CytoAutoCluster

Importing Header files

In [ ]:
```
import pandas as pd
import matplotlib.pyplot as plt
import numpy as np
import matplotlib.pyplot as plt
from sklearn.preprocessing import StandardScaler
from sklearn.decomposition import PCA
from sklearn.cluster import KMeans
from sklearn.semi_supervised import LabelPropagation
from sklearn.metrics import silhouette_score
from sklearn.manifold import TSNE
```

In [ ]:
```
from google.colab import drive
drive.mount('/content/drive')
```

```
Mounted at /content/drive
```

Displaying the data

In [ ]:
```
import pandas as pd

# Provide the URL of the file
url = '/content/drive/MyDrive/Datasets/Levine_32dim.fcs.csv'

# Load the dataset
df = pd.read_csv(url)

# Check the first few rows of the dataset
print(df.head())
```

```
   Event    Time  Cell_length      DNA1      DNA2    CD45RA     CD133  \
0      1  2693.0           22  4.391057  4.617262  0.162691 -0.029585
1      2  3736.0           35  4.340481  4.816692  0.701349 -0.038280
2      3  7015.0           32  3.838727  4.386369  0.603568 -0.032216
3      4  7099.0           29  4.255806  4.830048  0.433747 -0.027611
4      5  7700.0           25  3.976909  4.506433 -0.008809 -0.030297

       CD19      CD22     CD11b  ...     CD117     CD49d    HLA-DR      CD64
\
0 -0.006696  0.066388 -0.009184  ...  0.053050  0.853505  1.664480 -0.005376
1 -0.016654  0.074409  0.808031  ...  0.089660  0.197818  0.491592  0.144814
2  0.073855 -0.042977 -0.001881  ...  0.046222  2.586670  1.308337 -0.010961
3 -0.017661 -0.044072  0.733698  ...  0.066470  1.338669  0.140523 -0.013449
4  0.080423  0.495791  1.107627  ... -0.006223  0.180924  0.197332  0.076167

       CD41  Viability  file_number  event_number  label  individual
0 -0.001961   0.648429     3.627711           307    1.0           1
1  0.868014   0.561384     3.627711           545    1.0           1
2 -0.010413   0.643337     3.627711          1726    1.0           1
3 -0.026039  -0.026523     3.627711          1766    1.0           1
4 -0.040488   0.283287     3.627711          2031    1.0           1

[5 rows x 42 columns]
```

In [ ]:
```
df
```

Out[ ]:

	Event	Time	Cell_length	DNA1	DNA2	CD45RA	CD13
0	1	2693.00	22	4.391057	4.617262	0.162691	-0.02958
1	2	3736.00	35	4.340481	4.816692	0.701349	-0.03828
2	3	7015.00	32	3.838727	4.386369	0.603568	-0.03221
3	4	7099.00	29	4.255806	4.830048	0.433747	-0.02761
4	5	7700.00	25	3.976909	4.506433	-0.008809	-0.03029
...	...	...	...	...	...	...	
265622	265623	707951.44	41	6.826629	7.133022	1.474081	-0.01917
265623	265624	708145.44	45	6.787791	7.154026	0.116755	-0.05621
265624	265625	708398.44	41	6.889866	7.141219	0.684921	-0.00626
265625	265626	708585.44	39	6.865218	7.144353	0.288761	-0.01131
265626	265627	709122.44	41	6.887820	7.127359	0.360753	0.12860

265627 rows × 42 columns

In [ ]:
```
df.columns
```

Out[ ]:
```
Index(['Event', 'Time', 'Cell_length', 'DNA1', 'DNA2', 'CD45RA', 'CD133',
       'CD19', 'CD22', 'CD11b', 'CD4', 'CD8', 'CD34', 'Flt3', 'CD20', 'CXCR
4',
       'CD235ab', 'CD45', 'CD123', 'CD321', 'CD14', 'CD33', 'CD47', 'CD11
c',
       'CD7', 'CD15', 'CD16', 'CD44', 'CD38', 'CD13', 'CD3', 'CD61', 'CD11
7',
       'CD49d', 'HLA-DR', 'CD64', 'CD41', 'Viability', 'file_number',
       'event_number', 'label', 'individual'],
      dtype='object')
```

In [ ]:
```
df['Viability']
```

Out[ ]:

	Viability
0	0.648429
1	0.561384
2	0.643337
3	-0.026523
4	0.283287
...	...
265622	0.236957
265623	-0.003500
265624	0.107206
265625	0.620872
265626	0.310466

265627 rows × 1 columns

dtype: float64

In [ ]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 265627 entries, 0 to 265626
Data columns (total 42 columns):
 #   Column        Non-Null Count   Dtype  
---  ------        --------------   -----  
 0   Event         265627 non-null  int64  
 1   Time          265627 non-null  float64
 2   Cell_length   265627 non-null  int64  
 3   DNA1          265627 non-null  float64
 4   DNA2          265627 non-null  float64
 5   CD45RA        265627 non-null  float64
 6   CD133         265627 non-null  float64
 7   CD19          265627 non-null  float64
 8   CD22          265627 non-null  float64
 9   CD11b         265627 non-null  float64
 10  CD4           265627 non-null  float64
 11  CD8           265627 non-null  float64
 12  CD34          265627 non-null  float64
 13  Flt3          265627 non-null  float64
 14  CD20          265627 non-null  float64
 15  CXCR4         265627 non-null  float64
 16  CD235ab       265627 non-null  float64
 17  CD45          265627 non-null  float64
 18  CD123         265627 non-null  float64
 19  CD321         265627 non-null  float64
 20  CD14          265627 non-null  float64
 21  CD33          265627 non-null  float64
 22  CD47          265627 non-null  float64
 23  CD11c         265627 non-null  float64
 24  CD7           265627 non-null  float64
 25  CD15          265627 non-null  float64
 26  CD16          265627 non-null  float64
 27  CD44          265627 non-null  float64
 28  CD38          265627 non-null  float64
 29  CD13          265627 non-null  float64
 30  CD3           265627 non-null  float64
 31  CD61          265627 non-null  float64
 32  CD117         265627 non-null  float64
 33  CD49d         265627 non-null  float64
 34  HLA-DR        265627 non-null  float64
 35  CD64          265627 non-null  float64
 36  CD41          265627 non-null  float64
 37  Viability     265627 non-null  float64
 38  file_number   265627 non-null  float64
 39  event_number  265627 non-null  int64  
 40  label         104184 non-null  float64
 41  individual    265627 non-null  int64  
dtypes: float64(38), int64(4)
memory usage: 85.1 MB
```

In [ ]:

```
df.describe()
```

Out[ ]:

	Event	Time	Cell_length	DNA1	D
count	265627.000000	265627.000000	265627.000000	265627.000000	265627.00
mean	132814.000000	272948.345014	34.450572	4.606956	5.19
std	76680.054314	171220.139430	11.446694	1.312831	1.15
min	1.000000	1.000000	10.000000	2.786488	2.23
25%	66407.500000	120196.000000	26.000000	3.700023	4.40
50%	132814.000000	253276.000000	33.000000	4.022127	4.69
75%	199220.500000	424502.500000	41.000000	6.353313	6.76
max	265627.000000	709122.440000	65.000000	7.001489	7.47

8 rows × 42 columns

Finding the column containg null values

In [ ]:

```
null_count = df.isnull().sum()
print(null_count)
```

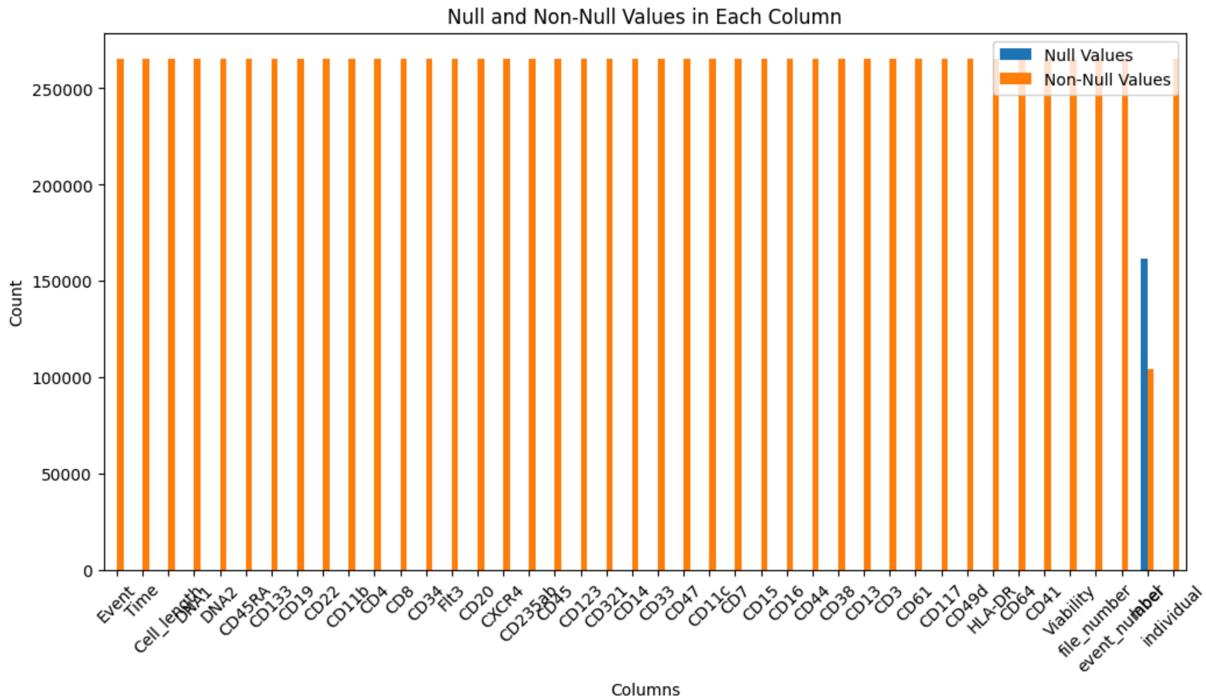
```
Event                0
Time                 0
Cell_length          0
DNA1                 0
DNA2                 0
CD45RA               0
CD133                0
CD19                 0
CD22                 0
CD11b                0
CD4                  0
CD8                  0
CD34                 0
Flt3                 0
CD20                 0
CXCR4                0
CD235ab              0
CD45                 0
CD123                0
CD321                0
CD14                 0
CD33                 0
CD47                 0
CD11c                0
CD7                  0
CD15                 0
CD16                 0
CD44                 0
CD38                 0
CD13                 0
CD3                  0
CD61                 0
CD117                0
CD49d                0
HLA-DR               0
CD64                 0
CD41                 0
Viability            0
file_number          0
event_number         0
label           161443
individual           0
dtype: int64
```

NULL VS NOT NULL

In [ ]:

```
df = pd.DataFrame(df)
null_values = df.isnull().sum()
non_null_values = df.notnull().sum()
plot_data = pd.DataFrame({
    'Null Values': null_values,
    'Non-Null Values': non_null_values
})
plot_data.plot(kind='bar', figsize=(12, 6))
plt.title('Null and Non-Null Values in Each Column')
```

```
plt.xlabel('Columns')
plt.ylabel('Count')
plt.xticks(rotation=45)
plt.legend(loc='upper right')
plt.show()
```

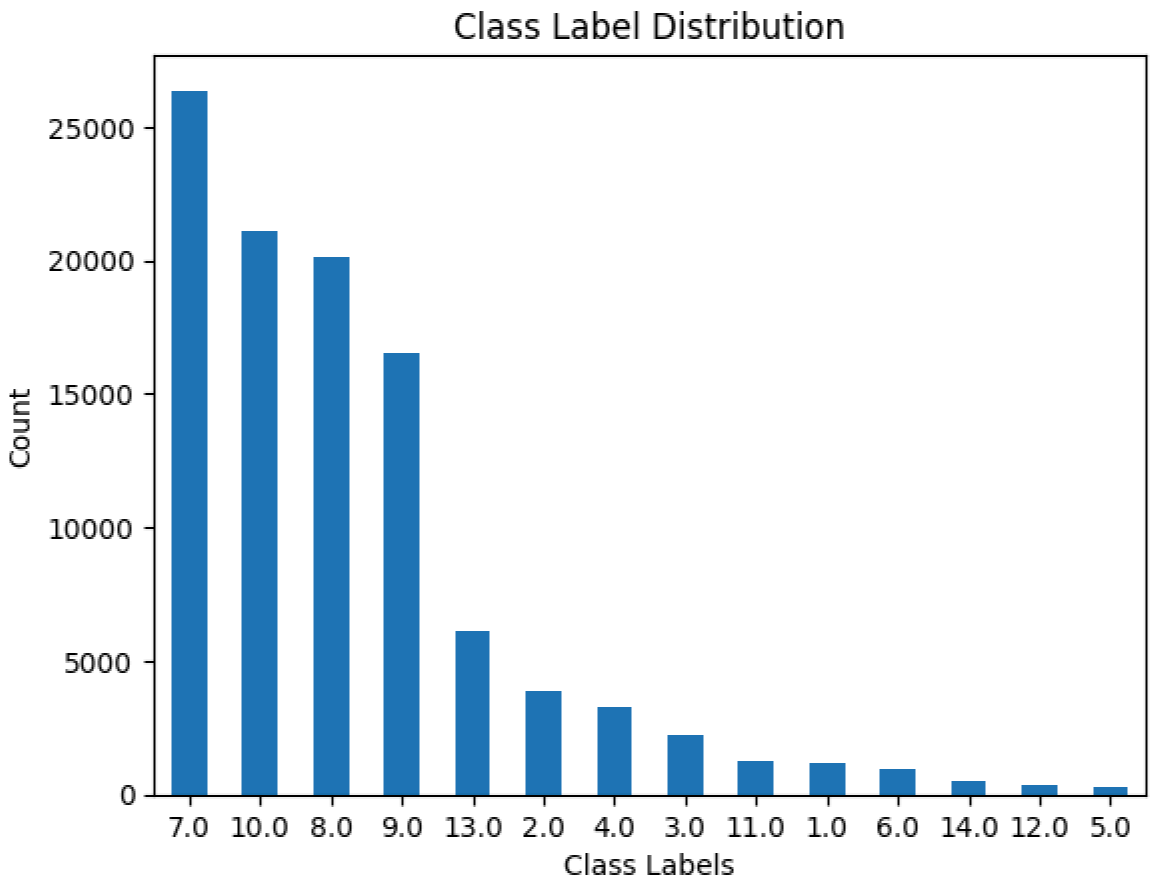


Droping Unnecessary Column

In [ ]:
```
df = df.drop(columns=['Event','Time','individual','file_number','event_numbe
```

Class Label Distribution

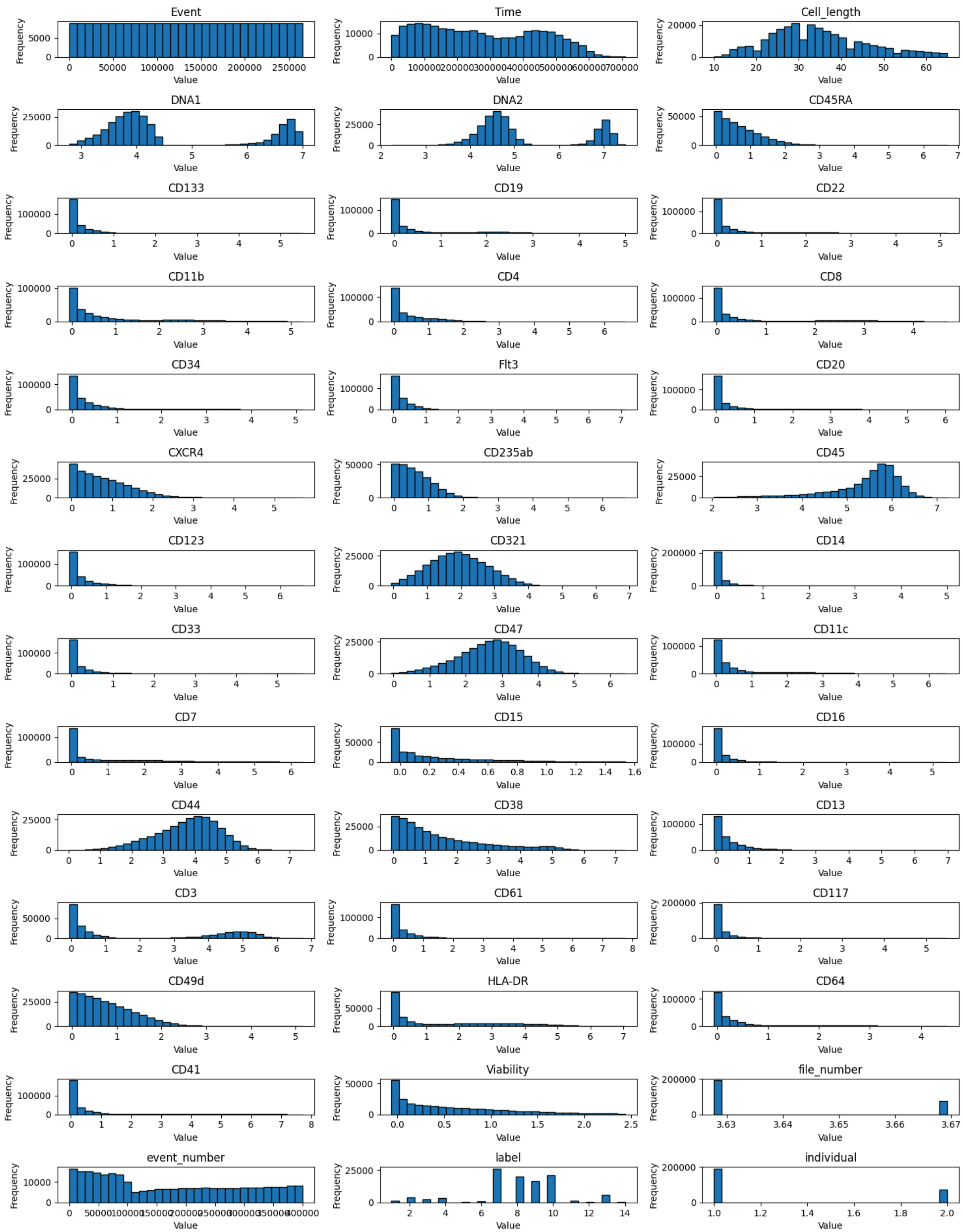
In [ ]:
```
import pandas as pd
import matplotlib.pyplot as plt

data = pd.read_csv('/content/drive/MyDrive/Datasets/Levine_32dim.fcs.csv')

class_counts = data['label'].value_counts()

class_counts.plot(kind='bar')

plt.title('Class Label Distribution')
plt.ylabel('Count')
plt.xlabel('Class Labels')
plt.xticks(rotation=0)
plt.show()
```



Histogram of each feature

In [ ]:

