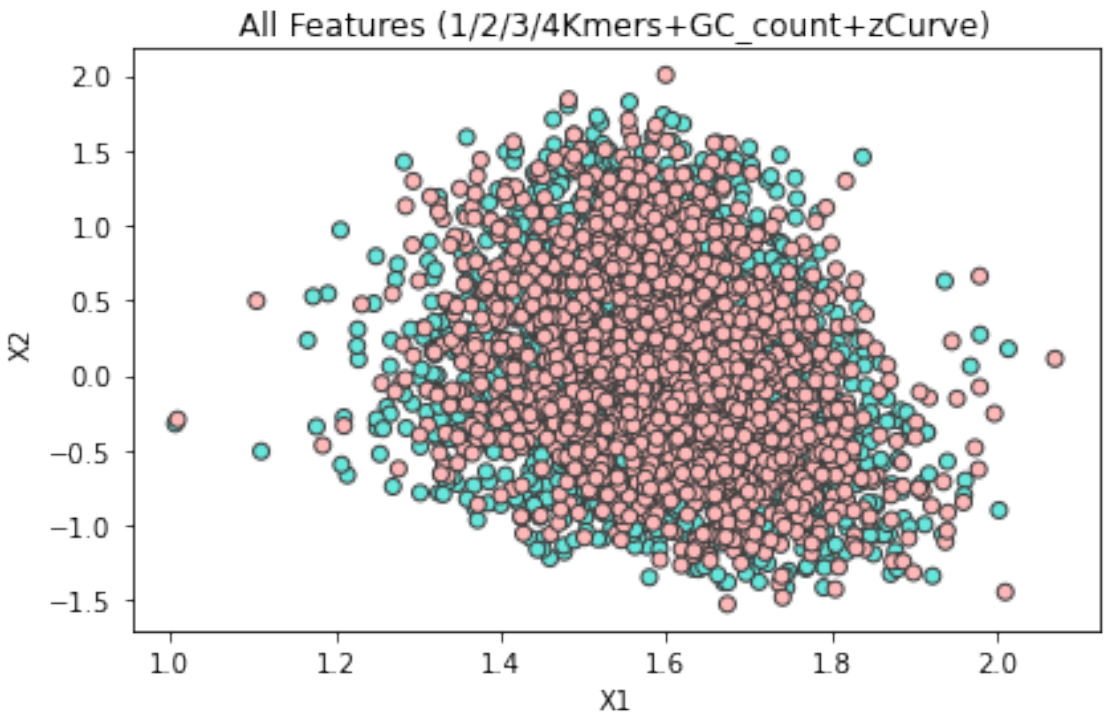


1.3 AUGC - DiMers

[8]:
```
two_mers = (X[:, 4:20])

two_mers = decomposition.TruncatedSVD(n_components=2).fit_transform(two_mers)

binaryThemeDark = ListedColormap(['#67e6dc', '#ffb8b8'])
plt.scatter(two_mers[:,0], two_mers[:,1],
            c=y, cmap=binaryThemeDark,
            edgecolor='#3d3d3d', linewidth=1)
plt.xlabel('X1')
plt.ylabel('X2')
plt.title('DiMers Counts')
plt.tight_layout()
plt.savefig("two_mers_counts",dpi=300)
plt.show()
```



[9]:
```
X_reduce = decomposition.TruncatedSVD(n_components=2).fit_transform(X)

binaryThemeDark = ListedColormap(['#67e6dc', '#ffb8b8'])
plt.scatter(X_reduce[:,0], X_reduce[:,1], c=y, cmap=binaryThemeDark,␣
 ↪edgecolor='#3d3d3d', linewidth=1)
plt.xlabel('X1')
plt.ylabel('X2')
plt.title('All Features (1/2/3/4Kmers+GC_count+zCurve)')
plt.tight_layout()
plt.savefig("All-Features",dpi=300)
plt.show()
```


All Features (1/2/3/4Kmers+GC_count+zCurve)
2.0
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
X2
1.0
1.2
1.4
1.6
1.8
2.0
X1