```
import pandas as pd
import matplotlib.pyplot as plt

data = pd.read_csv('/content/drive/MyDrive/Datasets/Levine_32dim.fcs.csv')

# Select only numerical columns for histogram plotting
numerical_columns = data.select_dtypes(include=['float64', 'int64']).columns

# Set up the figure for subplots
plt.figure(figsize=(15, 20))

# Iterate through numerical columns and create a histogram for each
for i, column in enumerate(numerical_columns, 1):
    plt.subplot(len(numerical_columns)//3 + 1, 3, i)
    plt.hist(data[column], bins=30, edgecolor='black')
    plt.title(column)
    plt.xlabel('Value')
    plt.ylabel('Frequency')

plt.tight_layout()
plt.show()
```

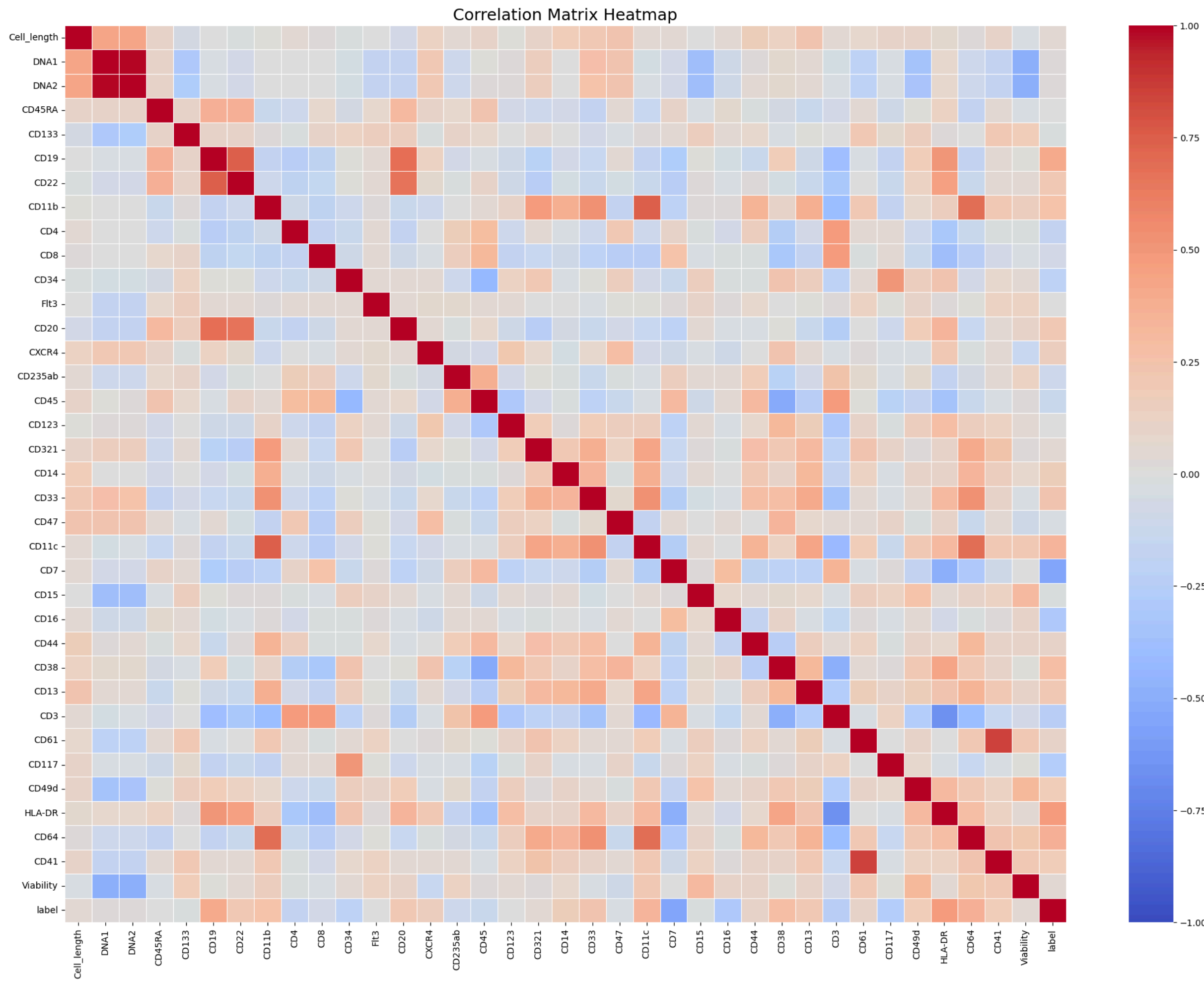


Correlation matrix

In [ ]:

```
import seaborn as sns
import matplotlib.pyplot as plt
# Compute the correlation matrix
correlation_matrix = df.corr()
# Display the correlation matrix
correlation_matrix.round(2)
```

```
# Set the figure size
plt.figure(figsize=(25, 18))
# Create a heatmap of the correlation matrix
sns.heatmap(correlation_matrix, annot= False , cmap='coolwarm',vmin=-1,vmax=
# Add a title
plt.title('Correlation Matrix Heatmap', fontsize=18)
# Show the plot
plt.show()
```



Setting the threshold

```
In [ ]: def correlation(dataset, threshold):
            col_corr = set() # Set of dll the names of correlated columns
            corr_matrix = dataset.corr()
            for i in range(len(corr_matrix.columns)):
                for j in range(i):
                    if abs(corr_matrix.iloc[i, j]) > threshold: # we are interested
                        colname = corr_matrix.columns[i] # getting the name of colum
                        col_corr.add(colname)
            return col_corr
```

```
In [ ]: corr_features = correlation(df, 0.8)
        len(set(corr_features))
```

Out[ ]: 2

In [ ]:
```
corr_features
```

Out[ ]: {'CD41', 'DNA2'}

Finding the range of each column

In [ ]:
```
# Select only numerical columns
numerical_columns = df.select_dtypes(include=['float64', 'int64']).columns

# Create a DataFrame to store max, min, and range values
summary_df = pd.DataFrame({
    'Max': df[numerical_columns].max(),
    'Min': df[numerical_columns].min(),
    'Range': df[numerical_columns].max() - df[numerical_columns].min()
})

# Display the summary DataFrame
print("Summary of Max, Min, and Range for Each Numerical Column:")
print(summary_df)
```

```
Summary of Max, Min, and Range for Each Numerical Column:
                   Max        Min      Range
Cell_length  65.000000  10.000000  55.000000
DNA1          7.001489   2.786488   4.215001
DNA2          7.472308   2.236450   5.235858
CD45RA        6.691197  -0.057305   6.748502
CD133         5.527494  -0.058081   5.585575
CD19          4.990085  -0.058089   5.048174
CD22          5.160477  -0.057342   5.217819
CD11b         5.260789  -0.058236   5.319025
CD4           6.581762  -0.057751   6.639513
CD8           4.693694  -0.058003   4.751697
CD34          5.147996  -0.058008   5.206004
Flt3          7.117323  -0.057884   7.175207
CD20          6.051411  -0.058132   6.109543
CXCR4         5.696674  -0.057042   5.753717
CD235ab       6.646699  -0.057612   6.704311
CD45          7.238076   2.040243   5.197833
CD123         6.640626  -0.058003   6.698630
CD321         6.867388  -0.053552   6.920940
CD14          5.006121  -0.057954   5.064075
CD33          5.612469  -0.058079   5.670548
CD47          6.402488  -0.055087   6.457575
CD11c         6.520939  -0.058053   6.578992
CD7           6.319219  -0.058162   6.377381
CD15          1.534151  -0.058077   1.592227
CD16          5.338305  -0.057780   5.396085
CD44          7.404564   0.026061   7.378503
CD38          7.293085  -0.057194   7.350279
CD13          6.981187  -0.057728   7.038915
CD3           6.748362  -0.058241   6.806603
CD61          7.748498  -0.057642   7.806139
CD117         5.502125  -0.057668   5.559793
CD49d         5.153438  -0.058064   5.211502
HLA-DR        7.052507  -0.057974   7.110481
CD64          4.517843  -0.058199   4.576042
CD41          7.718288  -0.058244   7.776532
Viability     2.433031  -0.057979   2.491010
label        14.000000   1.000000  13.000000
```

Boxplot

In [ ]:

```
n_cols = 6  # You can adjust this to 7, 8, 9, or 10 as needed
n_rows = (len(numerical_columns) + n_cols - 1) // n_cols  # Calculate number

# Set a suitable figure size
plt.figure(figsize=(n_cols * 5, n_rows * 5))  # Adjust height and width base

# Filter to include only valid numerical columns
valid_numerical_columns = [col for col in numerical_columns if col in df.col

# Loop through each valid numerical column to create individual box plots
for i, column in enumerate(valid_numerical_columns):
    plt.subplot(n_rows, n_cols, i + 1)  # Create a grid of subplots
    df.boxplot(column=column)
```

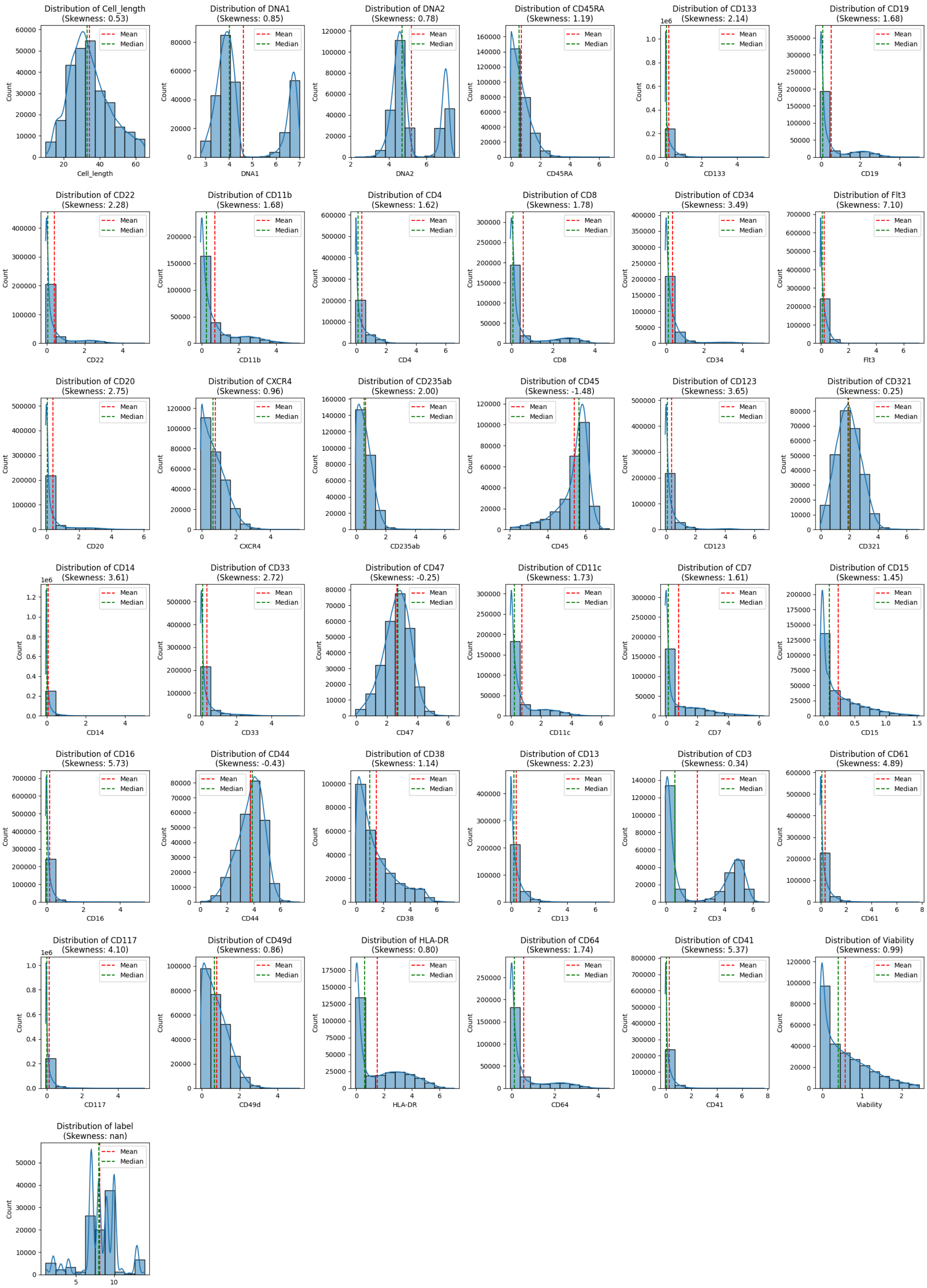
```python
    plt.title(f'Box Plot of {column}', fontsize=10)
    plt.ylabel('Value', fontsize=10)
    plt.xticks(rotation=45, fontsize=8)

# Adjust layout for better spacing
plt.tight_layout()
plt.show()
```

Skewness

In [ ]:
```python
import matplotlib.pyplot as plt
import seaborn as sns
```

```python
from scipy.stats import skew
import pandas as pd

skewness = df.apply(skew)

# Function to categorize skewness
def categorize_skewness(value):
    if value > 0.5:
        return 'Right-skewed'
    elif value < -0.5:
        return 'Left-skewed'
    else:
        return 'Approximately symmetrical'

# Apply the categorization
skewness_category = skewness.apply(categorize_skewness)

# Display skewness and its categorization
skewness_df = pd.DataFrame({'Skewness': skewness, 'Category': skewness_categ
print(skewness_df)

# Number of numerical columns
num_cols = len(df.columns)

# Create a grid of 6 plots per row
cols_per_row = 6
rows = (num_cols + cols_per_row - 1) // cols_per_row  # Calculate the number

# Create subplots
fig, axes = plt.subplots(rows, cols_per_row, figsize=(20, rows * 4))
axes = axes.flatten()  # Flatten to make it easier to iterate through

# Plot histograms for each numerical column
for i, col in enumerate(df.columns):
    sns.histplot(df[col], bins=10, kde=True, ax=axes[i])
    axes[i].set_title(f'Distribution of {col}\n(Skewness: {skewness[col]:.2f
    axes[i].axvline(df[col].mean(), color='red', linestyle='--', label='Mean
    axes[i].axvline(df[col].median(), color='green', linestyle='--', label='
    axes[i].legend()

# Remove any empty subplots
for j in range(i + 1, len(axes)):
    fig.delaxes(axes[j])

# Adjust layout
plt.tight_layout()
plt.show()
```

	Skewness	Category
Cell_length	0.527832	Right-skewed
DNA1	0.845010	Right-skewed
DNA2	0.779167	Right-skewed
CD45RA	1.191595	Right-skewed
CD133	2.141953	Right-skewed
CD19	1.682609	Right-skewed
CD22	2.283181	Right-skewed
CD11b	1.679089	Right-skewed
CD4	1.622044	Right-skewed
CD8	1.775713	Right-skewed
CD34	3.492437	Right-skewed
Flt3	7.098151	Right-skewed
CD20	2.754699	Right-skewed
CXCR4	0.955342	Right-skewed
CD235ab	2.001479	Right-skewed
CD45	-1.484824	Left-skewed
CD123	3.648890	Right-skewed
CD321	0.247097	Approximately symmetrical
CD14	3.609006	Right-skewed
CD33	2.724977	Right-skewed
CD47	-0.250323	Approximately symmetrical
CD11c	1.733888	Right-skewed
CD7	1.606528	Right-skewed
CD15	1.445147	Right-skewed
CD16	5.733203	Right-skewed
CD44	-0.431589	Approximately symmetrical
CD38	1.141482	Right-skewed
CD13	2.234311	Right-skewed
CD3	0.342239	Approximately symmetrical
CD61	4.894707	Right-skewed
CD117	4.097508	Right-skewed
CD49d	0.856805	Right-skewed
HLA-DR	0.795359	Right-skewed
CD64	1.743733	Right-skewed
CD41	5.366314	Right-skewed
Viability	0.985417	Right-skewed
label	NaN	Approximately symmetrical

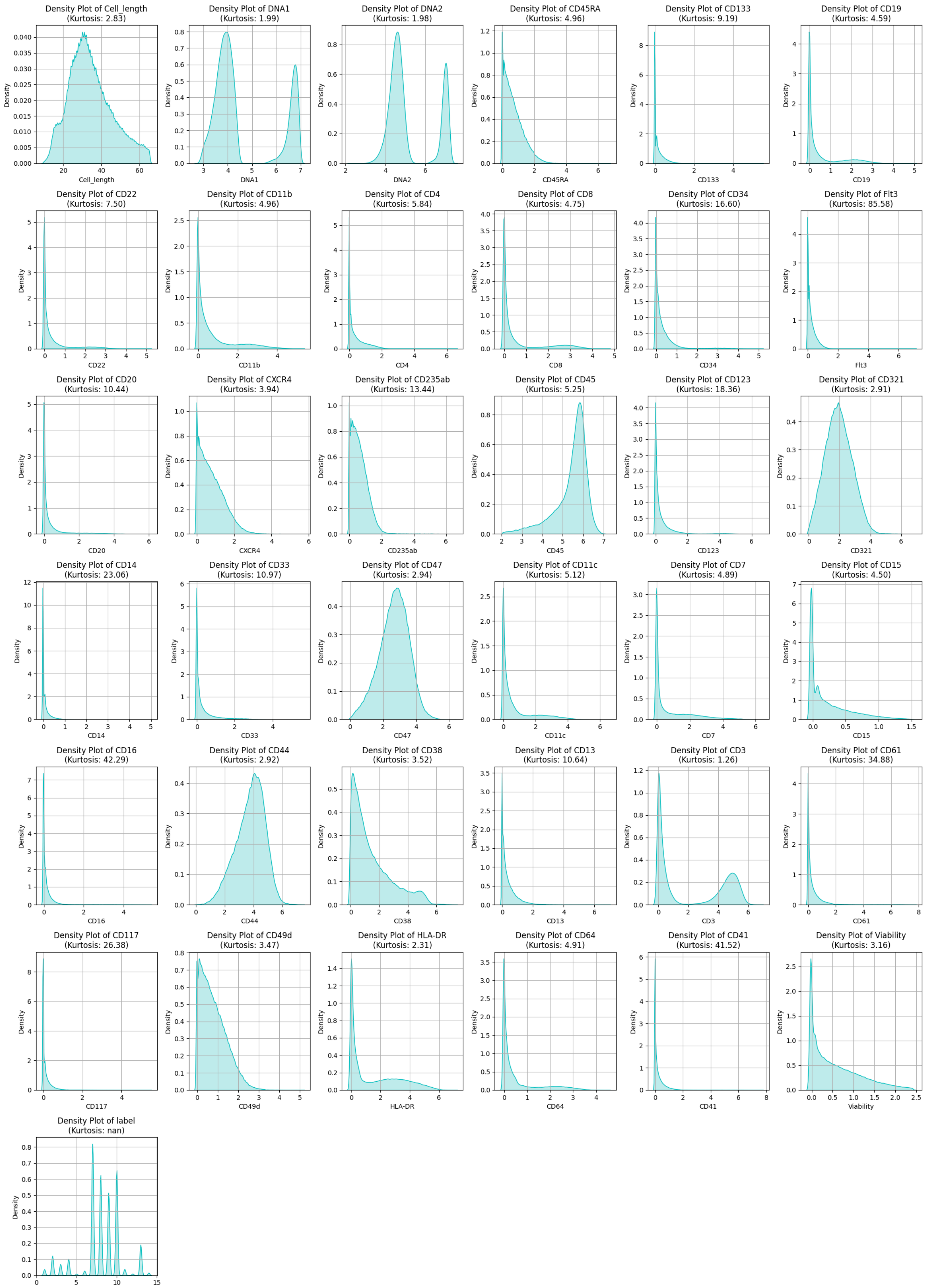

Distribution of Cell_length (Skewness: 0.53)
Distribution of DNA1 (Skewness: 0.85)
Distribution of DNA2 (Skewness: 0.78)
Distribution of CD45RA (Skewness: 1.19)
Distribution of CD133 (Skewness: 2.14)
Distribution of CD19 (Skewness: 1.68)
Distribution of CD22 (Skewness: 2.28)
Distribution of CD11b (Skewness: 1.68)
Distribution of CD4 (Skewness: 1.62)
Distribution of CD8 (Skewness: 1.78)
Distribution of CD34 (Skewness: 3.49)
Distribution of Flt3 (Skewness: 7.10)
Distribution of CD20 (Skewness: 2.75)
Distribution of CXCR4 (Skewness: 0.96)
Distribution of CD235ab (Skewness: 2.00)
Distribution of CD45 (Skewness: -1.48)
Distribution of CD123 (Skewness: 3.65)
Distribution of CD321 (Skewness: 0.25)
Distribution of CD14 (Skewness: 3.61)
Distribution of CD33 (Skewness: 2.72)
Distribution of CD47 (Skewness: -0.25)
Distribution of CD11c (Skewness: 1.73)
Distribution of CD7 (Skewness: 1.61)
Distribution of CD15 (Skewness: 1.45)
Distribution of CD16 (Skewness: 5.73)
Distribution of CD44 (Skewness: -0.43)
Distribution of CD38 (Skewness: 1.14)
Distribution of CD13 (Skewness: 2.23)
Distribution of CD3 (Skewness: 0.34)
Distribution of CD61 (Skewness: 4.89)
Distribution of CD117 (Skewness: 4.10)
Distribution of CD49d (Skewness: 0.86)
Distribution of HLA-DR (Skewness: 0.80)
Distribution of CD64 (Skewness: 1.74)
Distribution of CD41 (Skewness: 5.37)
Distribution of Viability (Skewness: 0.99)
Distribution of label (Skewness: nan)
Mean
Median
Count

Kurtosis

In [ ]:

```
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
from scipy.stats import kurtosis

# Calculate kurtosis for each column
kurtosis_values = df.apply(kurtosis, fisher=False)  # Pearson kurtosis (norm

# Create a DataFrame with kurtosis values
kurtosis_df = pd.DataFrame({'Column': df.columns, 'Kurtosis': kurtosis_value

# Categorize the kurtosis values (Leptokurtic, Mesokurtic, Platykurtic)
def categorize_kurtosis(value):
    if value > 3:
        return 'Leptokurtic (heavy tails)'
    elif value < 3:
        return 'Platykurtic (light tails)'
    else:
        return 'Mesokurtic (normal tails)'

kurtosis_df['Category'] = kurtosis_df['Kurtosis'].apply(categorize_kurtosis)

# Print the kurtosis values and their categories
print(kurtosis_df)

# Number of numerical columns
num_cols = len(df.columns)

# Create a grid of 6 plots per row
cols_per_row = 6
rows = (num_cols + cols_per_row - 1) // cols_per_row  # Calculate the number

# Create subplots
fig, axes = plt.subplots(rows, cols_per_row, figsize=(20, rows * 4))
axes = axes.flatten()  # Flatten the axes array to make iteration easier

# Plot density for each column
for i, column in enumerate(df.columns):
    sns.kdeplot(df[column].dropna(), color='c', fill=True, bw_adjust=0.5, ax
    axes[i].set_title(f'Density Plot of {column}\n(Kurtosis: {kurtosis_df.lo
    axes[i].set_xlabel(column)
    axes[i].set_ylabel('Density')
    axes[i].grid(True)

# Remove any empty subplots
for j in range(i + 1, len(axes)):
    fig.delaxes(axes[j])

# Adjust layout
plt.tight_layout()
plt.show()
```

	Column	Kurtosis	Category
Cell_length	Cell_length	2.834033	Platykurtic (light tails)
DNA1	DNA1	1.994037	Platykurtic (light tails)
DNA2	DNA2	1.975021	Platykurtic (light tails)
CD45RA	CD45RA	4.964272	Leptokurtic (heavy tails)
CD133	CD133	9.190066	Leptokurtic (heavy tails)
CD19	CD19	4.590887	Leptokurtic (heavy tails)
CD22	CD22	7.500223	Leptokurtic (heavy tails)
CD11b	CD11b	4.964495	Leptokurtic (heavy tails)
CD4	CD4	5.844261	Leptokurtic (heavy tails)
CD8	CD8	4.745776	Leptokurtic (heavy tails)
CD34	CD34	16.596416	Leptokurtic (heavy tails)
Flt3	Flt3	85.583534	Leptokurtic (heavy tails)
CD20	CD20	10.435449	Leptokurtic (heavy tails)
CXCR4	CXCR4	3.936307	Leptokurtic (heavy tails)
CD235ab	CD235ab	13.440586	Leptokurtic (heavy tails)
CD45	CD45	5.246770	Leptokurtic (heavy tails)
CD123	CD123	18.361217	Leptokurtic (heavy tails)
CD321	CD321	2.914593	Platykurtic (light tails)
CD14	CD14	23.062535	Leptokurtic (heavy tails)
CD33	CD33	10.967536	Leptokurtic (heavy tails)
CD47	CD47	2.943834	Platykurtic (light tails)
CD11c	CD11c	5.117156	Leptokurtic (heavy tails)
CD7	CD7	4.885115	Leptokurtic (heavy tails)
CD15	CD15	4.504387	Leptokurtic (heavy tails)
CD16	CD16	42.287749	Leptokurtic (heavy tails)
CD44	CD44	2.918792	Platykurtic (light tails)
CD38	CD38	3.521190	Leptokurtic (heavy tails)
CD13	CD13	10.637564	Leptokurtic (heavy tails)
CD3	CD3	1.264612	Platykurtic (light tails)
CD61	CD61	34.878020	Leptokurtic (heavy tails)
CD117	CD117	26.375108	Leptokurtic (heavy tails)
CD49d	CD49d	3.468119	Leptokurtic (heavy tails)
HLA-DR	HLA-DR	2.309924	Platykurtic (light tails)
CD64	CD64	4.910631	Leptokurtic (heavy tails)
CD41	CD41	41.521113	Leptokurtic (heavy tails)
Viability	Viability	3.156935	Leptokurtic (heavy tails)
label	label	NaN	Mesokurtic (normal tails)



Loading and Visualizing the MNIST Dataset

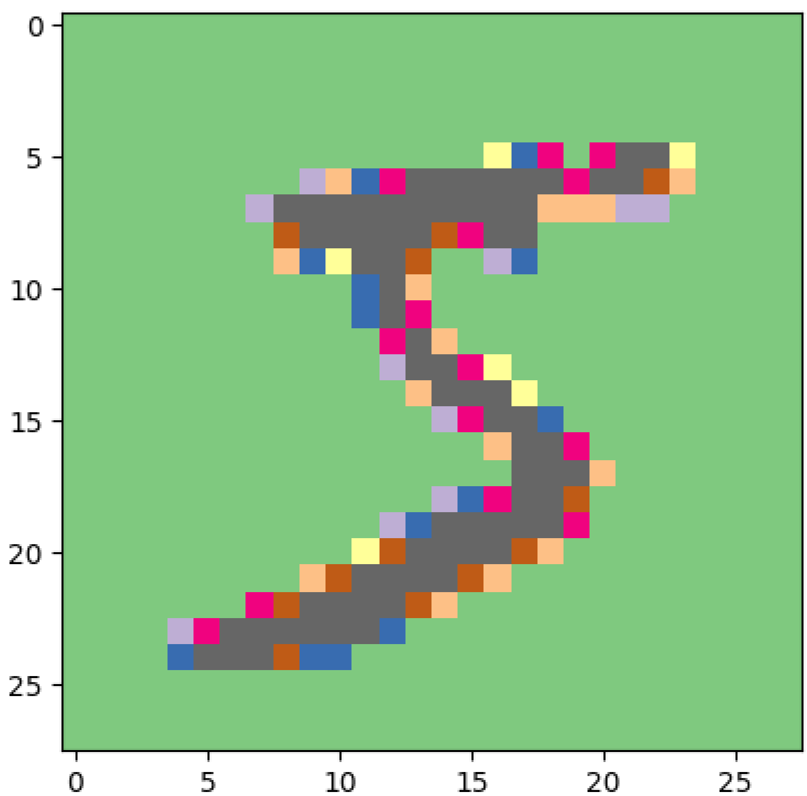
In [ ]:

```python
import tensorflow as tf

(train_images, train_labels), (test_images, test_labels) = tf.keras.datasets

train_images = train_images.astype('float32') / 255.0
test_images = test_images.astype('float32') / 255.0

print(f"Training images shape: {train_images.shape}")
print(f"Training labels shape: {train_labels.shape}")
print(f"Test images shape: {test_images.shape}")
print(f"Test labels shape: {test_labels.shape}")

import matplotlib.pyplot as plt

plt.imshow(train_images[0], cmap='Accent')
```

```
Downloading data from https://storage.googleapis.com/tensorflow/tf-keras-dat
asets/mnist.npz
11490434/11490434 ━━━━━━━━━━━━━━━━━━━━ 0s 0us/step
Training images shape: (60000, 28, 28)
Training labels shape: (60000,)
Test images shape: (10000, 28, 28)
Test labels shape: (10000,)
```

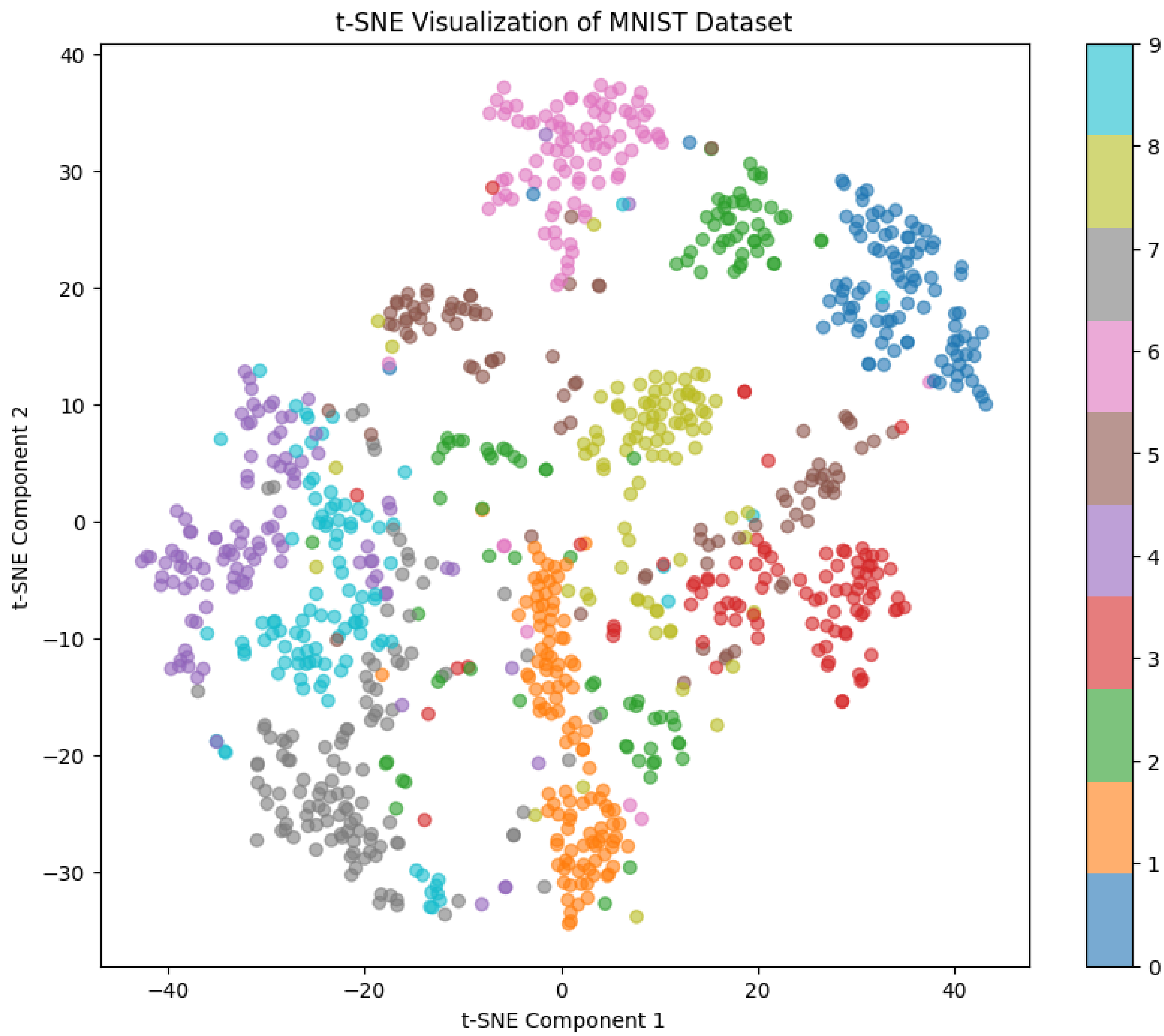
Out[ ]:

```
<matplotlib.image.AxesImage at 0x7a9c10029540>
```



t-SNE Visualization of MNIST Dataset with Subset of Samples

In [ ]:
```
import tensorflow as tf
from sklearn.manifold import TSNE
import matplotlib.pyplot as plt
import numpy as np

(train_images, train_labels), (test_images, test_labels) = tf.keras.datasets
train_images = train_images.astype('float32') / 255.0
test_images = test_images.astype('float32') / 255.0

n_samples = 1000
train_images_flat = train_images[:n_samples].reshape(n_samples, -1)
train_labels_subset = train_labels[:n_samples]

tsne = TSNE(n_components=2, random_state=42, perplexity=30)
train_images_tsne = tsne.fit_transform(train_images_flat)

# plot the results
plt.figure(figsize=(10, 8))
scatter = plt.scatter(train_images_tsne[:, 0], train_images_tsne[:, 1], c=tr
plt.colorbar(scatter, ticks=range(10))
plt.title('t-SNE Visualization of MNIST Dataset')
plt.xlabel('t-SNE Component 1')
plt.ylabel('t-SNE Component 2')
plt.show()
```



Standardizing the data

In [ ]:

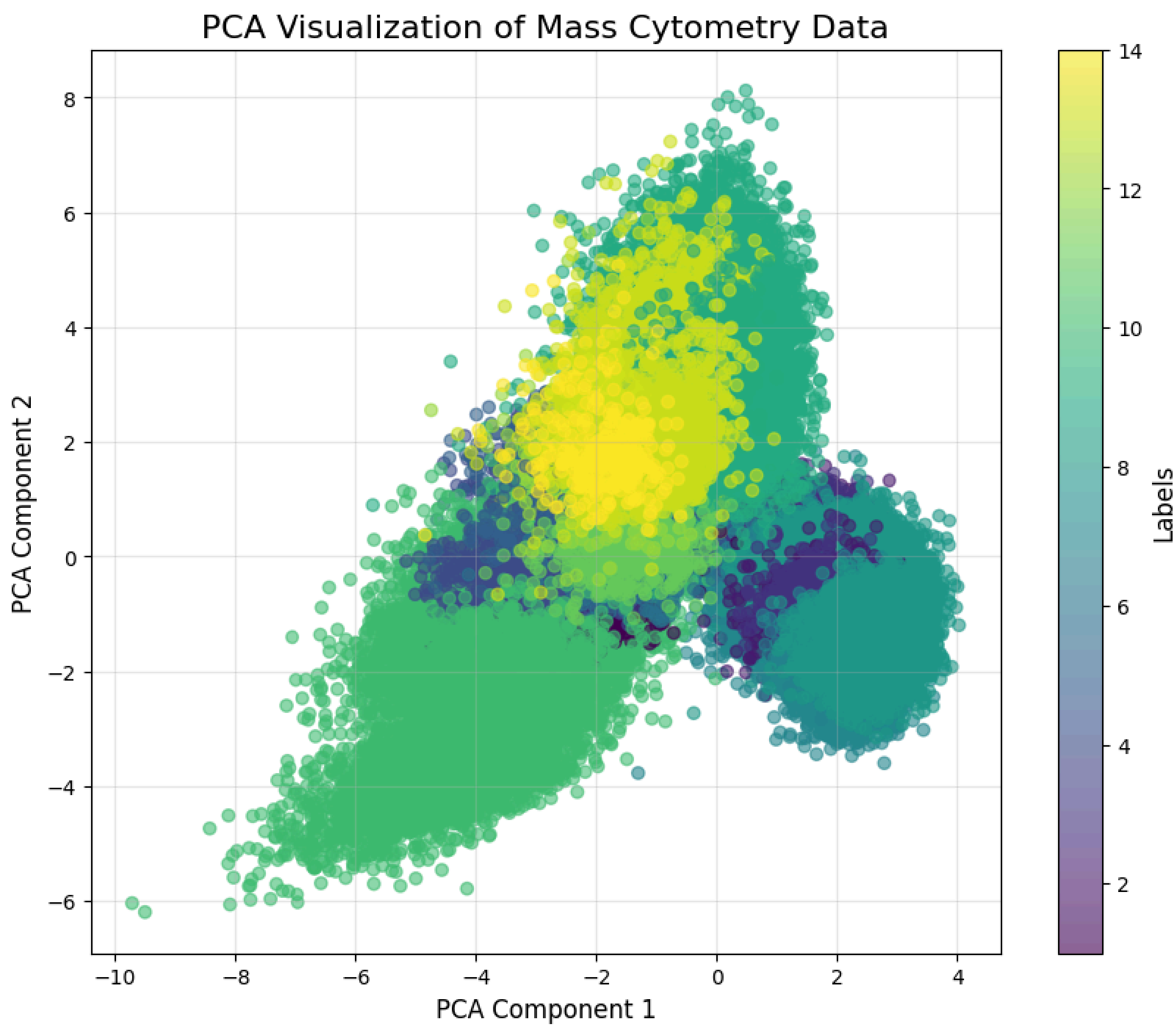
```
import pandas as pd
from sklearn.preprocessing import StandardScaler
# Initialize the StandardScaler
scaler = StandardScaler()

scaled_data = scaler.fit_transform(df)


scaled_df = pd.DataFrame(scaled_data, columns=df.columns)

#  Display the first few rows of the standardized data
print(scaled_df.head())
```

```
   Cell_length      DNA1      DNA2    CD45RA     CD133      CD19      CD22  \
0    -1.087702 -0.164453 -0.505101 -0.862639 -0.677085 -0.601774 -0.434227
1     0.047999 -0.202977 -0.331737  0.021706 -0.710621 -0.613387 -0.423702
2    -0.214086 -0.585171 -0.705816 -0.138826 -0.687231 -0.507832 -0.577727
3    -0.476171 -0.267476 -0.320127 -0.417630 -0.669470 -0.614562 -0.579163
4    -0.825617 -0.479916 -0.601444 -1.144201 -0.679832 -0.500173  0.129202

      CD11b       CD4       CD8  ...      CD13       CD3      CD61     CD117  \
0 -0.711371 -0.007722 -0.044861  ... -0.665941 -0.968994 -0.479732 -0.249511
1  0.096608 -0.778973 -0.573653  ...  2.197090 -0.973786  1.262168 -0.132623
2 -0.704150 -0.727475 -0.568752  ... -0.312734 -0.813227 -0.120582 -0.271310
3  0.023115 -0.747355 -0.507239  ...  0.294199 -0.927985 -0.532490 -0.206663
4  0.392818  0.357861 -0.531946  ...  0.438207 -0.894158 -0.242836 -0.438757

      CD49d    HLA-DR      CD64      CD41  Viability     label
0  0.093316  0.084209 -0.626606 -0.427371   0.132927 -2.895698
1 -0.951407 -0.608084 -0.457614  0.982491  -0.014673 -2.895698
2  2.854812 -0.126003 -0.632890 -0.441068   0.124292 -2.895698
3  0.866341 -0.815301 -0.635690 -0.466392  -1.011569 -2.895698
4 -0.978326 -0.781769 -0.534854 -0.489807  -0.486233 -2.895698

[5 rows x 37 columns]
```

PCA for 2D

In [ ]:
```python
import pandas as pd
import seaborn as sns
from sklearn.decomposition import PCA
from sklearn.preprocessing import StandardScaler
import matplotlib.pyplot as plt

# Scale the data using StandardScaler
# Use all columns except the 'label' column
scaler = StandardScaler()
scaled_data = scaler.fit_transform(df.drop(columns=['label']))

# Apply PCA to reduce dimensions to 2 components
pca = PCA(n_components=2)
pca_results = pca.fit_transform(scaled_data)

# Add PCA results back to the original DataFrame
df['PCA1'] = pca_results[:, 0]
df['PCA2'] = pca_results[:, 1]

# Create a scatter plot of the PCA results
plt.figure(figsize=(10, 8))
scatter = plt.scatter(
    df['PCA1'], df['PCA2'],
    c=df['label'],  # Use the label column for coloring
    cmap='viridis',  # 'viridis' colormap for smooth gradients
    alpha=0.6        # Set transparency for better visualization
)
```

```python
# Add a colorbar to explain the labels
cbar = plt.colorbar(scatter)
cbar.set_label('Labels', fontsize=12)

# Add plot title and axis labels
plt.title('PCA Visualization of Mass Cytometry Data', fontsize=16)
plt.xlabel('PCA Component 1', fontsize=12)
plt.ylabel('PCA Component 2', fontsize=12)

# Add grid for clarity
plt.grid(alpha=0.3)

# Show the final plot
plt.show()
```



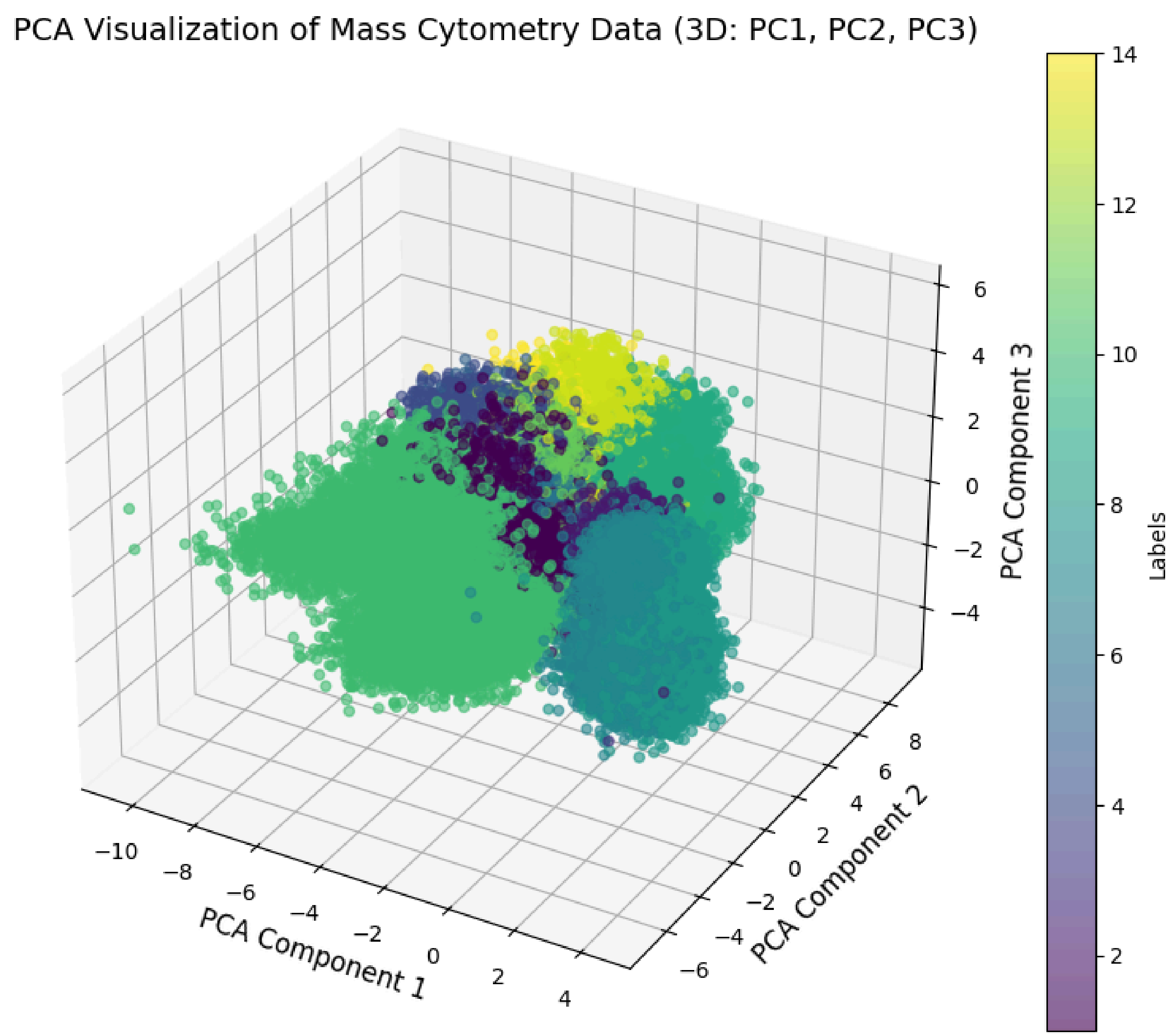
PCA for 3D

In [ ]:

```python
import pandas as pd
import numpy as np  # Ensure this is imported for mathematical operations
import matplotlib.pyplot as plt
from mpl_toolkits.mplot3d import Axes3D  # For 3D plotting
from sklearn.decomposition import PCA
from sklearn.preprocessing import StandardScaler
```

```
# Scale the data using StandardScaler
# Use all columns except 'label' for scaling
scaler = StandardScaler()
scaled_data = scaler.fit_transform(df.drop(columns=['label']))

# Apply PCA with 4 components
pca = PCA(n_components=4)
pca_results = pca.fit_transform(scaled_data)

# Add PCA results back to the DataFrame
df['PCA1'] = pca_results[:, 0]
df['PCA2'] = pca_results[:, 1]
df['PCA3'] = pca_results[:, 2]
df['PCA4'] = pca_results[:, 3]

# Print PCA explained variance results
explained_variance = pca.explained_variance_ratio_
cumulative_variance = explained_variance.cumsum()
standard_deviation = pca.singular_values_ / np.sqrt(len(df) - 1)

print(f"Standard deviation: {standard_deviation}")
print(f"Proportion of Variance: {explained_variance}")
print(f"Cumulative Proportion: {cumulative_variance}")

# 3D scatter plot of the PCA results (PC1, PC2, PC3)
fig = plt.figure(figsize=(10, 8))
ax = fig.add_subplot(111, projection='3d')

# Scatter plot using the 'viridis' colormap
scatter = ax.scatter(
    df['PCA1'], df['PCA2'], df['PCA3'],
    c=df['label'], cmap='viridis', alpha=0.6
)

# Add title and axis labels
ax.set_title('PCA Visualization of Mass Cytometry Data (3D: PC1, PC2, PC3)',
ax.set_xlabel('PCA Component 1', fontsize=12)
ax.set_ylabel('PCA Component 2', fontsize=12)
ax.set_zlabel('PCA Component 3', fontsize=12)

# Add a colorbar with a label
cbar = fig.colorbar(scatter, ax=ax, label='Labels')

# Show the plot
plt.show()
```

```
Standard deviation: [2.53583711 2.20245521 1.89526477 1.61107568]
Proportion of Variance: [0.16922225 0.12765239 0.09452671 0.06830408]
Cumulative Proportion: [0.16922225 0.29687464 0.39140135 0.45970543]
```



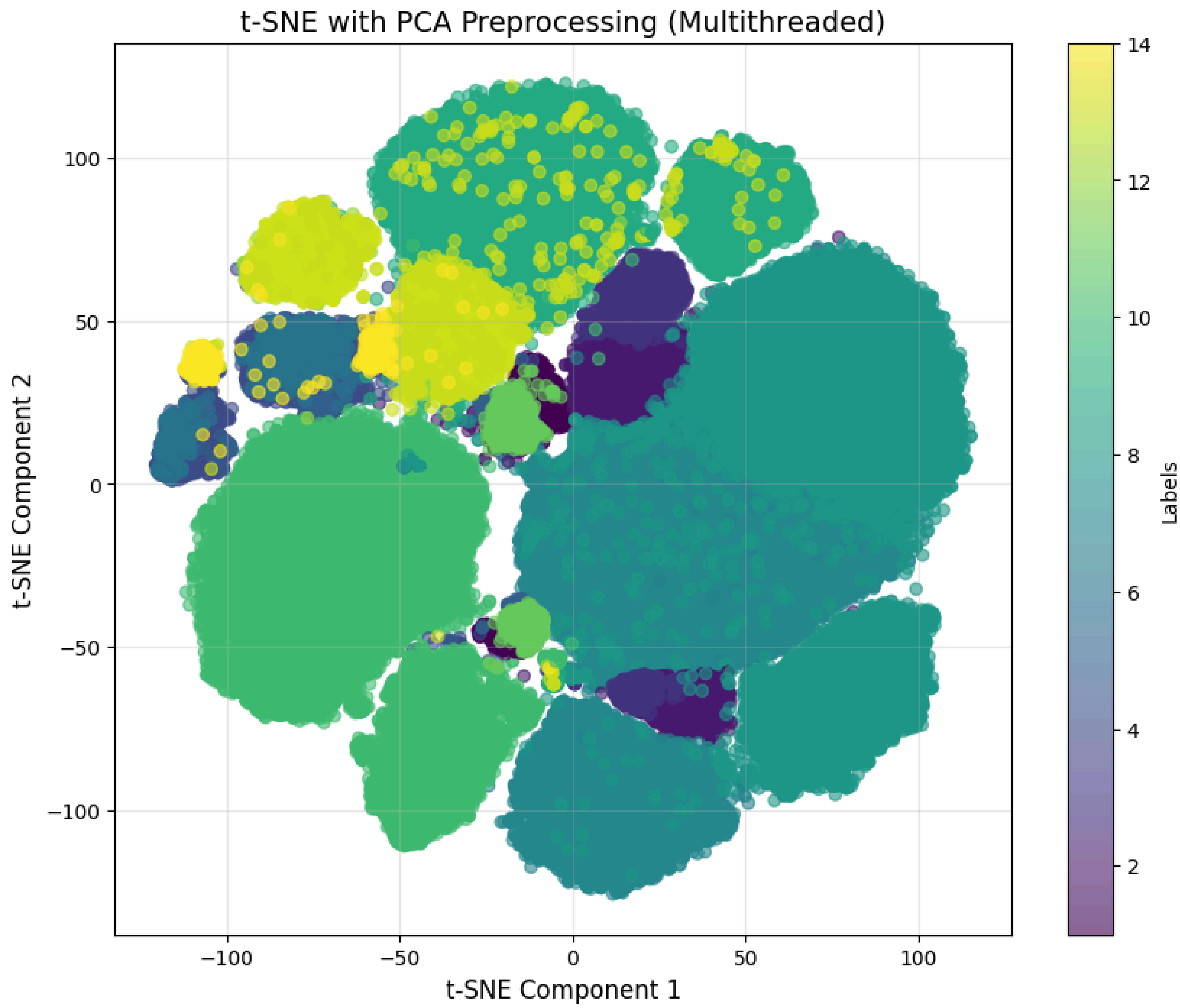
T-SNE

In [ ]:
```
pip install openTSNE
```

```
Collecting openTSNE
  Downloading openTSNE-1.0.2-cp310-cp310-manylinux_2_17_x86_64.manylinux2014
_x86_64.whl.metadata (7.8 kB)
Requirement already satisfied: numpy>=1.16.6 in /usr/local/lib/python3.10/di
st-packages (from openTSNE) (1.26.4)
Requirement already satisfied: scikit-learn>=0.20 in /usr/local/lib/python3.
10/dist-packages (from openTSNE) (1.5.2)
Requirement already satisfied: scipy in /usr/local/lib/python3.10/dist-packa
ges (from openTSNE) (1.13.1)
Requirement already satisfied: joblib>=1.2.0 in /usr/local/lib/python3.10/di
st-packages (from scikit-learn>=0.20->openTSNE) (1.4.2)
Requirement already satisfied: threadpoolctl>=3.1.0 in /usr/local/lib/python
3.10/dist-packages (from scikit-learn>=0.20->openTSNE) (3.5.0)
Downloading openTSNE-1.0.2-cp310-cp310-manylinux_2_17_x86_64.manylinux2014_x
86_64.whl (3.0 MB)
   ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 3.0/3.0 MB 22.8 MB/s eta 0:00:00
Installing collected packages: openTSNE
Successfully installed openTSNE-1.0.2
```

In [ ]:

```python
from openTSNE import TSNE
import matplotlib.pyplot as plt

# Step 1: Reduce dimensionality with PCA
from sklearn.decomposition import PCA

pca = PCA(n_components=20)
pca_result = pca.fit_transform(scaled_data)

# Step 2: Apply t-SNE using openTSNE (multithreaded)
# `n_jobs=-1` uses all available CPU cores
tsne = TSNE(
    n_components=2, perplexity=30, n_jobs=-1, random_state=42, initializatio
)
tsne_results = tsne.fit(pca_result)

# Step 3: Add t-SNE results to the dataframe
df['TSNE1'] = tsne_results[:, 0]
df['TSNE2'] = tsne_results[:, 1]

# Step 4: Plot the t-SNE results
plt.figure(figsize=(10, 8))
scatter = plt.scatter(
    df['TSNE1'], df['TSNE2'],
    c=df['label'], cmap='viridis', alpha=0.6
)

# Add a colorbar and labels
cbar = plt.colorbar(scatter, label='Labels')
plt.title('t-SNE with PCA Preprocessing (Multithreaded)', fontsize=14)
plt.xlabel('t-SNE Component 1', fontsize=12)
plt.ylabel('t-SNE Component 2', fontsize=12)
plt.grid(alpha=0.3)

# Show the plot
plt.show()
```



Applying Binary Mask, Shuffled Output and Corrupted DataFrame on example data

In [ ]:
```
import pandas as pd
import numpy as np

np.random.seed(42)
demo_data = pd.DataFrame({
    'A': [5, 11, 18, 8],
    'B': [10, 40, 15, 30],
    'C': [9, 25, 35, 20]
})

p_m = 0.5

data_array = demo_data.values
mask = np.random.binomial(1, p_m, data_array.shape)
print("Generated Mask (1 represents masked values):\n", mask)

masked_data = np.where(mask == 1, np.nan, data_array)
masked_demo_data = pd.DataFrame(masked_data, columns=demo_data.columns)
```

```
print("\nOriginal DataFrame:\n", demo_data)
print("\nMasked DataFrame:\n", masked_demo_data)
```

```
Generated Mask (1 represents masked values):
 [[0 1 1]
 [1 0 0]
 [0 1 1]
 [1 0 1]]

Original DataFrame:
     A   B   C
0   5  10   9
1  11  40  25
2  18  15  35
3   8  30  20

Masked DataFrame:
       A     B     C
0   5.0   NaN   NaN
1   NaN  40.0  25.0
2  18.0   NaN   NaN
3   NaN  30.0   NaN
```

In [ ]:

```
import pandas as pd
import numpy as np

data = {
    'A': [1, 2, 3, 4, 5],
    'B': [10, 20, 30, 40, 50],
    'C': [100, 200, 300, 400, 500],
    'D': [120,300,231,450,200],
    'E': [12,30,31,40,20]
}
df = pd.DataFrame(data)

shuffled_df = df.apply(np.random.permutation)

print("Original DataFrame:")
print(df)
print("\nDataFrame with shuffled column values:")
print(shuffled_df)
```

```
Original DataFrame:
   A   B    C    D   E
0  1  10  100  120  12
1  2  20  200  300  30
2  3  30  300  231  31
3  4  40  400  450  40
4  5  50  500  200  20

DataFrame with shuffled column values:
   A   B    C    D   E
0  1  30  300  300  12
1  3  20  400  450  20
2  5  50  100  231  31
3  2  10  500  200  40
4  4  40  200  120  30
```

In [ ]:

```
import pandas as pd
import numpy as np

data = {
    'A': [1, 2, 3, 4, 5],
    'B': [10, 20, 30, 40, 50],
    'C': [100, 200, 300, 400, 500],
    'D': [1000, 2000, 3000, 4000, 5000],
    'E': [10000, 20000, 30000, 40000, 50000]
}
x = pd.DataFrame(data)

m = pd.DataFrame(np.random.binomial(1, 0.5, x.shape), columns=x.columns)
x_shuffled = x.apply(np.random.permutation)
x_corrupted = x * (1 - m) + x_shuffled * m

print("Original DataFrame (x):")
print(x)
print("\nBinary Mask (m):")
print(m)
print("\nShuffled DataFrame (x_shuffled):")
print(x_shuffled)
print("\nCorrupted DataFrame (x_corrupted):")
print(x_corrupted)
```

```
Original DataFrame (x):
   A   B    C     D      E
0  1  10  100  1000  10000
1  2  20  200  2000  20000
2  3  30  300  3000  30000
3  4  40  400  4000  40000
4  5  50  500  5000  50000

Binary Mask (m):
   A  B  C  D  E
0  0  1  0  1  0
1  1  1  0  0  1
2  1  0  0  0  0
3  1  1  1  0  0
4  0  1  0  0  1

Shuffled DataFrame (x_shuffled):
   A   B    C     D      E
0  1  10  100  5000  30000
1  4  30  500  3000  20000
2  2  50  300  2000  10000
3  3  20  200  1000  40000
4  5  40  400  4000  50000

Corrupted DataFrame (x_corrupted):
   A   B    C     D      E
0  1  10  100  5000  10000
1  4  30  200  2000  20000
2  2  30  300  3000  30000
3  3  20  200  4000  40000
4  5  40  500  5000  50000
```

Applying Binary Mask, Shuffled Output and Corrupted DataFrame on Original Data

In [ ]:

```
# Separate labeled and unlabeled data based on non-NaN and NaN values in the
df_labeled = df[df['label'].notnull()]
df_unlabeled = df[df['label'].isnull()]

# Print the shapes of labeled and unlabeled data
print("Labeled Data Shape:", df_labeled.shape)
print("Unlabeled Data Shape:", df_unlabeled.shape)
```

```
Labeled Data Shape: (104184, 37)
Unlabeled Data Shape: (161443, 37)
```

Split labelled dataset into x_test,x_train and y_test and y_train . train = 70% and test = 30%

In [ ]:

```
from sklearn.model_selection import train_test_split
# Separate labeled and unlabeled data
```

```
df_labeled = df[df['label'].notnull()]  # Labeled data
df_unlabeled = df[df['label'].isnull()]  # Unlabeled data

# Separate features and target for labeled data
x_labeled = df_labeled.drop(columns=['label'])  # Features
y_labeled = df_labeled['label']                  # Target

# Separate features for unlabeled data
x_unlabeled = df_unlabeled.drop(columns=['label'])  # Features (no labels)

# Split the labeled data into training and testing sets (e.g., 70% train, 30
x_train, x_test, y_train, y_test = train_test_split(x_labeled, y_labeled, te

print("\nTraining Features (x_train):\n", x_train.head())
print("\nTraining Labels (y_train):\n", y_train.head())
print("\nTesting Features (x_test):\n", x_test.head())
print("\nTesting Labels (y_test):\n", y_test.head())
```

```
Training Features (x_train):
        Cell_length      DNA1      DNA2    CD45RA     CD133      CD19  \
64113           25  3.899656  4.594272  0.976652  0.302811  0.154761
82744           31  6.592998  6.901888  0.431481 -0.052898 -0.037690
24294           41  3.543583  4.467671  0.377192  0.219081  0.245478
7820            38  4.305227  4.881685  0.199351  0.100678 -0.025812
43295           26  4.159271  4.861015  0.831285  0.191518  2.002712

           CD22     CD11b       CD4       CD8  ...      CD38      CD13  \
64113 -0.011676  3.180236  1.465950  0.086209  ...  1.563844  0.480488
82744 -0.029715 -0.040846  0.914311  0.022305  ...  1.232765  0.100678
24294  0.193328  0.075123  0.936352 -0.044813  ...  0.486930  0.046766
7820  -0.002898  1.437247 -0.013400 -0.001012  ...  1.250272  0.731957
43295  3.387782  0.179219  0.115231 -0.010963  ...  2.883403  0.345273

            CD3      CD61     CD117     CD49d    HLA-DR      CD64      CD41
\
64113  0.017010  0.051464 -0.003680  1.260410  0.700093  2.355886  0.125409
82744  5.722406 -0.036430  0.021689  0.034946 -0.055651 -0.023248 -0.054842
24294  4.061728  1.003383  0.406137  1.928676 -0.046849  0.229309  0.937020
7820   0.245939 -0.007282  1.421540  1.443145  2.461705  0.528679  0.072205
43295  0.226596 -0.040754  0.060944  1.294561  3.085858 -0.014128  0.479256

       Viability
64113   0.840205
82744  -0.009329
24294   1.231347
7820    0.892480
43295   2.269233

[5 rows x 36 columns]

Training Labels (y_train):
 64113    10.0
82744     7.0
24294     7.0
7820      6.0
43295     9.0
Name: label, dtype: float64

Testing Features (x_test):
        Cell_length      DNA1      DNA2    CD45RA     CD133      CD19  \
60544           49  3.618797  4.144135  0.198186  0.000282  0.253703
50673           27  3.660988  4.497041  1.272625  0.129642  3.054480
50682           23  3.854865  4.663734  1.527763  0.151383  2.361353
1761            17  3.716473  4.465312  0.375236 -0.037150 -0.035385
98760           32  6.826030  7.007709  0.223441 -0.048813 -0.018816

           CD22     CD11b       CD4       CD8  ...      CD38      CD13  \
60544 -0.018972  2.665005  0.079150 -0.002045  ...  2.479135  1.419488
50673  2.493220  0.189975 -0.024412  0.186744  ...  2.212054 -0.020246
50682  2.281009  0.528589 -0.014516 -0.002732  ...  0.787080 -0.010742
1761   0.127904  0.415204  0.226788  2.802413  ...  0.042091 -0.018271
98760 -0.045954  4.067125  0.004401 -0.012083  ...  1.382377  0.154702

            CD3      CD61     CD117     CD49d    HLA-DR      CD64      CD41
```

```
\
60544  0.643676  0.307357  0.208639  2.039954  2.847283  2.798986  1.090235
50673  0.054290  0.084448  0.033192  0.004637  4.488360  0.866820 -0.002174
50682  0.068448 -0.041903 -0.026017  0.109363  2.328828 -0.008223 -0.018680
1761  -0.039628 -0.001024 -0.017034  0.023385  0.120367  0.472159 -0.014919
98760  0.250393 -0.029816 -0.046020  0.140410  0.735830  1.011186 -0.044875

       Viability
60544   1.005784
50673   0.917810
50682   1.091297
1761    0.620643
98760   0.149759

[5 rows x 36 columns]

Testing Labels (y_test):
 60544    10.0
50673     9.0
50682     9.0
1761      2.0
98760    10.0
Name: label, dtype: float64
```

In [ ]:

```
from sklearn.preprocessing import StandardScaler

# Initialize the scaler
scaler = StandardScaler()

# Fit and transform the unlabeled data
x_unlabeled_scaled = scaler.fit_transform(x_unlabeled)

# Convert back to a DataFrame if needed (optional, for better readability)
x_unlabeled_scaled = pd.DataFrame(x_unlabeled_scaled, columns=x_unlabeled.co
```

In [ ]:

```
from sklearn.model_selection import train_test_split
df_labeled = df[df['label'].notnull()]  # Labeled data
df_unlabeled = df[df['label'].isnull()]  # Unlabeled data

# Separate features and target for labeled data
X_labeled = df_labeled.drop(columns=['label'])  # Features
y_labeled = df_labeled['label']                  # Target


# Split the labeled data into training and testing sets (e.g., 70% train, 30
X_train, X_test, y_train, y_test = train_test_split(X_labeled, y_labeled, te

# Print the shapes of the training and testing sets
print("Shape of Training Features (X_train):", X_train.shape)
print("Shape of Training Labels (y_train):", y_train.shape)
print("Shape of Testing Features (X_test):", X_test.shape)
```

```
Shape of Training Features (X_train): (72928, 36)
Shape of Training Labels (y_train): (72928,)
Shape of Testing Features (X_test): (31256, 36)
```

Logistic Regression Model

In [ ]:

```
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import log_loss

def logit(x_train, y_train, x_test):
    """Logistic Regression.

    Args:
        x_train: Training features.
        y_train: Training labels.
        x_test: Testing features.

    Returns:
        y_test_hat: Predicted probabilities for x_test.
    """
    # Convert labels into proper format
    if len(y_train.shape) > 1:
        y_train = donvert_matrix_to_vector(y_train)

    # Define and fit the model on the training dataset
    model = LogisticRegression()
    model.fit(x_train, y_train)

    # Predict probabilities on x_test
    y_test_hat = model.predict_proba(x_test)

    return y_test_hat
```

In [ ]:

```
y_test_prob = logit(X_train, y_train, X_test)

# Display the probabilities
print("Predicted probabilities for the test set:")
print(y_test_prob)

# Compute log loss
log_loss_value = log_loss(y_test, y_test_prob)

# Display log loss
print("Log loss for the test set:", log_loss_value)
```

```
Predicted probabilities for the test set:
[[1.27832255e-12 2.06977665e-16 3.99046638e-17 ... 7.92486068e-13
  3.66276613e-14 1.83700781e-13]
 [3.53829724e-14 5.62561775e-14 9.40919132e-16 ... 1.07032765e-11
  2.42897888e-04 1.52985856e-10]
 [9.66721886e-11 2.33132685e-10 3.73727689e-12 ... 1.13644612e-10
  1.28665515e-06 3.89190497e-11]
 ...
 [8.97193682e-08 1.11777043e-05 1.13462283e-08 ... 2.18504192e-08
  2.32788580e-10 2.44061608e-10]
 [4.43450554e-09 3.80180801e-10 2.59394355e-11 ... 1.75572500e-08
  5.96201221e-06 2.02390897e-07]
 [2.07984818e-09 7.62212185e-09 7.21995065e-11 ... 3.49653489e-11
  5.64646108e-08 4.47350113e-12]]
Log loss for the test set: 0.033144266653965554
```

```
/usr/local/lib/python3.10/dist-packages/sklearn/linear_model/_logistic.py:46
9: ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regre
ssion
  n_iter_i = _check_optimize_result(
```

XGBoost Model

In [ ]:

```
from xgboost import XGBClassifier
from sklearn.metrics import log_loss
import numpy as np

def xgboost_model(x_train, y_train, x_test):
    """XGBoost Classifier.

    Args:
        x_train: Training features.
        y_train: Training labels.
        x_test: Testing features.

    Returns:
        y_test_prob: Predicted probabilities for x_test.
    """
    # Convert labels to proper format and zero-based index if necessary
    if len(y_train.shape) > 1:
        y_train = donvert_matrix_to_vector(y_train)

    y_train = y_train.astype(int) - 1  # Convert to integer and zero-based i

    # Define and fit the XGBoost model on the training dataset
    model = XGBClassifier(use_label_encoder=False, eval_metric='logloss')
    model.fit(x_train, y_train)

    # Predict probabilities on x_test
```

```
    y_test_prob = model.predict_proba(x_test)

    return y_test_prob

# Example usage
# Assuming y_test is the true labels for X_test
y_test_zero_based = y_test.astype(int) - 1  # Adjust y_test for log loss cal
y_test_prob = xgboost_model(X_train, y_train, X_test)

# Display the probabilities
print("Predicted probabilities for the test set:")
print(y_test_prob)

# Compute log loss
log_loss_value = log_loss(y_test_zero_based, y_test_prob)
print("Log loss for the test set:", log_loss_value)
```

```
/usr/local/lib/python3.10/dist-packages/xgboost/core.py:158: UserWarning: [1
4:16:17] WARNING: /workspace/src/learner.cc:740:
Parameters: { "use_label_encoder" } are not used.

  warnings.warn(smsg, UserWarning)
Predicted probabilities for the test set:
[[5.1860439e-07 5.7017002e-07 3.9342234e-07 ... 8.7231638e-07
  7.8322529e-07 5.8524296e-07]
 [8.1559443e-07 1.7004106e-06 6.5709958e-07 ... 1.0578590e-06
  1.6773043e-05 2.0757868e-06]
 [5.4707510e-07 7.7939086e-07 5.7252436e-07 ... 1.0011939e-06
  4.1819862e-06 9.0937459e-07]
 ...
 [7.2769092e-07 3.8095675e-06 7.3217876e-07 ... 6.5145679e-07
  5.3072574e-07 4.8228475e-07]
 [2.6380076e-06 2.8987354e-06 2.4175074e-06 ... 4.4621897e-06
  1.0261622e-05 3.1510957e-05]
 [8.4509293e-07 7.6321942e-07 6.7003754e-07 ... 7.0236740e-07
  3.7610098e-06 9.6112626e-07]]
Log loss for the test set: 0.00400363072165128
```

AUTOENCODER

In [ ]:
```
def binary_mask(p_m, data):
    """Generates a binary mask with probability p_m for corruption."""
    return pd.DataFrame(np.random.binomial(1, p_m, data.shape), columns=data

def x_corruption(mask, data):
    """Applies corruption to the data using the mask."""
    shuffled = data.apply(lambda col: np.random.permutation(col))
    return data * (1 - mask) + shuffled * mask
```

In [ ]:
```
from keras.layers import Input,Dense
from keras.models import Model
from keras import models
import numpy as np
```

```python
def self_supervised(x_unlabeled_scaled,p_m, alpha, parameters):

  # extract the batch_size and epochs
  epochs = parameters['epochs']
  batch_size = parameters['batch_size']
  _,dimension = x_unlabeled_scaled.shape

  # model creation
  # defining an encoder
  # auto encoder ---> corrupted input ---> encoder ----> latent space ---> c
  # working on the encoder part and extracting the latent space
  # creating a fully connecting network with the number of neurons in the fc
  # input_layer will be of size 37
  input_layer = Input(shape=(dimension,))

  #encoder model
  h = Dense(int(dimension),activation='relu')(input_layer)

  #output1 ---> mask estimation
  output1 = Dense(int(dimension) , activation='sigmoid', name='mask_estimati

  #output2 ---> feature estimation
  output2 = Dense(int(dimension) , activation='sigmoid', name='feature_estim

  model = Model(inputs = input_layer, outputs=[output1,output2])
  model.compile(optimizer="rmsprop",loss={'mask_estimation': 'binary_crosser

  # Generate corrupted data and mask
  corruption_mask = binary_mask(p_m,x_unlabeled_scaled)
  x_unlabeled_corrupted = x_corruption(corruption_mask, x_unlabeled_scaled)
  m_label = (x_unlabeled_scaled != x_unlabeled_corrupted).astype(int) # Calc

  # Fit the model
  model.fit(x_unlabeled_corrupted,{'mask_estimation':m_label,'feature_estima

  name_of_layer = model.layers[1].name # Assuming the encoder layer is the s
  layer_output = model.get_layer(name_of_layer).output
  encoder = models.Model(inputs=model.input , outputs=layer_output)
  model.summary()
  return encoder
```

In [ ]:

```python
x_unlab = x_unlabeled_scaled

p_m=0.3

alpha= 2.0

parameters={'batch_size':128,
            'epochs':50,
            }

encoder_model =self_supervised(x_unlab,p_m, alpha, parameters)
```

```
Epoch 1/50
1262/1262 3s 2ms/step - feature_estimation_loss: 0.6362
- loss: 2.3662 - mask_estimation_loss: 1.7301
Epoch 2/50
1262/1262 4s 3ms/step - feature_estimation_loss: 0.6104
- loss: 1.9978 - mask_estimation_loss: 1.3874
Epoch 3/50
1262/1262 3s 2ms/step - feature_estimation_loss: 0.6089
- loss: 1.9796 - mask_estimation_loss: 1.3707
Epoch 4/50
1262/1262 3s 2ms/step - feature_estimation_loss: 0.6082
- loss: 1.9750 - mask_estimation_loss: 1.3668
Epoch 5/50
1262/1262 2s 2ms/step - feature_estimation_loss: 0.6081
- loss: 1.9691 - mask_estimation_loss: 1.3610
Epoch 6/50
1262/1262 2s 2ms/step - feature_estimation_loss: 0.6081
- loss: 1.9639 - mask_estimation_loss: 1.3559
Epoch 7/50
1262/1262 4s 3ms/step - feature_estimation_loss: 0.6074
- loss: 1.9607 - mask_estimation_loss: 1.3534
Epoch 8/50
1262/1262 4s 2ms/step - feature_estimation_loss: 0.6075
- loss: 1.9604 - mask_estimation_loss: 1.3529
Epoch 9/50
1262/1262 3s 2ms/step - feature_estimation_loss: 0.6069
- loss: 1.9645 - mask_estimation_loss: 1.3576
Epoch 10/50
1262/1262 3s 2ms/step - feature_estimation_loss: 0.6069
- loss: 1.9605 - mask_estimation_loss: 1.3536
Epoch 11/50
1262/1262 3s 2ms/step - feature_estimation_loss: 0.6067
- loss: 1.9599 - mask_estimation_loss: 1.3532
Epoch 12/50
1262/1262 5s 2ms/step - feature_estimation_loss: 0.6061
- loss: 1.9534 - mask_estimation_loss: 1.3473
Epoch 13/50
1262/1262 2s 2ms/step - feature_estimation_loss: 0.6056
- loss: 1.9571 - mask_estimation_loss: 1.3516
Epoch 14/50
1262/1262 3s 2ms/step - feature_estimation_loss: 0.6056
- loss: 1.9571 - mask_estimation_loss: 1.3515
Epoch 15/50
1262/1262 2s 2ms/step - feature_estimation_loss: 0.6052
- loss: 1.9524 - mask_estimation_loss: 1.3472
Epoch 16/50
1262/1262 3s 3ms/step - feature_estimation_loss: 0.6052
- loss: 1.9559 - mask_estimation_loss: 1.3507
Epoch 17/50
1262/1262 3s 3ms/step - feature_estimation_loss: 0.6052
- loss: 1.9553 - mask_estimation_loss: 1.3501
Epoch 18/50
1262/1262 4s 2ms/step - feature_estimation_loss: 0.6053
- loss: 1.9567 - mask_estimation_loss: 1.3514
Epoch 19/50
1262/1262 2s 2ms/step - feature_estimation_loss: 0.6051
```

```
- loss: 1.9537 - mask_estimation_loss: 1.3485
Epoch 20/50
1262/1262 ━━━━━━━━━━━━━━━━━━━━ 2s 2ms/step - feature_estimation_loss: 0.6049
- loss: 1.9525 - mask_estimation_loss: 1.3476
Epoch 21/50
1262/1262 ━━━━━━━━━━━━━━━━━━━━ 3s 3ms/step - feature_estimation_loss: 0.6050
- loss: 1.9503 - mask_estimation_loss: 1.3454
Epoch 22/50
1262/1262 ━━━━━━━━━━━━━━━━━━━━ 4s 2ms/step - feature_estimation_loss: 0.6048
- loss: 1.9495 - mask_estimation_loss: 1.3447
Epoch 23/50
1262/1262 ━━━━━━━━━━━━━━━━━━━━ 2s 2ms/step - feature_estimation_loss: 0.6052
- loss: 1.9566 - mask_estimation_loss: 1.3515
Epoch 24/50
1262/1262 ━━━━━━━━━━━━━━━━━━━━ 2s 2ms/step - feature_estimation_loss: 0.6047
- loss: 1.9552 - mask_estimation_loss: 1.3504
Epoch 25/50
1262/1262 ━━━━━━━━━━━━━━━━━━━━ 2s 2ms/step - feature_estimation_loss: 0.6048
- loss: 1.9539 - mask_estimation_loss: 1.3490
Epoch 26/50
1262/1262 ━━━━━━━━━━━━━━━━━━━━ 3s 2ms/step - feature_estimation_loss: 0.6052
- loss: 1.9536 - mask_estimation_loss: 1.3484
Epoch 27/50
1262/1262 ━━━━━━━━━━━━━━━━━━━━ 4s 3ms/step - feature_estimation_loss: 0.6044
- loss: 1.9500 - mask_estimation_loss: 1.3456
Epoch 28/50
1262/1262 ━━━━━━━━━━━━━━━━━━━━ 2s 2ms/step - feature_estimation_loss: 0.6046
- loss: 1.9539 - mask_estimation_loss: 1.3492
Epoch 29/50
1262/1262 ━━━━━━━━━━━━━━━━━━━━ 3s 2ms/step - feature_estimation_loss: 0.6047
- loss: 1.9525 - mask_estimation_loss: 1.3478
Epoch 30/50
1262/1262 ━━━━━━━━━━━━━━━━━━━━ 2s 2ms/step - feature_estimation_loss: 0.6046
- loss: 1.9547 - mask_estimation_loss: 1.3501
Epoch 31/50
1262/1262 ━━━━━━━━━━━━━━━━━━━━ 2s 2ms/step - feature_estimation_loss: 0.6047
- loss: 1.9525 - mask_estimation_loss: 1.3478
Epoch 32/50
1262/1262 ━━━━━━━━━━━━━━━━━━━━ 3s 3ms/step - feature_estimation_loss: 0.6044
- loss: 1.9513 - mask_estimation_loss: 1.3469
Epoch 33/50
1262/1262 ━━━━━━━━━━━━━━━━━━━━ 3s 3ms/step - feature_estimation_loss: 0.6042
- loss: 1.9487 - mask_estimation_loss: 1.3445
Epoch 34/50
1262/1262 ━━━━━━━━━━━━━━━━━━━━ 2s 2ms/step - feature_estimation_loss: 0.6042
- loss: 1.9495 - mask_estimation_loss: 1.3453
Epoch 35/50
1262/1262 ━━━━━━━━━━━━━━━━━━━━ 2s 2ms/step - feature_estimation_loss: 0.6044
- loss: 1.9479 - mask_estimation_loss: 1.3435
Epoch 36/50
1262/1262 ━━━━━━━━━━━━━━━━━━━━ 2s 2ms/step - feature_estimation_loss: 0.6044
- loss: 1.9523 - mask_estimation_loss: 1.3479
Epoch 37/50
1262/1262 ━━━━━━━━━━━━━━━━━━━━ 2s 2ms/step - feature_estimation_loss: 0.6047
- loss: 1.9536 - mask_estimation_loss: 1.3489
Epoch 38/50
```

```
1262/1262 ━━━━━━━━━━━━━━━━━━━━ 4s 3ms/step - feature_estimation_loss: 0.6046
- loss: 1.9518 - mask_estimation_loss: 1.3471
Epoch 39/50
1262/1262 ━━━━━━━━━━━━━━━━━━━━ 4s 2ms/step - feature_estimation_loss: 0.6045
- loss: 1.9507 - mask_estimation_loss: 1.3462
Epoch 40/50
1262/1262 ━━━━━━━━━━━━━━━━━━━━ 2s 2ms/step - feature_estimation_loss: 0.6040
- loss: 1.9508 - mask_estimation_loss: 1.3468
Epoch 41/50
1262/1262 ━━━━━━━━━━━━━━━━━━━━ 2s 2ms/step - feature_estimation_loss: 0.6042
- loss: 1.9549 - mask_estimation_loss: 1.3507
Epoch 42/50
1262/1262 ━━━━━━━━━━━━━━━━━━━━ 2s 2ms/step - feature_estimation_loss: 0.6039
- loss: 1.9559 - mask_estimation_loss: 1.3520
Epoch 43/50
1262/1262 ━━━━━━━━━━━━━━━━━━━━ 4s 3ms/step - feature_estimation_loss: 0.6042
- loss: 1.9491 - mask_estimation_loss: 1.3449
Epoch 44/50
1262/1262 ━━━━━━━━━━━━━━━━━━━━ 3s 2ms/step - feature_estimation_loss: 0.6037
- loss: 1.9524 - mask_estimation_loss: 1.3487
Epoch 45/50
1262/1262 ━━━━━━━━━━━━━━━━━━━━ 4s 2ms/step - feature_estimation_loss: 0.6039
- loss: 1.9499 - mask_estimation_loss: 1.3460
Epoch 46/50
1262/1262 ━━━━━━━━━━━━━━━━━━━━ 3s 2ms/step - feature_estimation_loss: 0.6040
- loss: 1.9524 - mask_estimation_loss: 1.3484
Epoch 47/50
1262/1262 ━━━━━━━━━━━━━━━━━━━━ 2s 2ms/step - feature_estimation_loss: 0.6037
- loss: 1.9508 - mask_estimation_loss: 1.3472
Epoch 48/50
1262/1262 ━━━━━━━━━━━━━━━━━━━━ 4s 3ms/step - feature_estimation_loss: 0.6040
- loss: 1.9489 - mask_estimation_loss: 1.3449
Epoch 49/50
1262/1262 ━━━━━━━━━━━━━━━━━━━━ 5s 4ms/step - feature_estimation_loss: 0.6039
- loss: 1.9511 - mask_estimation_loss: 1.3472
Epoch 50/50
1262/1262 ━━━━━━━━━━━━━━━━━━━━ 12s 6ms/step - feature_estimation_loss: 0.603
9 - loss: 1.9540 - mask_estimation_loss: 1.3501
```

Model: "functional"

Layer (type)	Output Shape	Param #
input_layer (InputLayer)	(None, 36)	0
dense (Dense)	(None, 36)	1,332
mask_estimation (Dense)	(None, 36)	1,332
feature_estimation (Dense)	(None, 36)	1,332

Total params: 7,994 (31.23 KB)

Trainable params: 3,996 (15.61 KB)

Non-trainable params: 0 (0.00 B)

Optimizer params: 3,998 (15.62 KB)

Saving Autoencoder

In [40]:
```
import os

# Define the path where you want to save the model
encoder_path = "content/encoder_model.keras"

# Create the directory if it doesn't exist
os.makedirs(os.path.dirname(encoder_path), exist_ok=True)

# Save the model
encoder_model.save(encoder_path)

print(f"Model saved to {encoder_path}")
```

```
Model saved to content/encoder_model.keras
```

In [41]:
```
from keras.models import load_model
encoder=load_model(encoder_path)
```

Evaluating Encoded Features with Logistic Regression and XGBoost

In [ ]:
```
import numpy as np
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import log_loss
import xgboost as xgb

# Adjust y_train and y_test labels to start from 0 by subtracting the minimu
y_train -= y_train.min()
y_test -= y_test.min()

scaler = StandardScaler()
x_train_scaled = scaler.fit_transform(x_train)  # Scale training data
x_test_scaled = scaler.transform(x_test)

# Step 1: Define the encoder model and train it on x_unlab (assumed to be do
# For demonstration, use the encoder to transform train and test data

# Use the encoder to get the encoded data for training and testing
x_train_scaled_encoded = encoder.predict(x_train_scaled)
x_test_scaled_encoded = encoder.predict(x_test_scaled)

# Check shapes
print("Encoded x_train shape:", x_train_scaled_encoded.shape)
print("Encoded x_test shape:", x_test_scaled_encoded.shape)

# Step 2: Logistic Regression
log_reg = LogisticRegression(max_iter=1000)  # Set max_iter to a higher valu
log_reg.fit(x_train_scaled_encoded, y_train)
```

```python
# Predict on the test set using Logistic Regression
y_encoded_log_reg = log_reg.predict_proba(x_test_scaled_encoded)

# Compute log loss for logistic regression predictions
log_reg_loss = log_loss(y_test, y_encoded_log_reg)
print("Log Loss for Logistic Regression:", log_reg_loss)

# Step 3: XGBoost Model
xgb_model = xgb.XGBClassifier(eval_metric='logloss', random_state=42)
xgb_model.fit(x_train_scaled_encoded, y_train)

# Predict on the test set using XGBoost
y_encoded_xgb = xgb_model.predict_proba(x_test_scaled_encoded)

# Compute log loss for XGBoost predictions
xgb_loss = log_loss(y_test, y_encoded_xgb)
print("Log Loss for XGBoost:", xgb_loss)
```

```
2279/2279 ━━━━━━━━━━━━━━━━━━━━ 4s 2ms/step
977/977 ━━━━━━━━━━━━━━━━━━━━ 2s 2ms/step
Encoded x_train shape: (72928, 36)
Encoded x_test shape: (31256, 36)
Log Loss for Logistic Regression: 0.03150809857009143
Log Loss for XGBoost: 0.051473070193110836
```

SEMI SUPERVISED

In [ ]:

```python
import numpy as np
import tensorflow as tf
from tensorflow.keras import layers, optimizers, losses
from tensorflow.keras.utils import to_categorical
from tensorflow.keras.models import load_model
import pandas as pd

# Define the model
def model(input_dimension, hidden_dimension, label_dimension, activation=tf.
    inputs = tf.keras.Input(shape=input_dimension, name='model_input')
    x = layers.Dense(hidden_dimension, activation=activation, name='model_de
    x = layers.Dense(hidden_dimension, activation=activation, name='model_de
    y_logit = layers.Dense(label_dimension, activation=None, name='model_log
    y = layers.Activation('softmax', name='model_output')(y_logit)
    return tf.keras.Model(inputs=inputs, outputs=[y_logit, y], name="model")

# Training function
def train(feature_batch, label_batch, unlabeled_feature_batch, model, beta,
    with tf.GradientTape() as tape:
        # Labeled data loss
        y_logit, _ = model(feature_batch, training=True)
        y_loss = supv_loss_fn(label_batch, y_logit)

        # Unlabeled data loss
        unlabeled_y_logit, _ = model(unlabeled_feature_batch, training=True)
        _, variance = tf.nn.moments(unlabeled_y_logit, axes=0)
        unlabeled_y_loss = tf.reduce_mean(variance)
```

```
        # Total loss
        total_loss = y_loss + beta * unlabeled_y_loss

    # Gradient computation and update
    grads = tape.gradient(total_loss, model.trainable_weights)
    optimizer.apply_gradients(zip(grads, model.trainable_weights))
    return total_loss

# Semi-supervised function
def semi_supervised(x_train, y_train, x_unlabeled, x_test, parameters, mask_
    # Ensure NumPy arrays
    if isinstance(x_train, pd.DataFrame):
        x_train = x_train.values
    if isinstance(y_train, pd.Series):
        y_train = y_train.values
    if isinstance(x_unlabeled, pd.DataFrame):
        x_unlabeled = x_unlabeled.values
    if isinstance(x_test, pd.DataFrame):
        x_test = x_test.values

    # Hyperparameters
    hidden_dimension = parameters['hidden_dim']
    batch_size = parameters['batch_size']
    epochs = parameters['iterations']
    input_dimension = x_train.shape[1]

    # Label preprocessing: One-hot encoding for CategoricalCrossentropy
    unique_classes = np.unique(y_train)
    label_dimension = len(unique_classes)
    class_mapping = {label: idx for idx, label in enumerate(unique_classes)}
    y_train_mapped = np.vectorize(class_mapping.get)(y_train)
    y_train_one_hot = to_categorical(y_train_mapped, num_classes=label_dimer

    # Data splitting
    index = np.random.permutation(x_train.shape[0])
    train_index = index[:int(len(index) * 0.9)]
    valid_index = index[int(len(index) * 0.9):]
    splitted_train_x, splitted_train_y = x_train[train_index], y_train_one_h
    splitted_valid_x, splitted_valid_y = x_train[valid_index], y_train_one_h

    # Load pre-trained encoder
    encoder = load_model(encoder_path)
    x_valid_encoded = encoder.predict(splitted_valid_x)
    x_test_encoded = encoder.predict(x_test)

    # Initialize the supervised model
    supervised_model = model(input_dimension=(encoder.output_shape[1],),
                             hidden_dimension=hidden_dimension,
                             label_dimension=label_dimension)

    optimizer = optimizers.Adam()
    supv_loss_fn = losses.CategoricalCrossentropy(from_logits=True)

    # Training loop
    for epoch in range(epochs):
        batch_index = np.random.choice(splitted_train_x.shape[0], batch_size
```

```
        batch_x, batch_y = splitted_train_x[batch_index], splitted_train_y[b
        batch_x_encoded = encoder.predict(batch_x)

        batch_unlabeled_index = np.random.choice(x_unlabeled.shape[0], batch
        batch_unlabeled_x = x_unlabeled[batch_unlabeled_index]

        batch_unlabeled_x_shuffled = []
        for _ in range(K):
            mask = np.random.binomial(1, mask_probability, batch_unlabeled_x
            corrupted_data = batch_unlabeled_x * (1 - mask) + np.random.perm
            corrupted_data_encoded = encoder.predict(corrupted_data)
            batch_unlabeled_x_shuffled.append(corrupted_data_encoded)
        batch_unlabeled_x_shuffled = np.concatenate(batch_unlabeled_x_shuffl

        total_loss = train(batch_x_encoded, batch_y, batch_unlabeled_x_shuff

        y_valid_logit, _ = supervised_model(x_valid_encoded, training=False)
        y_valid_loss = supv_loss_fn(splitted_valid_y, y_valid_logit)

        if epoch % 100 == 0:
            print(f'Epoch: {epoch}/{epochs}, Validation Loss: {y_valid_loss:

    y_test_logit, _ = supervised_model(x_test_encoded, training=False)
    return y_test_logit, supervised_model

# Hyperparameters
mask_probability = 0.3
K = 3
beta = 1.0
parameters = {
    'hidden_dim': 100,
    'batch_size': 128,
    'iterations': 1100
}

# Assuming x_train, y_train, x_unlabeled_scaled, x_test are defined
encoder_path = "content/encoder_model.keras"  # Replace with your encoder pa
y_test_model, model_instance = semi_supervised(x_train, y_train, x_unlabelec
                                         parameters, mask_probability, K, be
```

```
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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Epoch: 100/1100, Validation Loss: 0.3188
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
Epoch: 200/1100, Validation Loss: 0.1738
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 7ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 8ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
Epoch: 300/1100, Validation Loss: 0.1321
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 7ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
Epoch: 400/1100, Validation Loss: 0.1101
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 7ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 7ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
Epoch: 500/1100, Validation Loss: 0.0929
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 8ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 7ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 7ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 7ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 8ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 7ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
Epoch: 600/1100, Validation Loss: 0.0844
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 7ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
Epoch: 700/1100, Validation Loss: 0.0787
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 8ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 10ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 7ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 8ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 10ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
Epoch: 800/1100, Validation Loss: 0.0757
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 7ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
Epoch: 900/1100, Validation Loss: 0.0983
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 7ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 7ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
Epoch: 1000/1100, Validation Loss: 0.0736
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 2ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step
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4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 4ms/step
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```

Performace Metrics

In [27]:

```python
from sklearn.metrics import accuracy_score, roc_auc_score
from sklearn.preprocessing import label_binarize
import numpy as np

def perf_metric(metric, y_test, y_test_hat):
    """
    Evaluate the performance of a classification model using accuracy or AUR
```

```
    Parameters:
    - metric (str): 'acc' for accuracy or 'auc' for AUROC.
    - y_test (np.array): Ground truth labels, integer encoded, shape: (n_sam
    - y_test_hat (np.array): Predicted probabilities, shape: (n_samples, n_c

    Returns:
    - float: Calculated performance metric.
    """
    # Validate input
    if metric not in ['acc', 'auc']:
        raise ValueError("Unsupported metric. Use 'acc' for accuracy or 'auc

    # Accuracy metric
    if metric == 'acc':
        # Convert predicted probabilities to class labels
        y_pred = np.argmax(y_test_hat, axis=1)
        return accuracy_score(y_test, y_pred)

    # AUROC metric
    elif metric == 'auc':
        n_classes = y_test_hat.shape[1]
        if n_classes == 2:  # Binary classification
            # Use probabilities of the positive class
            y_pred_prob = y_test_hat[:, 1]
            return roc_auc_score(y_test, y_pred_prob)
        elif n_classes > 2:  # Multiclass classification
            # Use one-vs-rest approach
            y_test_bin = label_binarize(y_test, classes=np.unique(y_test))
            return roc_auc_score(y_test_bin, y_test_hat, average='macro', mu
        else:
            raise ValueError("AUROC is not defined for single-class tasks.")
```

In [28]:

```
# Evaluate Accuracy
accuracy = perf_metric('acc', y_test, y_test_model)
print(f"Accuracy: {accuracy:.4f}")

# Evaluate AUROC
auroc = perf_metric('auc', y_test, y_test_model)
print(f"AUROC: {auroc:.4f}")
```

```
Accuracy: 0.9766
AUROC: 0.9952
```

Predictions

In [29]:

```
def generate_unlabeled_predictions(x_unlab, encoder, predictor):
    """
    Generate predictions for unlabeled data using an encoder and predictor.

    Parameters:
    - x_unlab: Unlabeled feature data.
    - encoder: Pretrained encoder model to encode features.
    - predictor: Trained classification model.
```

```
    Returns:
    - y_unlab_pred: Predicted labels for unlabeled data.
    """
    # Encode unlabeled data
    x_unlab_encoded = encoder.predict(x_unlab)

    # Predict with the classifier
    _, y_unlab_hat = predictor(x_unlab_encoded, training=False)

    # Convert probabilities to predicted class labels
    y_unlab_pred = np.argmax(y_unlab_hat, axis=1)
    return y_unlab_pred

# Generate predictions for the unlabeled data
y_unlab_pred = generate_unlabeled_predictions(x_unlabeled_scaled, encoder, m
print(f"Predicted Labels for Unlabeled Data:\n{y_unlab_pred}")
```

```
5046/5046 ━━━━━━━━━━━━━━━━━━━━ 15s 3ms/step
Predicted Labels for Unlabeled Data:
[1 1 1 ... 1 1 1]
```

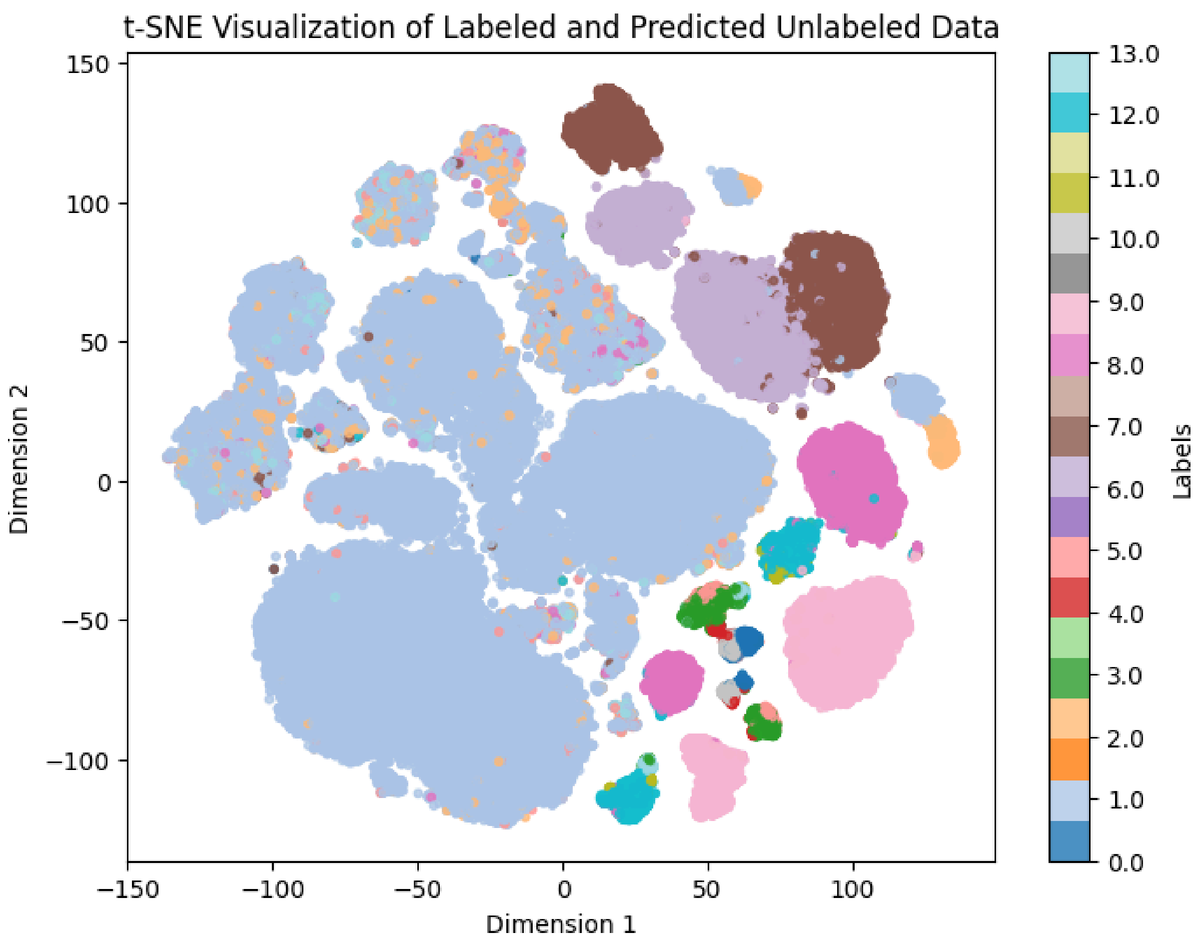
TSNE after semi-superivised

In [30]:
```
pip install openTSNE
```

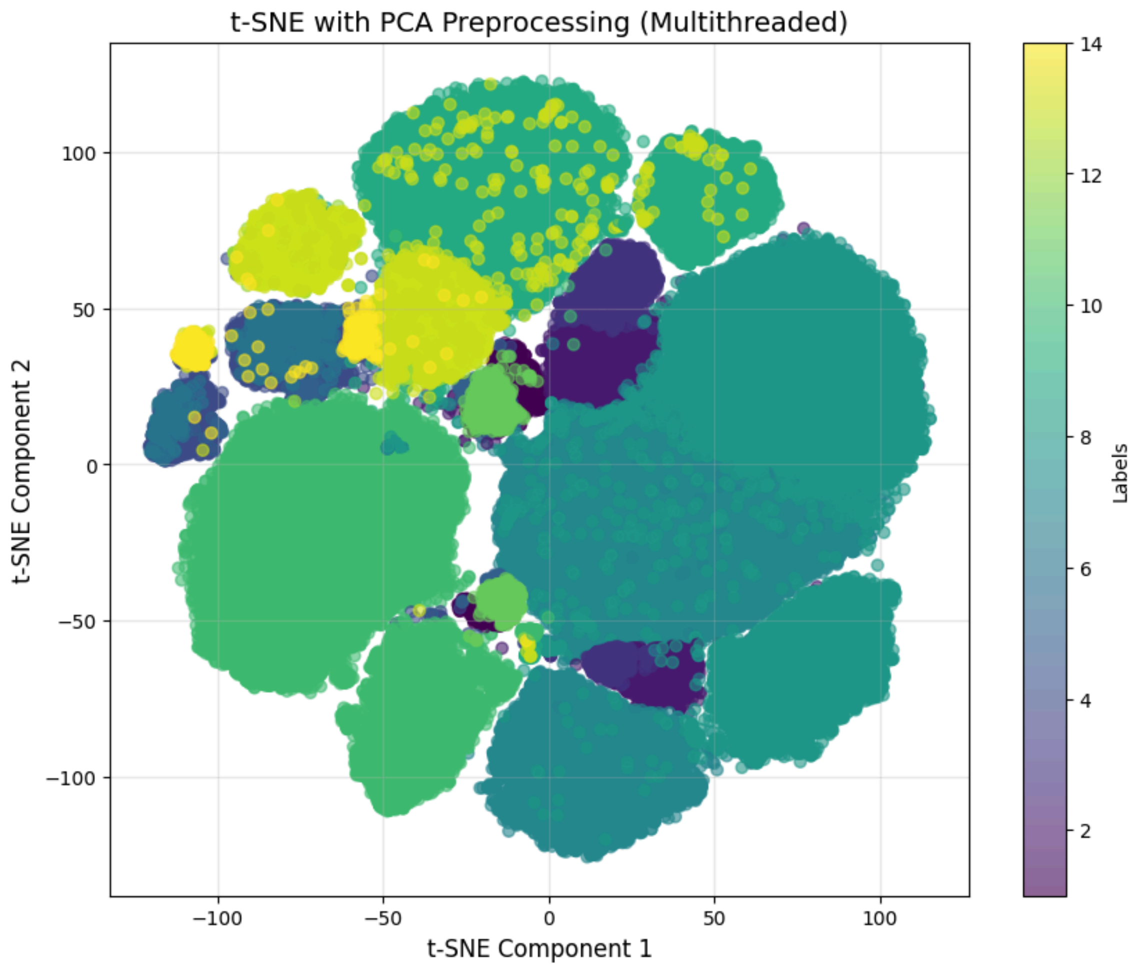
```
Requirement already satisfied: openTSNE in /usr/local/lib/python3.10/dist-pa
ckages (1.0.2)
Requirement already satisfied: numpy>=1.16.6 in /usr/local/lib/python3.10/di
st-packages (from openTSNE) (1.26.4)
Requirement already satisfied: scikit-learn>=0.20 in /usr/local/lib/python3.
10/dist-packages (from openTSNE) (1.5.2)
Requirement already satisfied: scipy in /usr/local/lib/python3.10/dist-packa
ges (from openTSNE) (1.13.1)
Requirement already satisfied: joblib>=1.2.0 in /usr/local/lib/python3.10/di
st-packages (from scikit-learn>=0.20->openTSNE) (1.4.2)
Requirement already satisfied: threadpoolctl>=3.1.0 in /usr/local/lib/python
3.10/dist-packages (from scikit-learn>=0.20->openTSNE) (3.5.0)
```

In [46]:
```
from matplotlib.colors import ListedColormap
import matplotlib.pyplot as plt
from openTSNE import TSNE
import numpy as np
from matplotlib import cm

def plot_tsne_custom_color(features, labels, title="t-SNE Visualization"):
    """
    Generate t-SNE visualization using OpenTSNE with a custom color scheme.

    Parameters:
    - features: The feature matrix (e.g., encoded or raw features).
    - labels: Labels corresponding to the features (should be integers or ca
    - title: Title of the plot.
    """
    # Perform t-SNE with OpenTSNE
    tsne = TSNE(n_components=2, perplexity=30, n_iter=1000, random_state=42)
```

```
    tsne_result = tsne.fit(features)

    # Generate a custom color map for better visual differentiation of clust
    num_classes = len(np.unique(labels))
    if num_classes <= 20:
        colors = cm.tab20.colors  # A colormap with 20 distinct colors
    else:
        colors = cm.nipy_spectral(np.linspace(0, 1, num_classes))  # A more
    cmap = ListedColormap(colors)

    # Plot the results
    plt.figure(figsize=(8, 6))
    scatter = plt.scatter(tsne_result[:, 0], tsne_result[:, 1], c=labels, cm
    plt.title(title)
    plt.xlabel('Dimension 1')
    plt.ylabel('Dimension 2')
    cbar = plt.colorbar(scatter, ticks=np.unique(labels))
    cbar.set_label('Labels')
    cbar.ax.set_yticklabels([str(label) for label in np.unique(labels)])
    plt.show()

# Features (scaled unlabeled data) and predicted labels
scaled_features = np.vstack([x_train_scaled_encoded, x_unlabeled_scaled])  #
combined_labels = np.hstack([y_train, y_unlab_pred])  # Combine true and pre

# Call the t-SNE plotting function
plot_tsne_custom_color(scaled_features, combined_labels, title="t-SNE Visual
```



Intial TSNE for Comparison



In [34]:

```
!pip install gradio
```

```
Collecting gradio
  Downloading gradio-5.6.0-py3-none-any.whl.metadata (16 kB)
Collecting aiofiles<24.0,>=22.0 (from gradio)
  Downloading aiofiles-23.2.1-py3-none-any.whl.metadata (9.7 kB)
Requirement already satisfied: anyio<5.0,>=3.0 in /usr/local/lib/python3.10/
dist-packages (from gradio) (3.7.1)
Collecting fastapi<1.0,>=0.115.2 (from gradio)
  Downloading fastapi-0.115.5-py3-none-any.whl.metadata (27 kB)
Collecting ffmpy (from gradio)
  Downloading ffmpy-0.4.0-py3-none-any.whl.metadata (2.9 kB)
Collecting gradio-client==1.4.3 (from gradio)
  Downloading gradio_client-1.4.3-py3-none-any.whl.metadata (7.1 kB)
Requirement already satisfied: httpx>=0.24.1 in /usr/local/lib/python3.10/di
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Requirement already satisfied: huggingface-hub>=0.25.1 in /usr/local/lib/pyt
hon3.10/dist-packages (from gradio) (0.26.2)
Requirement already satisfied: jinja2<4.0 in /usr/local/lib/python3.10/dist-
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Collecting markupsafe~=2.0 (from gradio)
  Downloading MarkupSafe-2.1.5-cp310-cp310-manylinux_2_17_x86_64.manylinux20
14_x86_64.whl.metadata (3.0 kB)
Requirement already satisfied: numpy<3.0,>=1.0 in /usr/local/lib/python3.10/
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Requirement already satisfied: pandas<3.0,>=1.0 in /usr/local/lib/python3.1
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Requirement already satisfied: pillow<12.0,>=8.0 in /usr/local/lib/python3.1
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Requirement already satisfied: pydantic>=2.0 in /usr/local/lib/python3.10/di
st-packages (from gradio) (2.9.2)
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Requirement already satisfied: pyyaml<7.0,>=5.0 in /usr/local/lib/python3.1
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Collecting ruff>=0.2.2 (from gradio)
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4.whl.metadata (25 kB)
Collecting safehttpx<1.0,>=0.1.1 (from gradio)
  Downloading safehttpx-0.1.1-py3-none-any.whl.metadata (4.1 kB)
Collecting semantic-version~=2.0 (from gradio)
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Collecting starlette<1.0,>=0.40.0 (from gradio)
  Downloading starlette-0.41.3-py3-none-any.whl.metadata (6.0 kB)
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  Downloading tomlkit-0.12.0-py3-none-any.whl.metadata (2.7 kB)
Requirement already satisfied: typer<1.0,>=0.12 in /usr/local/lib/python3.1
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Requirement already satisfied: typing-extensions~=4.0 in /usr/local/lib/pyth
on3.10/dist-packages (from gradio) (4.12.2)
Collecting uvicorn>=0.14.0 (from gradio)
  Downloading uvicorn-0.32.1-py3-none-any.whl.metadata (6.6 kB)
```

```
Requirement already satisfied: fsspec in /usr/local/lib/python3.10/dist-pack
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Collecting websockets<13.0,>=10.0 (from gradio-client==1.4.3->gradio)
  Downloading websockets-12.0-cp310-cp310-manylinux_2_5_x86_64.manylinux1_x8
6_64.manylinux_2_17_x86_64.manylinux2014_x86_64.whl.metadata (6.6 kB)
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t-packages (from anyio<5.0,>=3.0->gradio) (1.3.1)
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kages (from httpx>=0.24.1->gradio) (2024.8.30)
Requirement already satisfied: httpcore==1.* in /usr/local/lib/python3.10/di
st-packages (from httpx>=0.24.1->gradio) (1.0.7)
Requirement already satisfied: h11<0.15,>=0.13 in /usr/local/lib/python3.10/
dist-packages (from httpcore==1.*->httpx>=0.24.1->gradio) (0.14.0)
Requirement already satisfied: filelock in /usr/local/lib/python3.10/dist-pa
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Requirement already satisfied: python-dateutil>=2.8.2 in /usr/local/lib/pyth
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Requirement already satisfied: pytz>=2020.1 in /usr/local/lib/python3.10/dis
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n3.10/dist-packages (from pydantic>=2.0->gradio) (2.23.4)
Requirement already satisfied: click>=8.0.0 in /usr/local/lib/python3.10/dis
t-packages (from typer<1.0,>=0.12->gradio) (8.1.7)
Requirement already satisfied: shellingham>=1.3.0 in /usr/local/lib/python3.
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Requirement already satisfied: rich>=10.11.0 in /usr/local/lib/python3.10/di
st-packages (from typer<1.0,>=0.12->gradio) (13.9.4)
Requirement already satisfied: six>=1.5 in /usr/local/lib/python3.10/dist-pa
ckages (from python-dateutil>=2.8.2->pandas<3.0,>=1.0->gradio) (1.16.0)
Requirement already satisfied: markdown-it-py>=2.2.0 in /usr/local/lib/pytho
n3.10/dist-packages (from rich>=10.11.0->typer<1.0,>=0.12->gradio) (3.0.0)
Requirement already satisfied: pygments<3.0.0,>=2.13.0 in /usr/local/lib/pyt
hon3.10/dist-packages (from rich>=10.11.0->typer<1.0,>=0.12->gradio) (2.18.
0)
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Requirement already satisfied: urllib3<3,>=1.21.1 in /usr/local/lib/python3.
10/dist-packages (from requests->huggingface-hub>=0.25.1->gradio) (2.2.3)
Requirement already satisfied: mdurl~=0.1 in /usr/local/lib/python3.10/dist-
packages (from markdown-it-py>=2.2.0->rich>=10.11.0->typer<1.0,>=0.12->gradi
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Downloading aiofiles-23.2.1-py3-none-any.whl (15 kB)
Downloading fastapi-0.115.5-py3-none-any.whl (94 kB)
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Downloading starlette-0.41.3-py3-none-any.whl (73 kB)
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Downloading pydub-0.25.1-py2.py3-none-any.whl (32 kB)
Downloading websockets-12.0-cp310-cp310-manylinux_2_5_x86_64.manylinux1_x86_
64.manylinux_2_17_x86_64.manylinux2014_x86_64.whl (130 kB)
   ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 130.2/130.2 kB 9.0 MB/s eta 0:0
0:00
Installing collected packages: pydub, websockets, uvicorn, tomlkit, semantic
-version, ruff, python-multipart, markupsafe, ffmpy, aiofiles, starlette, sa
fehttpx, gradio-client, fastapi, gradio
  Attempting uninstall: markupsafe
    Found existing installation: MarkupSafe 3.0.2
    Uninstalling MarkupSafe-3.0.2:
      Successfully uninstalled MarkupSafe-3.0.2
Successfully installed aiofiles-23.2.1 fastapi-0.115.5 ffmpy-0.4.0 gradio-5.
6.0 gradio-client-1.4.3 markupsafe-2.1.5 pydub-0.25.1 python-multipart-0.0.1
2 ruff-0.8.0 safehttpx-0.1.1 semantic-version-2.10.0 starlette-0.41.3 tomlki
t-0.12.0 uvicorn-0.32.1 websockets-12.0
```

In [45]:

```python
import gradio as gr
import pandas as pd
import numpy as np
from openTSNE import TSNE
import matplotlib.pyplot as plt
from matplotlib import colormaps
from tensorflow.keras.models import load_model

# Function to generate predictions for unlabeled data
def generate_predictions_for_unlabeled(x_unlab, encoder, predictor):
    """Encode data and generate predictions for unlabeled samples."""
    encoded_data = encoder.predict(x_unlab)  # Encode data using the encoder
    predictions = predictor(encoded_data, training=False)  # Get the predict
    predicted_classes = np.argmax(predictions, axis=1)  # Get predicted clas
```

```
    return predicted_classes


# Function for t-SNE visualization
def create_tsne_visualization(features, labels, title="t-SNE Visualization")
    """Perform t-SNE dimensionality reduction and visualize with distinct cl
    tsne = TSNE(n_components=2, perplexity=30, n_iter=1000, random_state=42)
    tsne_result = tsne.fit(features)

    unique_labels = np.unique(labels)
    label_to_index = {label: idx for idx, label in enumerate(unique_labels)}
    color_indices = np.array([label_to_index[label] for label in labels])

    cmap = colormaps.get_cmap('tab10')  # Get the colormap
    fig, ax = plt.subplots(figsize=(8, 6))
    scatter = ax.scatter(
        tsne_result[:, 0],
        tsne_result[:, 1],
        c=color_indices,
        cmap=cmap,
        s=5,
        alpha=0.7
    )
    ax.set_title(title)
    ax.set_xlabel('t-SNE Dimension 1')
    ax.set_ylabel('t-SNE Dimension 2')

    # Add legend for cluster labels
    legend_handles = [
        plt.Line2D([], [], marker='o', color=cmap(idx / len(unique_labels)),
        for idx in range(len(unique_labels))
    ]
    ax.legend(legend_handles, unique_labels, title="Clusters", loc="best", b

    return fig

# Function to process and visualize predictions and t-SNE
def process_and_visualize_data(start_row, end_row):
    """
    Process a subset of the x_unlabeled dataset, predict labels, and generat
    """
    global x_unlabeled  # Ensure x_unlabeled is loaded

    # Parse input row indices
    start_row = int(start_row)
    end_row = int(end_row)

    # Select subset of data
    x_subset = x_unlabeled[start_row:end_row]

    # Load pre-trained encoder and predictor
    encoder = load_model(encoder_path)
    trained_model = encoder
    predictor = trained_model  # Assume predictor is preloaded

    # Predict labels for the subset
```

```python
    predicted_labels = generate_predictions_for_unlabeled(x_subset, encoder,

    # Create t-SNE visualization
    tsne_figure = create_tsne_visualization(x_subset, predicted_labels, titl

    # Return visualization and predictions
    return tsne_figure, pd.DataFrame({"Predicted Labels": predicted_labels})

# Set up Gradio interface
inputs = [
    gr.Number(label="Start Row", value=3, precision=0),  # Starting row inpu
    gr.Number(label="End Row", value=109, precision=0)   # Ending row input
]

outputs = [
    gr.Plot(label="t-SNE Visualization"),              # t-SNE plot
    gr.Dataframe(label="Predicted Labels (Top 10)")     # Dataframe for prec
]

gr.Interface(
    fn=process_and_visualize_data,
    inputs=inputs,
    outputs=outputs,
    title="Self-Supervised Learning Visualization",
    description="Generate predictions and visualize data with t-SNE."
).launch(debug=True)
```

```
Running Gradio in a Colab notebook requires sharing enabled. Automatically s
etting `share=True` (you can turn this off by setting `share=False` in `laun
ch()` explicitly).

Colab notebook detected. This cell will run indefinitely so that you can see
errors and logs. To turn off, set debug=False in launch().
* Running on public URL: https://459f058217e09b9478.gradio.live

This share link expires in 72 hours. For free permanent hosting and GPU upgr
ades, run `gradio deploy` from the terminal in the working directory to depl
oy to Hugging Face Spaces (https://huggingface.co/spaces)
```

No interface is running right now

```
1/4 ━━━━━━━━━━━━━━━━━━━━ 0s 38ms/step
WARNING:tensorflow:5 out of the last 28676 calls to <function TensorFlowTrai
ner.make_predict_function.<locals>.one_step_on_data_distributed at 0x7bd4bc5
af250> triggered tf.function retracing. Tracing is expensive and the excessi
ve number of tracings could be due to (1) creating @tf.function repeatedly i
n a loop, (2) passing tensors with different shapes, (3) passing Python obje
cts instead of tensors. For (1), please define your @tf.function outside of
the loop. For (2), @tf.function has reduce_retracing=True option that can av
oid unnecessary retracing. For (3), please refer to https://www.tensorflow.o
rg/guide/function#controlling_retracing and https://www.tensorflow.org/api_d
ocs/python/tf/function for  more details.
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 9ms/step
WARNING:tensorflow:6 out of the last 28677 calls to <function TensorFlowTrai
ner.make_predict_function.<locals>.one_step_on_data_distributed at 0x7bd4b5d
bfb50> triggered tf.function retracing. Tracing is expensive and the excessi
ve number of tracings could be due to (1) creating @tf.function repeatedly i
n a loop, (2) passing tensors with different shapes, (3) passing Python obje
cts instead of tensors. For (1), please define your @tf.function outside of
the loop. For (2), @tf.function has reduce_retracing=True option that can av
oid unnecessary retracing. For (3), please refer to https://www.tensorflow.o
rg/guide/function#controlling_retracing and https://www.tensorflow.org/api_d
ocs/python/tf/function for  more details.
2/2 ━━━━━━━━━━━━━━━━━━━━ 0s 22ms/step
```

```
WARNING:openTSNE.affinity:Perplexity value 30 is too high. Using perplexity
15.33 instead
32/32 ━━━━━━━━━━━━━━━━━━━━ 0s 3ms/step
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 8ms/step
Keyboard interruption in main thread... closing server.
Killing tunnel 127.0.0.1:7860 <> https://459f058217e09b9478.gradio.live
```

Out[45]: