CytoAutoCluster

Importing Dataset

In [ ]:
```python
import pandas as pd
```

In [ ]:
```python
data= pd.read_csv('/content/drive/MyDrive/Datasets/Levine_32dim.fcs.csv')
```

In [ ]:
```python
data.head()
```

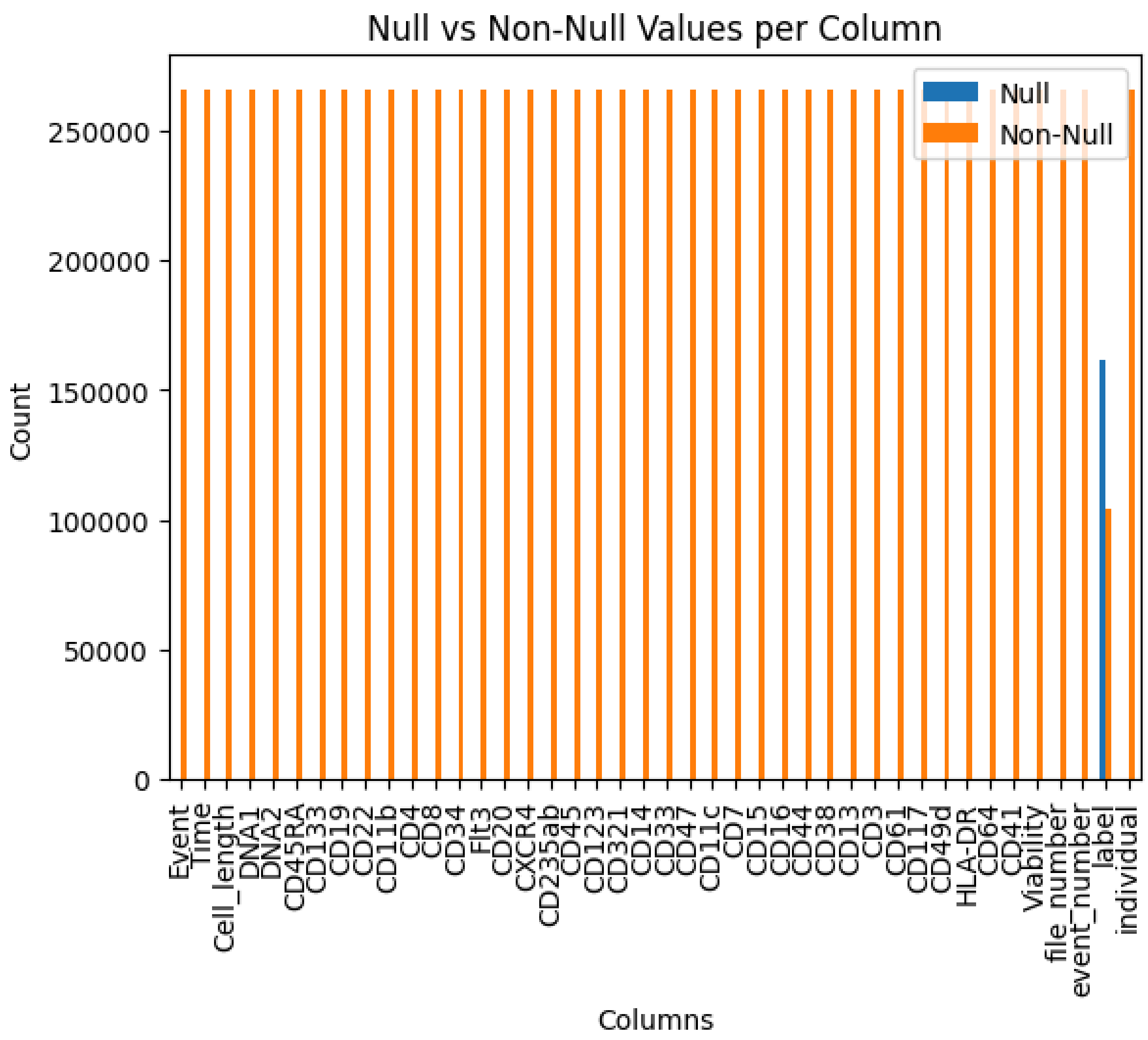
Out[ ]:

	Event	Time	Cell_length	DNA1	DNA2	CD45RA	CD133	CD1
0	1	2693.0	22	4.391057	4.617262	0.162691	-0.029585	-0.0066
1	2	3736.0	35	4.340481	4.816692	0.701349	-0.038280	-0.0166
2	3	7015.0	32	3.838727	4.386369	0.603568	-0.032216	0.0738
3	4	7099.0	29	4.255806	4.830048	0.433747	-0.027611	-0.0176
4	5	7700.0	25	3.976909	4.506433	-0.008809	-0.030297	0.0804

5 rows × 42 columns

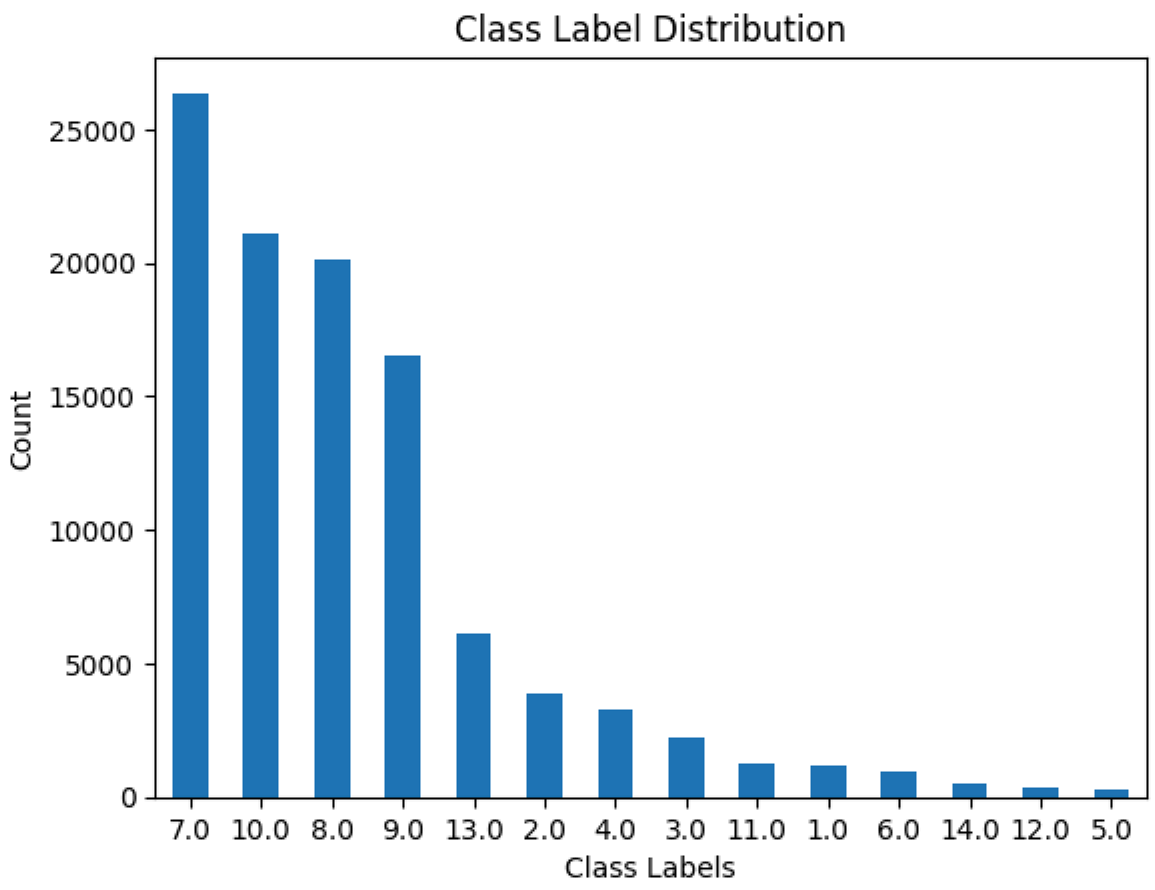
NULL VS NOT NULL

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

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

null_counts = data.isnull().sum()
non_null_counts = data.notnull().sum()

counts_df = pd.DataFrame({
    'Null': null_counts,
    'Non-Null': non_null_counts
})


counts_df.plot(kind='bar')

plt.title('Null vs Non-Null Values per Column')
plt.ylabel('Count')
plt.xlabel('Columns')
plt.xticks(rotation=90)
plt.show()
```



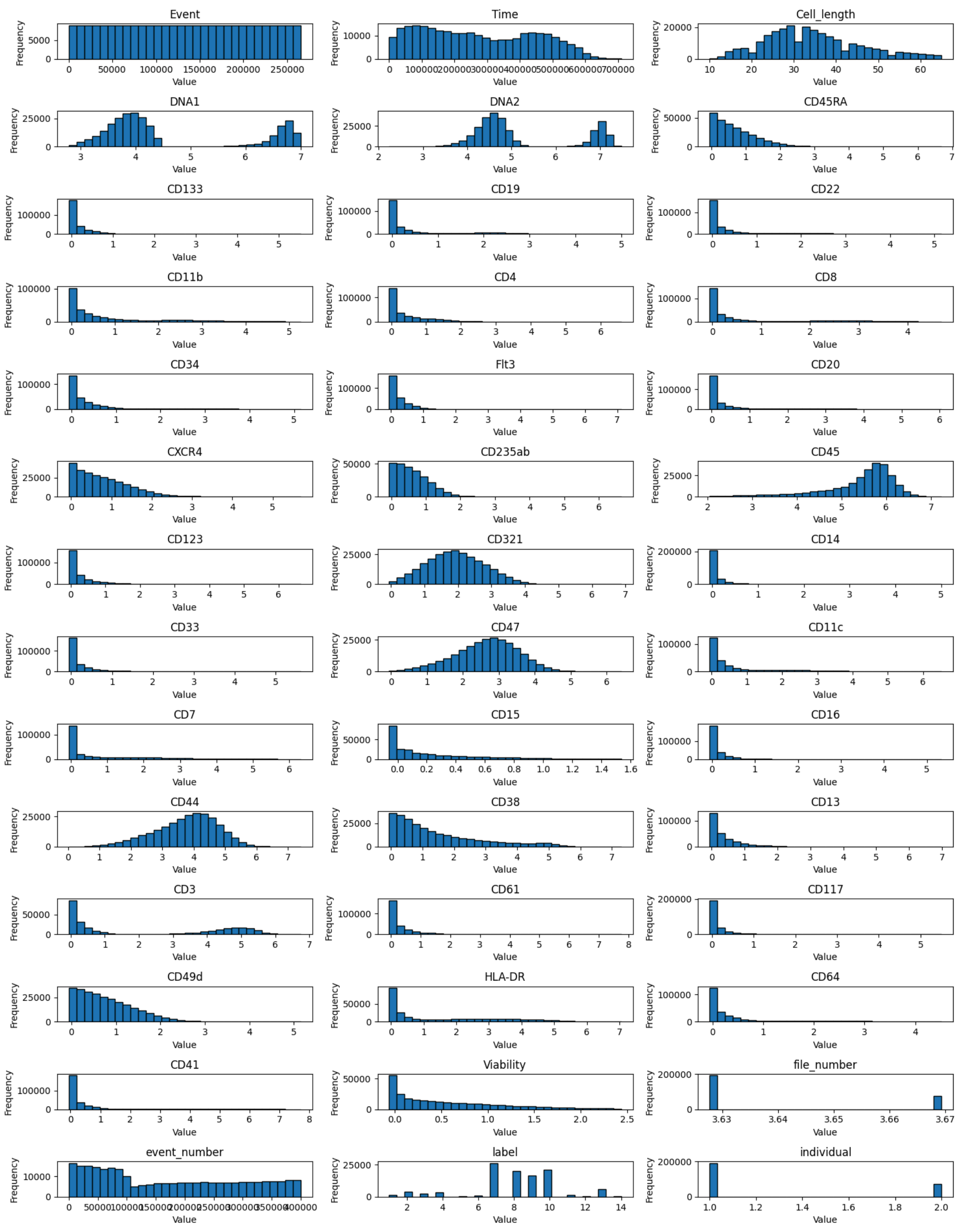
CLASS LABEL DISTRIBUTION

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()
```



Histograms of each feature

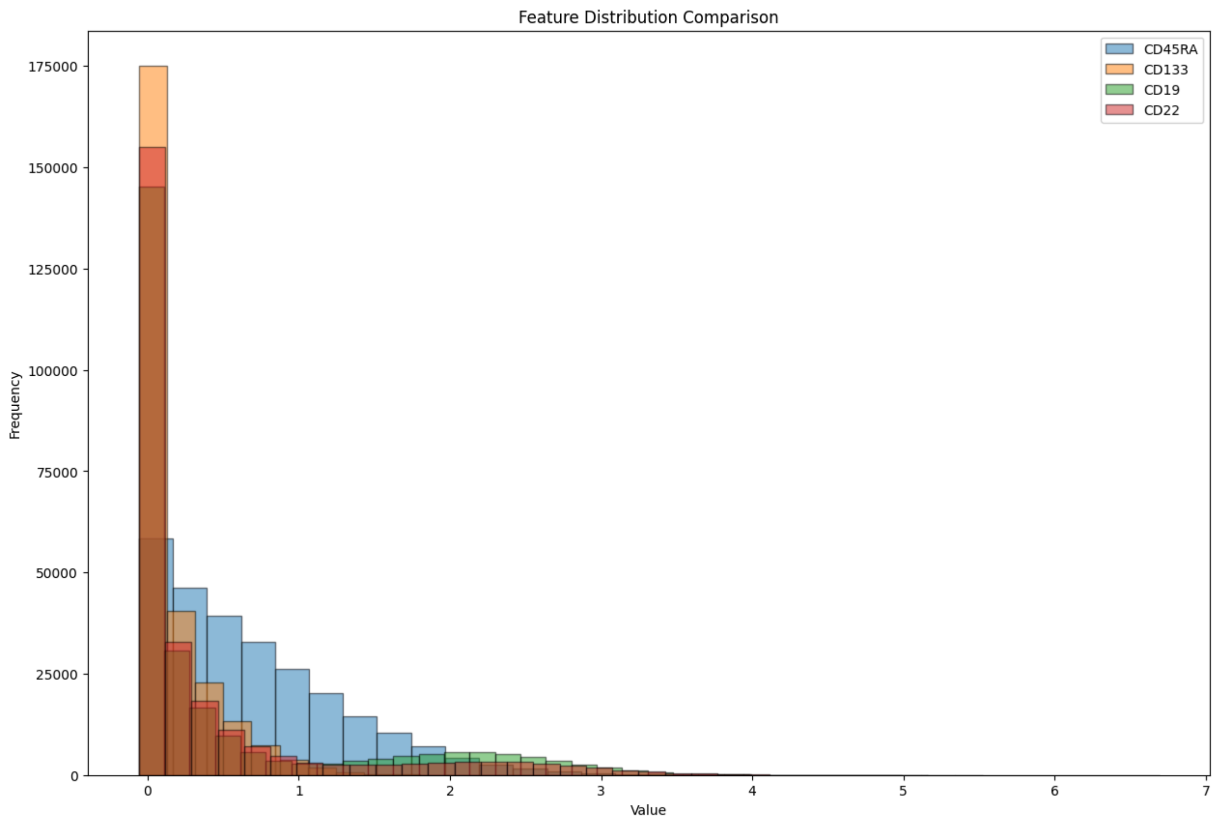
In [ ]:
```
import pandas as pd
import matplotlib.pyplot as plt

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()
```

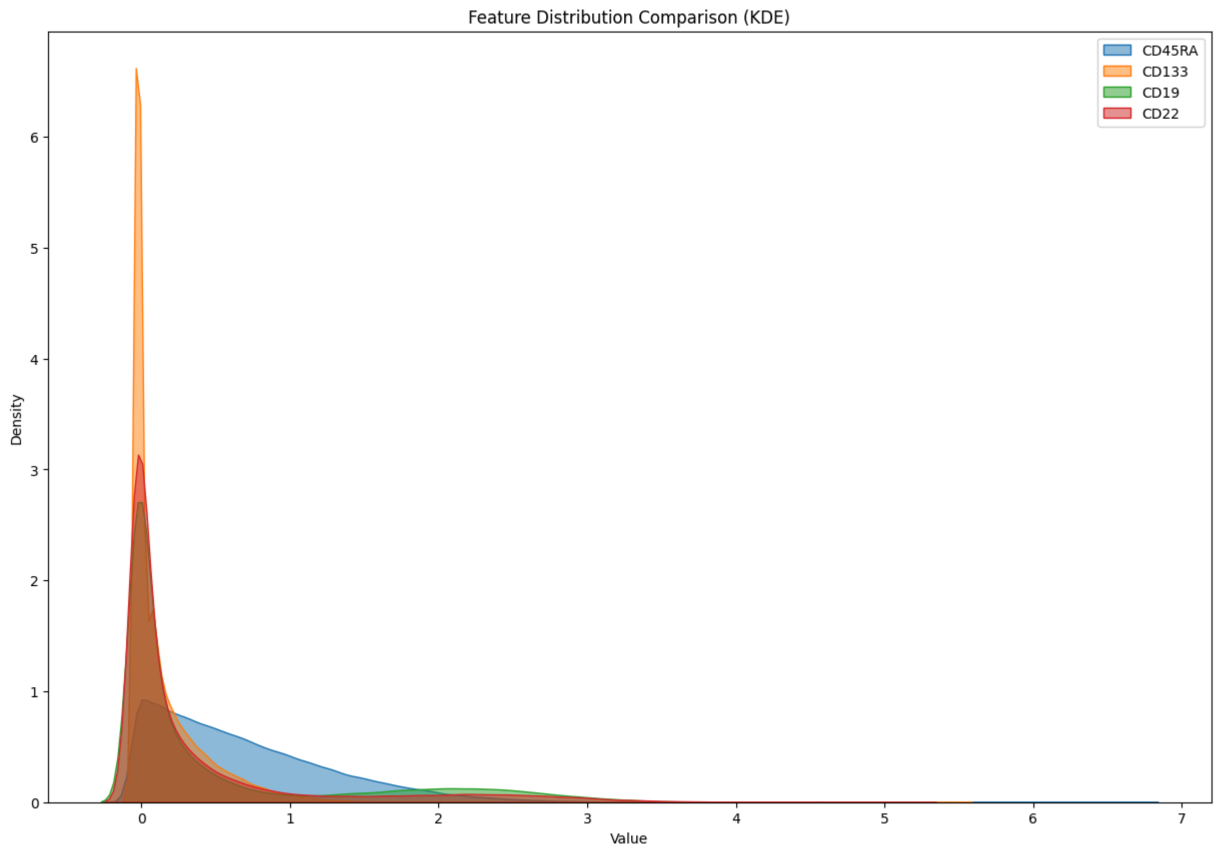


Feature Distribution Comparison Using Histograms and KDE

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

```
# Load the dataset
data = pd.read_csv('/content/drive/MyDrive/Datasets/Levine_32dim.fcs.csv')

# Select features for comparison (adjust based on your dataset)
features_to_compare = ['CD45RA', 'CD133', 'CD19', 'CD22']  # Example feature

# Step 1: Histograms for feature distribution comparison
plt.figure(figsize=(15, 10))

for feature in features_to_compare:
    plt.hist(data[feature], bins=30, alpha=0.5, label=feature, edgecolor='bl

plt.title('Feature Distribution Comparison')
plt.xlabel('Value')
plt.ylabel('Frequency')
plt.legend()
plt.show()

# Step 2: Kernel Density Estimation (KDE) for smoother distribution comparis
plt.figure(figsize=(15, 10))

for feature in features_to_compare:
    sns.kdeplot(data[feature], label=feature, fill=True, alpha=0.5)

plt.title('Feature Distribution Comparison (KDE)')
plt.xlabel('Value')
plt.ylabel('Density')
plt.legend()
plt.show()
```

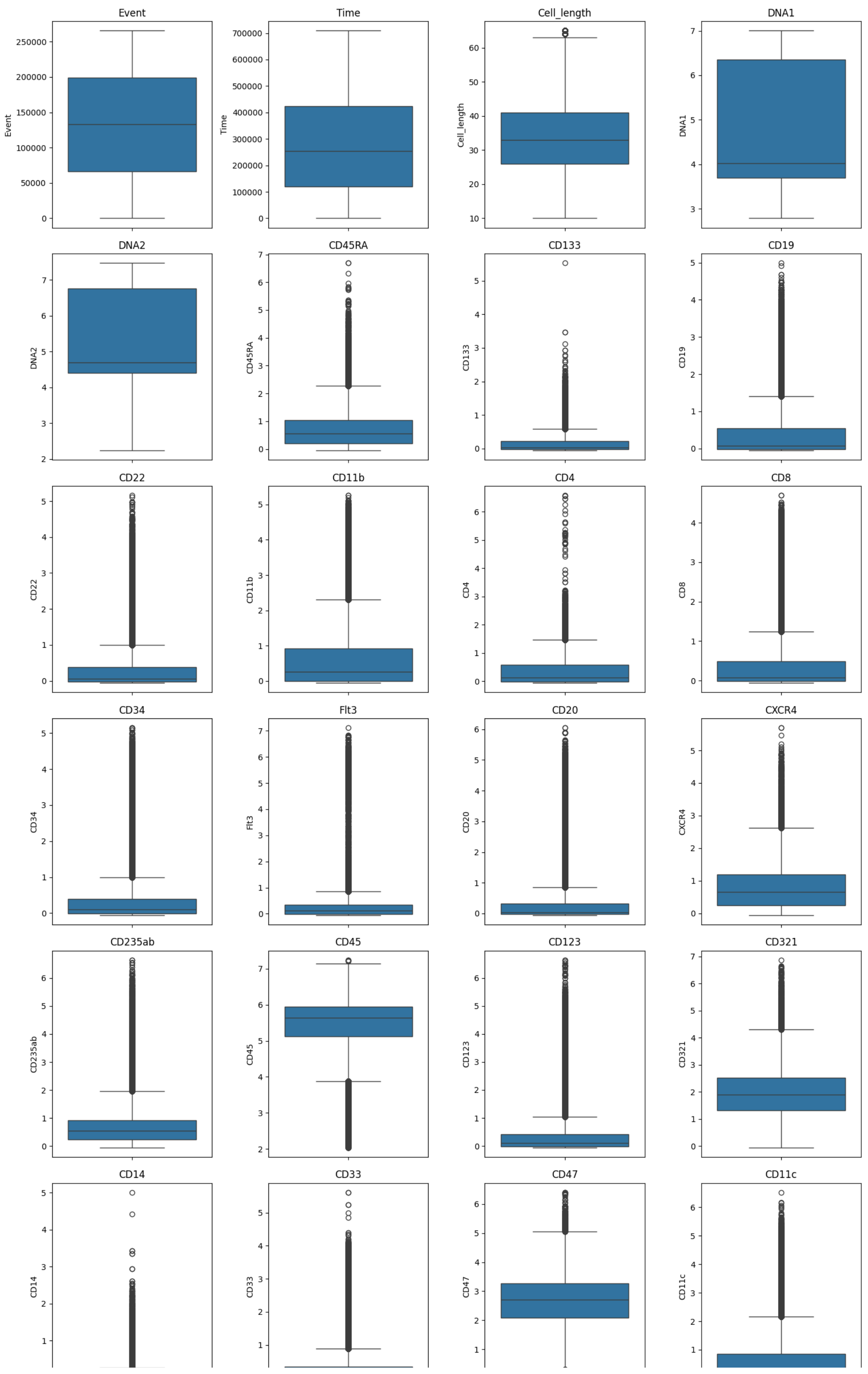


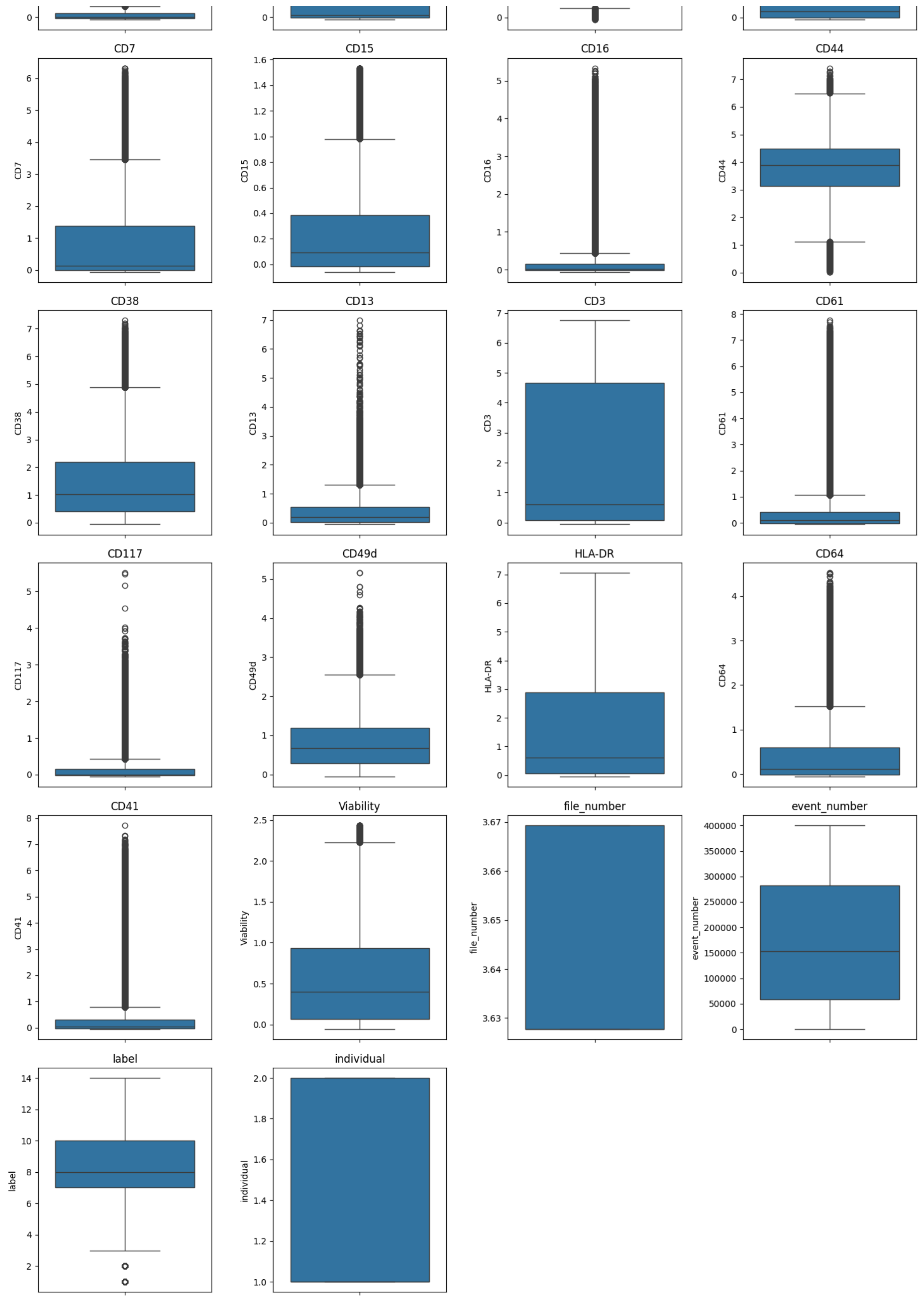


Box Plot

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

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

        # Step 1: Box Plots for Numerical Features
        numerical_features = data.select_dtypes(include=['float64', 'int64']).columr
        rows = (len(numerical_features) // 4) + 1  # Calculate the number of rows ne

        plt.figure(figsize=(15, rows * 4))
        for i, feature in enumerate(numerical_features):
            plt.subplot(rows, 4, i + 1)
            sns.boxplot(data[feature])
            plt.title(feature)
        plt.tight_layout()
        plt.show()

        # Step 2: Count Plots for Categorical Features
        categorical_features = data.select_dtypes(include=['object']).columns  # Sel

        plt.figure(figsize=(15, 10))
        for i, feature in enumerate(categorical_features):
            plt.subplot(2, 2, i + 1)
            sns.countplot(x=data[feature], order=data[feature].value_counts().index)
```

```
    plt.title(feature)
    plt.xticks(rotation=45)
plt.tight_layout()
plt.show()
```

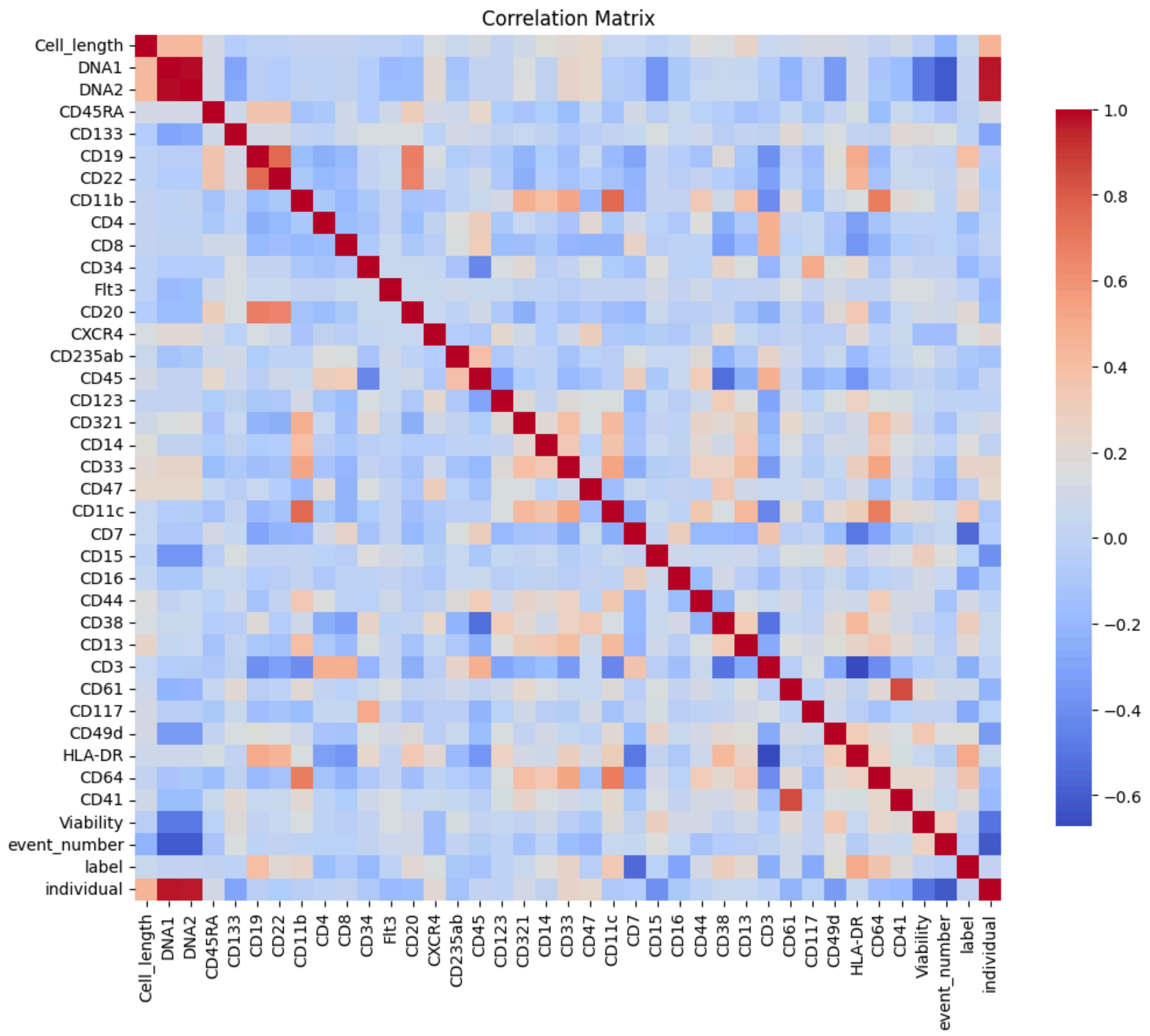

Event
Time
Cell_length
DNA1
DNA2
CD45RA
CD133
CD19
CD22
CD11b
CD4
CD8
CD34
Flt3
CD20
CXCR4
CD235ab
CD45
CD123
CD321
CD14
CD33
CD47
CD11c



```
<Figure size 1500x1000 with 0 Axes>
```

Correlation Matrix

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

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

        # Drop the specified columns
        data = data.drop(columns=['file_number', 'Event', 'Time'])

        # Calculate the correlation matrix
        correlation_matrix = data.corr()

        # Set up the matplotlib figure
        plt.figure(figsize=(12, 10))

        # Create a heatmap using Seaborn without annotations
        sns.heatmap(correlation_matrix, annot=False, cmap='coolwarm', square=True, c

        plt.title('Correlation Matrix')
        plt.show()
```

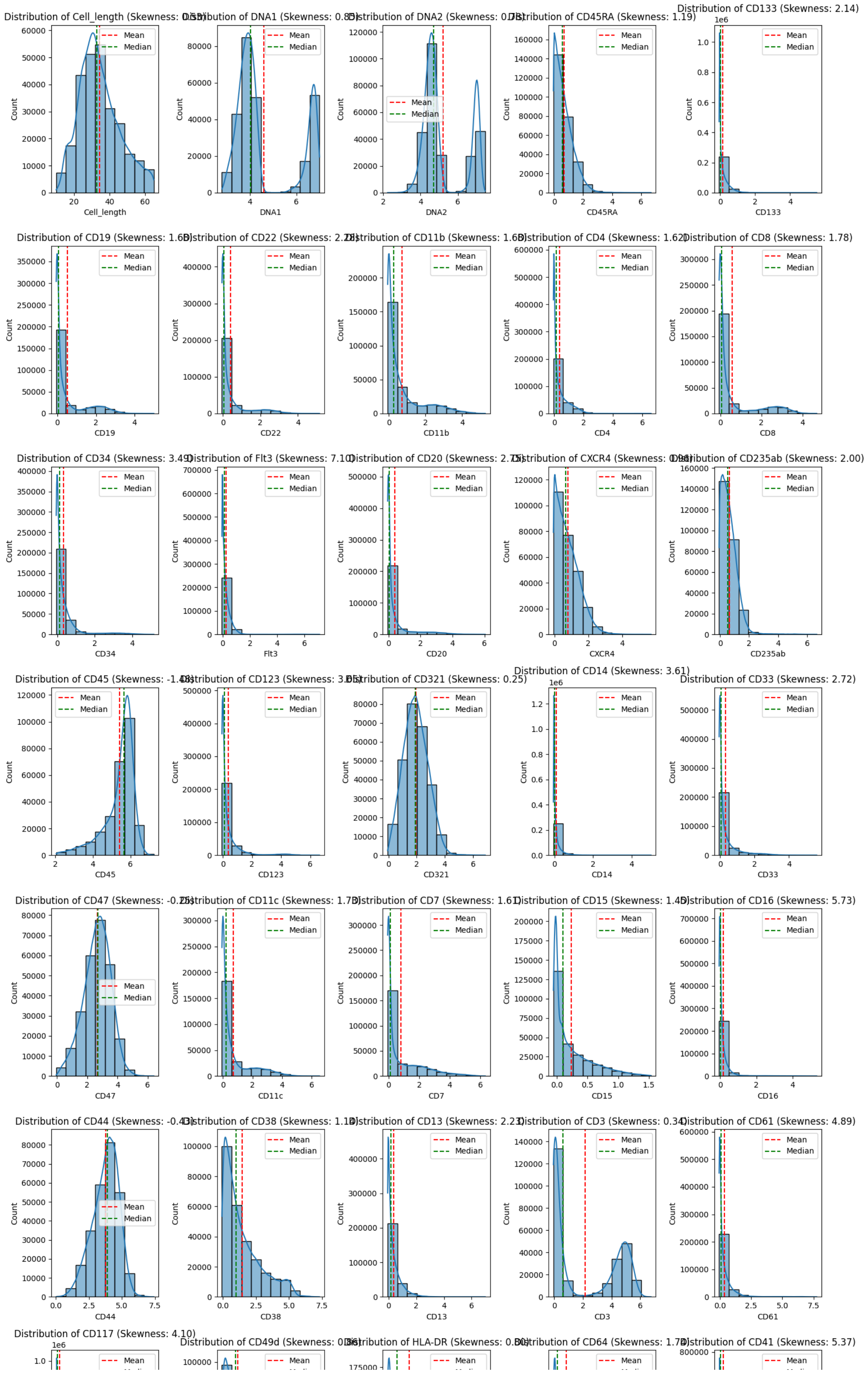


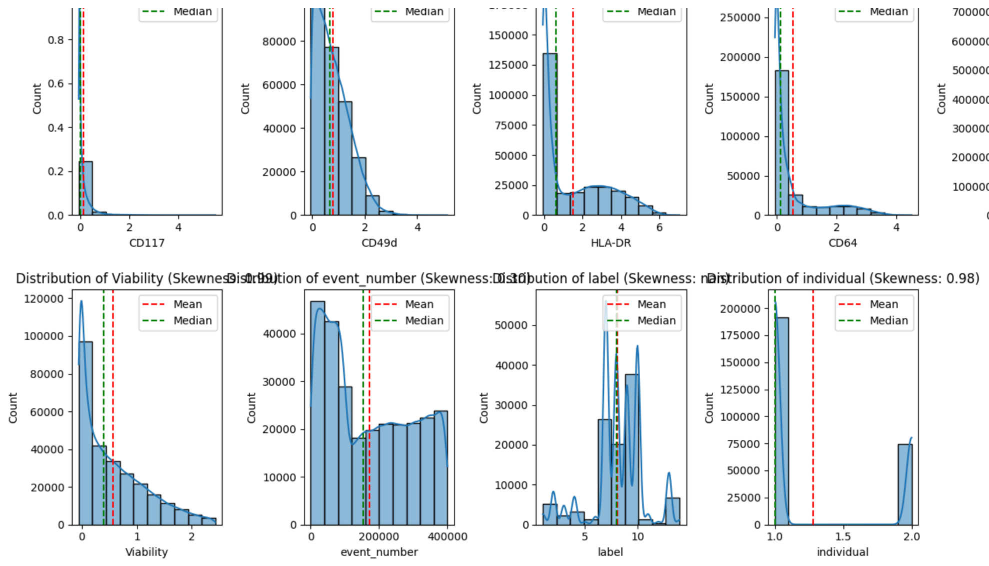
Skewness

```
In [ ]: import pandas as pd
        from scipy.stats import skew
        import matplotlib.pyplot as plt
        import seaborn as sns
        import math

        # Load the data
        data = pd.read_csv('/content/drive/MyDrive/Datasets/Levine_32dim.fcs.csv')
        data = data.drop(columns=['file_number', 'Event', 'Time'])

        # Calculate skewness
        skewness = data.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)

        # Set the number of columns in the grid
        n_cols = 5  # Adjust this value for number of plots per row
        n_plots = len(data.columns)
        n_rows = math.ceil(n_plots / n_cols)

        # Create subplots grid
        fig, axes = plt.subplots(n_rows, n_cols, figsize=(15, 4 * n_rows))  # Adjust
        axes = axes.flatten()  # Flatten axes array to make it easier to index

        # Loop through columns and plot histograms on each subplot
        for idx, col in enumerate(data.columns):
            sns.histplot(data[col], bins=10, kde=True, ax=axes[idx])
            axes[idx].set_title(f'Distribution of {col} (Skewness: {skewness[col]:.2
            axes[idx].axvline(data[col].mean(), color='red', linestyle='--', label='
            axes[idx].axvline(data[col].median(), color='green', linestyle='--', lab
            axes[idx].legend()

        # Remove any unused subplots (if n_plots is not a perfect multiple of n_cols
        for i in range(n_plots, len(axes)):
            fig.delaxes(axes[i])

        # Ensure the layout is tight and the plot is shown properly
```

```python
plt.tight_layout()
plt.show(block=True)  # Ensure plt.show() does not block rendering
```

```
               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
event_number   0.304116  Approximately symmetrical
label               NaN  Approximately symmetrical
individual     0.982030            Right-skewed
```


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: 1.60)
Distribution of CD22 (Skewness: 2.20)
Distribution of CD11b (Skewness: 1.60)
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: -1.40)
Distribution of CD123 (Skewness: 3.85)
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: 1.10)
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: 0.36)
Distribution of HLA-DR (Skewness: 0.30)
Distribution of CD64 (Skewness: 1.70)
Distribution of CD41 (Skewness: 5.37)
Mean
Median
Count



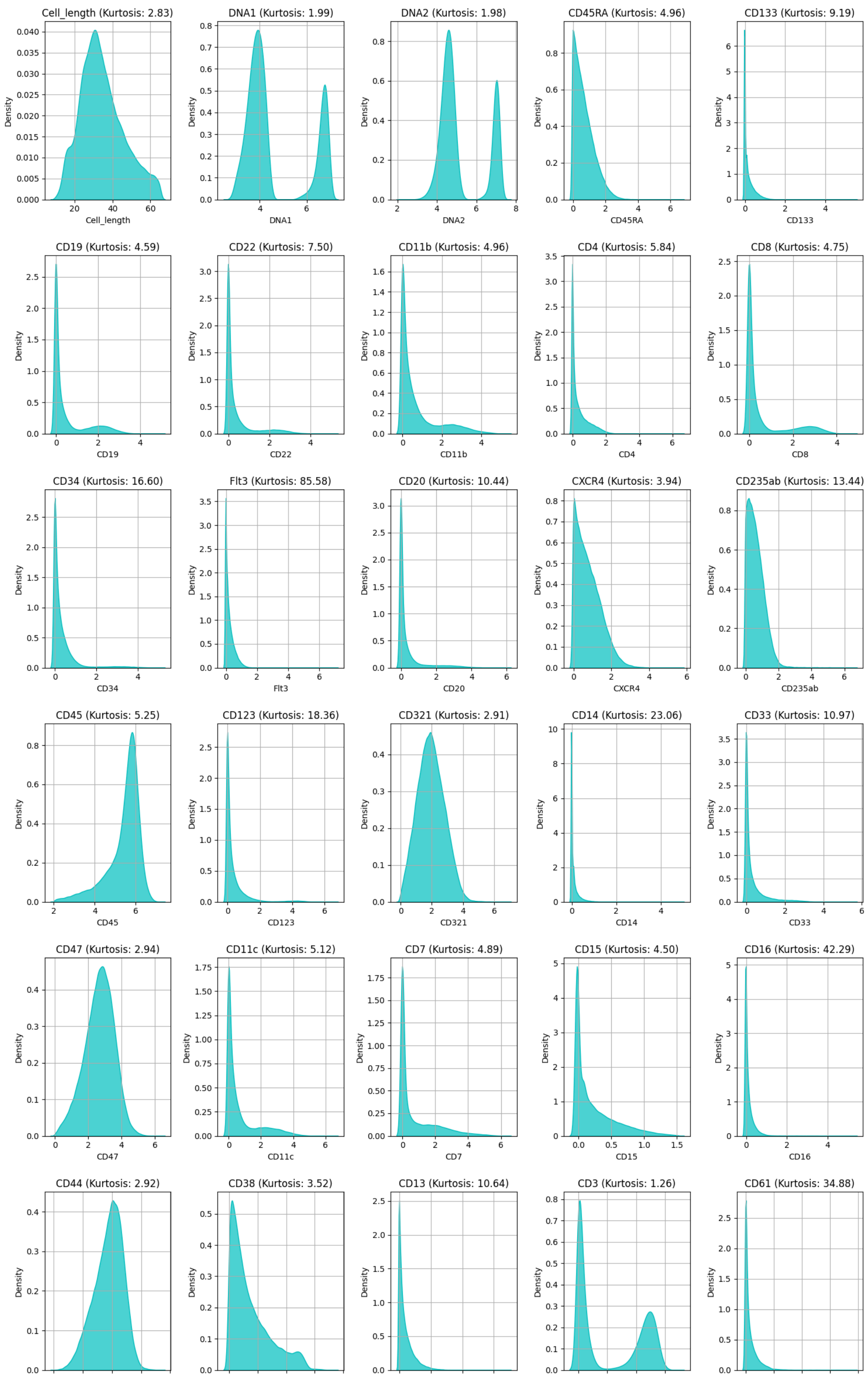
In [ ]:

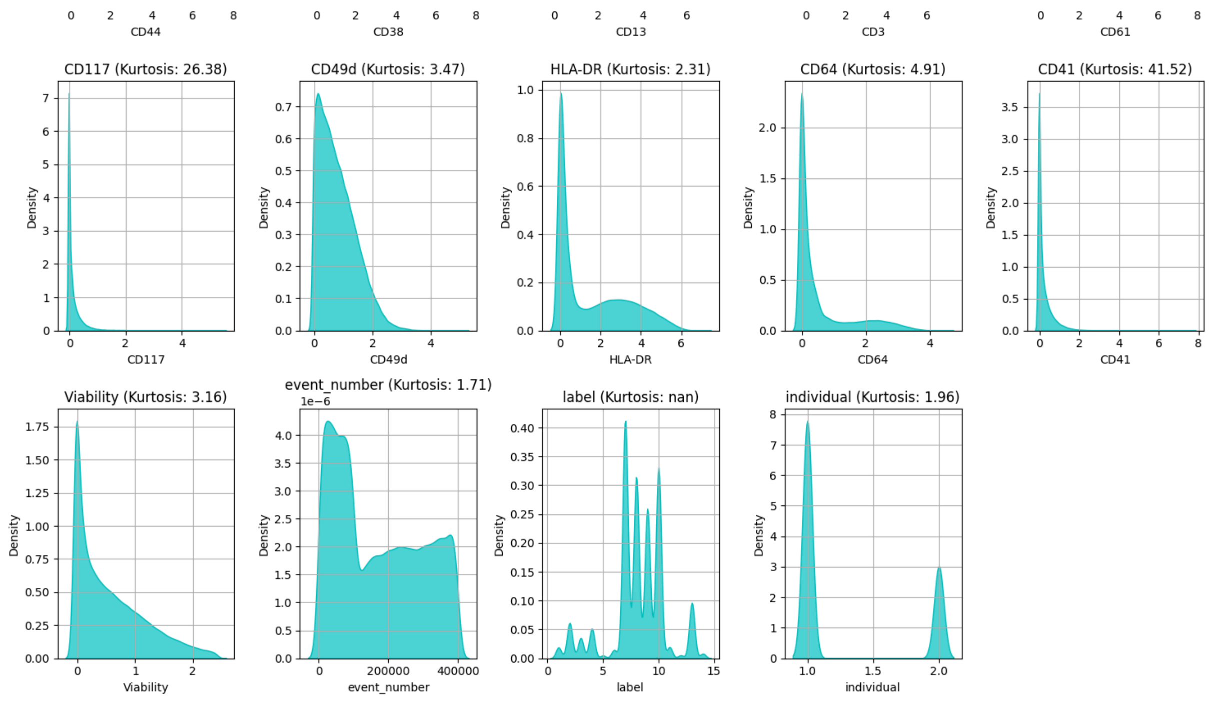
Kurtosis

In [ ]:
```python
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
from scipy.stats import kurtosis
import math

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

# Drop the specified columns
data = data.drop(columns=['file_number', 'Event', 'Time'])

# Calculate kurtosis for each column
kurtosis_values = data.apply(kurtosis, fisher=False)  # Fisher=False gives P

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

# 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)

# Set the number of columns in the grid
```

```
n_cols = 5  # You can adjust this to control how many plots per row
n_plots = len(data.columns)
n_rows = math.ceil(n_plots / n_cols)

# Create subplots grid
fig, axes = plt.subplots(n_rows, n_cols, figsize=(15, 4 * n_rows))  # Adjust
axes = axes.flatten()  # Flatten axes array to make it easier to index

# Loop through columns and plot KDE on each subplot
for idx, column in enumerate(data.columns):
    sns.kdeplot(data[column].dropna(), color='c', fill=True, alpha=0.7, ax=a
    axes[idx].set_title(f'{column} (Kurtosis: {kurtosis_df.loc[kurtosis_df["
    axes[idx].set_xlabel(column)
    axes[idx].set_ylabel('Density')
    axes[idx].grid(True)

# Remove any unused subplots (if n_plots is not a perfect multiple of n_cols
for i in range(n_plots, len(axes)):
    fig.delaxes(axes[i])

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)
event_number  event_number   1.706183  Platykurtic (light tails)
label                label        NaN  Mesokurtic (normal tails)
individual      individual   1.964382  Platykurtic (light tails)
```

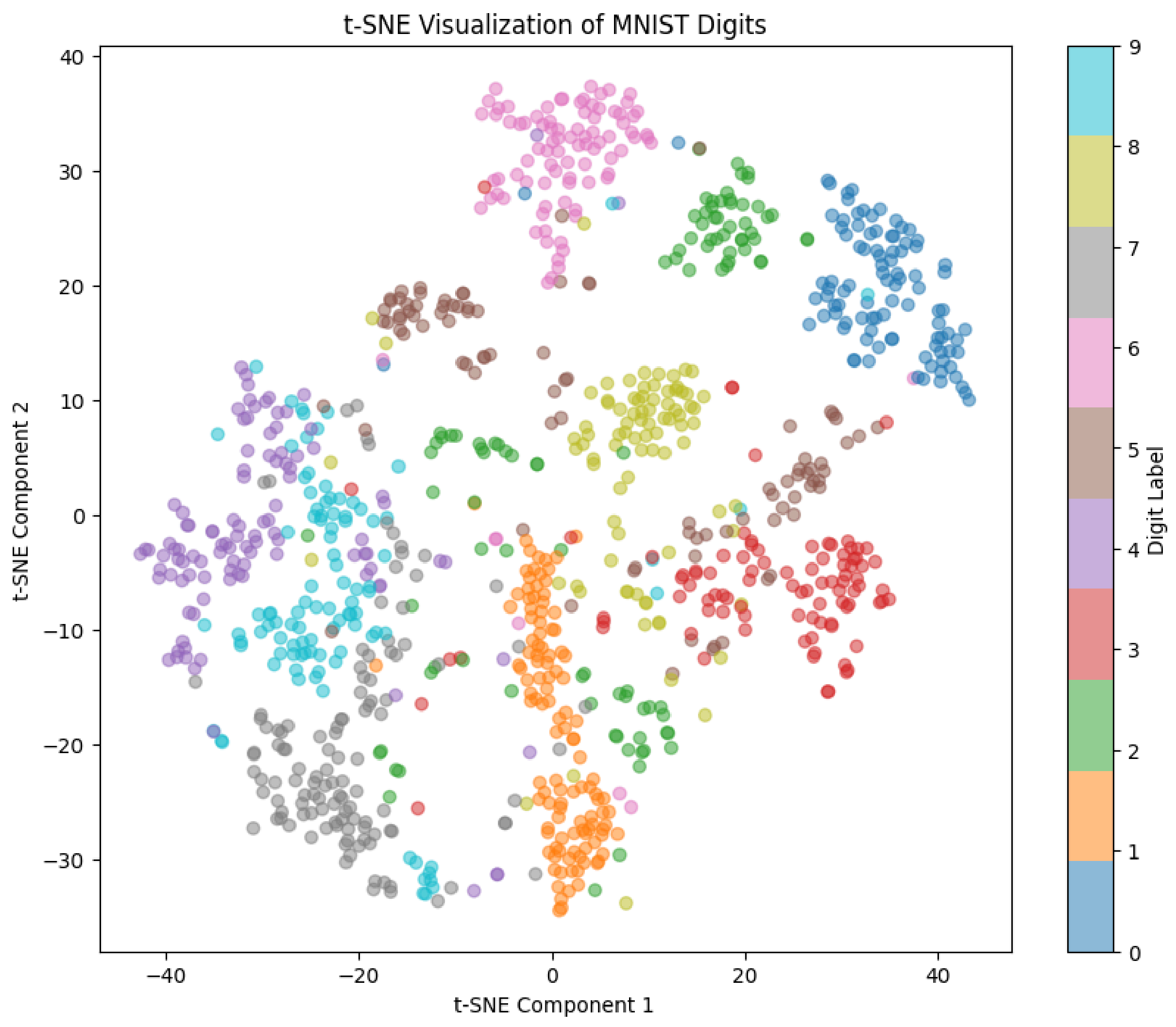

Cell_length (Kurtosis: 2.83)
DNA1 (Kurtosis: 1.99)
DNA2 (Kurtosis: 1.98)
CD45RA (Kurtosis: 4.96)
CD133 (Kurtosis: 9.19)
CD19 (Kurtosis: 4.59)
CD22 (Kurtosis: 7.50)
CD11b (Kurtosis: 4.96)
CD4 (Kurtosis: 5.84)
CD8 (Kurtosis: 4.75)
CD34 (Kurtosis: 16.60)
Flt3 (Kurtosis: 85.58)
CD20 (Kurtosis: 10.44)
CXCR4 (Kurtosis: 3.94)
CD235ab (Kurtosis: 13.44)
CD45 (Kurtosis: 5.25)
CD123 (Kurtosis: 18.36)
CD321 (Kurtosis: 2.91)
CD14 (Kurtosis: 23.06)
CD33 (Kurtosis: 10.97)
CD47 (Kurtosis: 2.94)
CD11c (Kurtosis: 5.12)
CD7 (Kurtosis: 4.89)
CD15 (Kurtosis: 4.50)
CD16 (Kurtosis: 42.29)
CD44 (Kurtosis: 2.92)
CD38 (Kurtosis: 3.52)
CD13 (Kurtosis: 10.64)
CD3 (Kurtosis: 1.26)
CD61 (Kurtosis: 34.88)
Density



CLASS WORK CODE

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

        # Load the MNIST dataset
        (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

        # Flatten the images and take a subset
        n_samples = 1000
        train_images_flat = train_images[:n_samples].reshape(n_samples, -1)
        train_labels_subset = train_labels[:n_samples]

        # Perform t-SNE
        tsne = TSNE(n_components=2, random_state=42, perplexity=30)
        train_images_embedded = tsne.fit_transform(train_images_flat)

        # Plot the t-SNE results
        plt.figure(figsize=(10, 8))
        scatter = plt.scatter(train_images_embedded[:, 0], train_images_embedded[:,
        plt.colorbar(scatter, label='Digit Label')
        plt.title('t-SNE Visualization of MNIST Digits')
        plt.xlabel('t-SNE Component 1')
        plt.ylabel('t-SNE Component 2')
        plt.show()
```

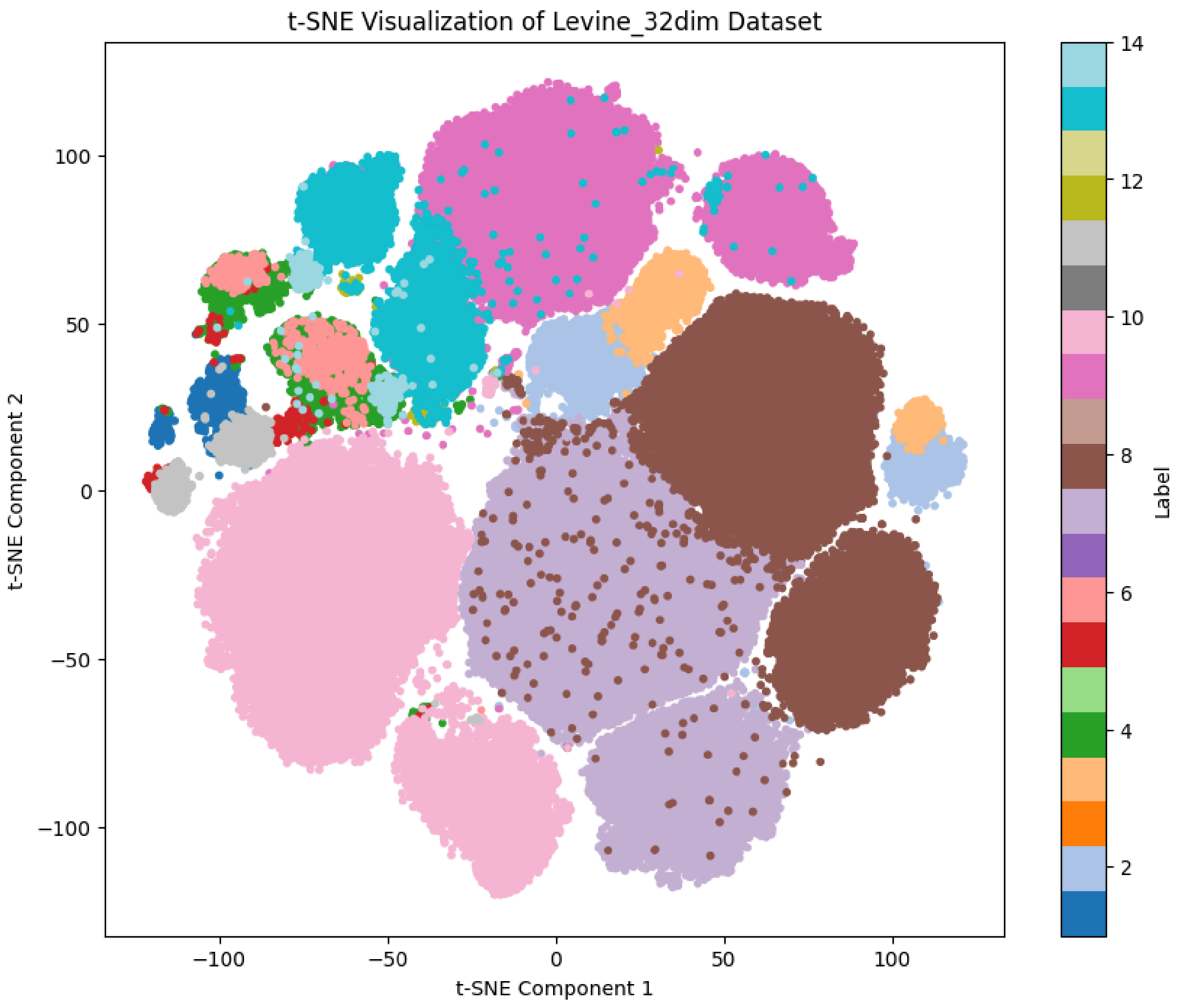
```
Downloading data from https://storage.googleapis.com/tensorflow/tf-keras-dat
asets/mnist.npz
11490434/11490434 ━━━━━━━━━━━━━━━━━━━━ 0s 0us/step
```



T-SNE

```
In [ ]: import pandas as pd
        from sklearn.preprocessing import StandardScaler
        from sklearn.manifold import TSNE
        import matplotlib.pyplot as plt

        # Load the dataset
        data = pd.read_csv('/content/Levine_32dim.fcs.csv')

        # Exclude the specified columns
        exclude_columns = ['Event', 'Time', 'Cell_length', 'file_number', 'event_num
        data_filtered = data.drop(columns=exclude_columns)

        # Standardize the data (z-score normalization)
        scaler = StandardScaler()
        data_standardized = scaler.fit_transform(data_filtered)

        # Perform t-SNE
        tsne = TSNE(n_components=2, random_state=42, perplexity=30)  # You can adjus
        tsne_results = tsne.fit_transform(data_standardized)
```

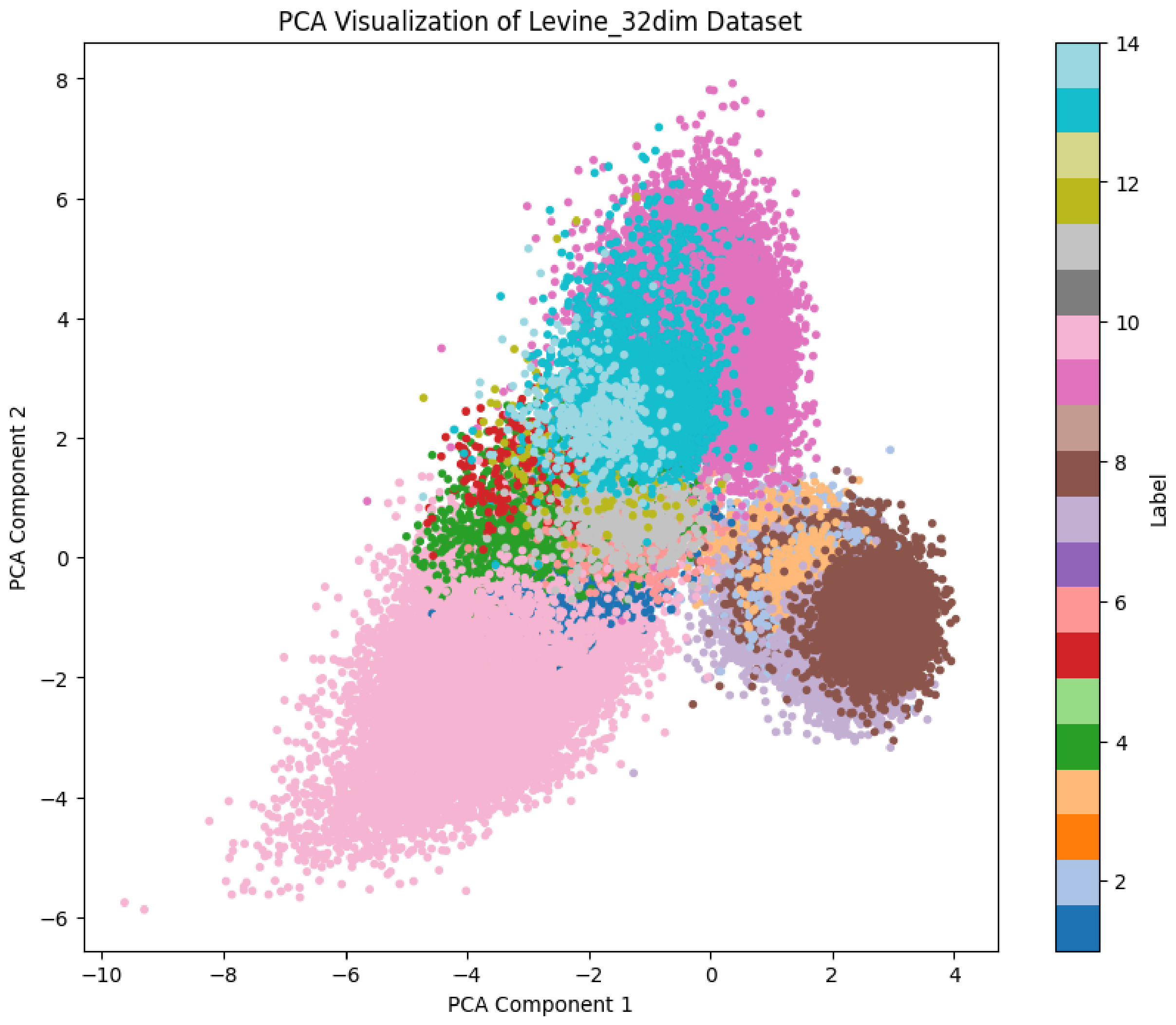
```
# Add the t-SNE results to the original data for visualization
data['t-SNE Component 1'] = tsne_results[:, 0]
data['t-SNE Component 2'] = tsne_results[:, 1]

# Plot the t-SNE visualization
plt.figure(figsize=(10, 8))
scatter = plt.scatter(data['t-SNE Component 1'], data['t-SNE Component 2'],
plt.colorbar(scatter, label='Label')
plt.title('t-SNE Visualization of Levine_32dim Dataset')
plt.xlabel('t-SNE Component 1')
plt.ylabel('t-SNE Component 2')
plt.show()
```



PCA

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

# Load the dataset
data = pd.read_csv('/content/Levine_32dim.fcs.csv')
```

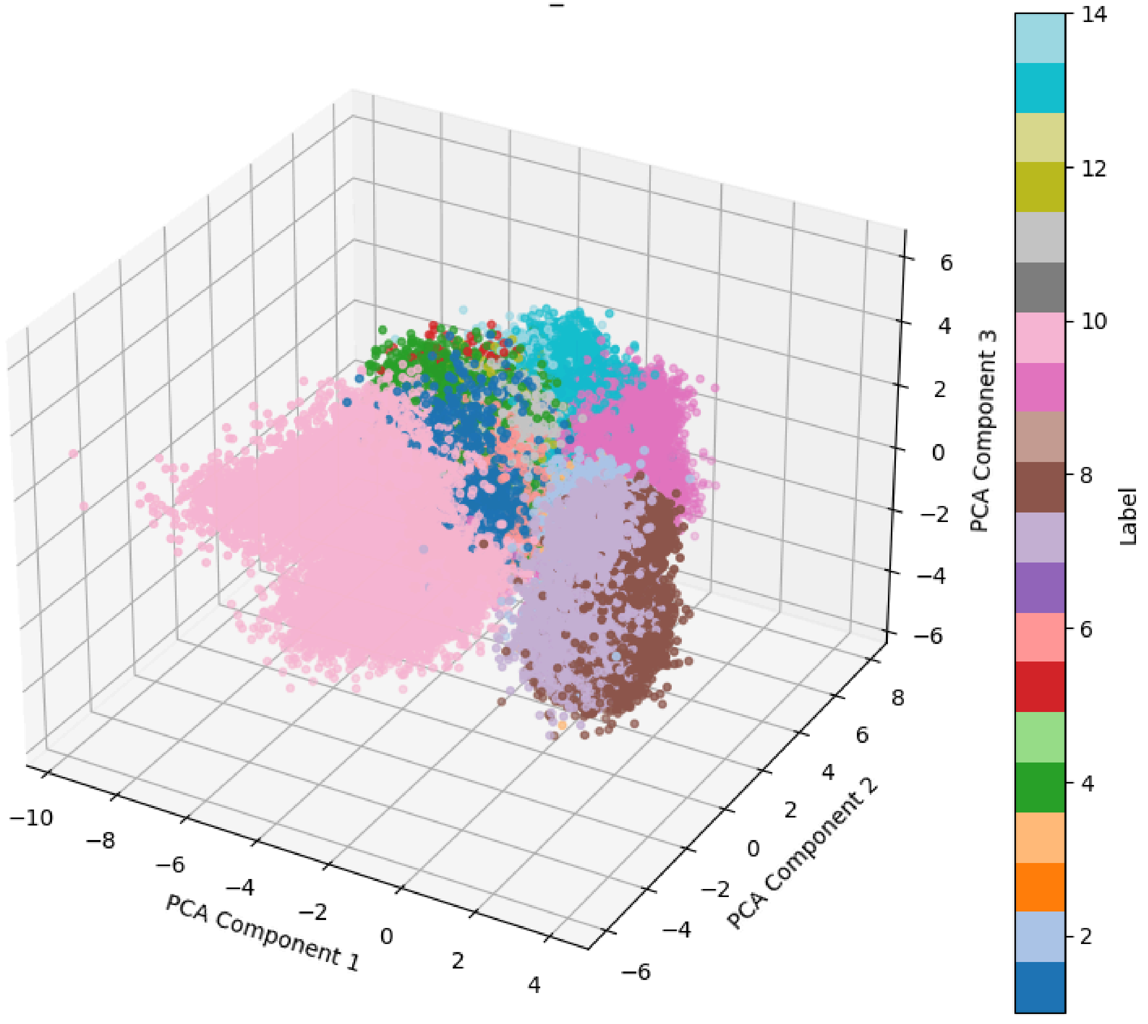
```
# Exclude the specified columns
exclude_columns = ['Event', 'Time', 'Cell_length', 'file_number', 'event_num
data_filtered = data.drop(columns=exclude_columns)

# Standardize the data (z-score normalization)
scaler = StandardScaler()
data_standardized = scaler.fit_transform(data_filtered)

# Perform PCA
pca = PCA(n_components=2)  # Reduce to 2 dimensions for visualization
pca_result = pca.fit_transform(data_standardized)

# Add the PCA results to the original data for visualization
data['PCA Component 1'] = pca_result[:, 0]
data['PCA Component 2'] = pca_result[:, 1]

# Plot the PCA results
plt.figure(figsize=(10, 8))
scatter = plt.scatter(data['PCA Component 1'], data['PCA Component 2'], c=da
plt.colorbar(scatter, label='Label')
plt.title('PCA Visualization of Levine_32dim Dataset')
plt.xlabel('PCA Component 1')
plt.ylabel('PCA Component 2')
plt.show()
```



3D PCA graph

```
In [ ]: import pandas as pd
        from sklearn.preprocessing import StandardScaler
        from sklearn.decomposition import PCA
        import matplotlib.pyplot as plt
        from mpl_toolkits.mplot3d import Axes3D  # Importing 3D plotting

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

        # Exclude the specified columns
        exclude_columns = ['Event', 'Time', 'Cell_length', 'file_number', 'event_num
        data_filtered = data.drop(columns=exclude_columns)

        # Standardize the data (z-score normalization)
        scaler = StandardScaler()
        data_standardized = scaler.fit_transform(data_filtered)

        # Perform PCA
        pca = PCA(n_components=3)  # Reduce to 3 dimensions for 3D visualization
        pca_result = pca.fit_transform(data_standardized)

        # Add the PCA results to the original data for visualization
        data['PCA Component 1'] = pca_result[:, 0]
        data['PCA Component 2'] = pca_result[:, 1]
        data['PCA Component 3'] = pca_result[:, 2]

        # Plot the PCA results in 3D
        fig = plt.figure(figsize=(10, 8))
        ax = fig.add_subplot(111, projection='3d')

        # Create a 3D scatter plot
        scatter = ax.scatter(data['PCA Component 1'], data['PCA Component 2'], data[
                             c=data['label'], cmap='tab20', s=10)

        # Add color bar and labels
        plt.colorbar(scatter, label='Label')
        ax.set_title('3D PCA Visualization of Levine_32dim Dataset')
        ax.set_xlabel('PCA Component 1')
        ax.set_ylabel('PCA Component 2')
        ax.set_zlabel('PCA Component 3')

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

3D PCA Visualization of Levine_32dim Dataset



Variance, Cumulative Proportion and S.D.

In [ ]:
```python
import pandas as pd
from sklearn.preprocessing import StandardScaler
from sklearn.decomposition import PCA

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

# Exclude the specified columns
exclude_columns = ['Event', 'Time', 'Cell_length', 'file_number', 'event_num
data_filtered = data.drop(columns=exclude_columns)

# Standardize the data (z-score normalization)
scaler = StandardScaler()
data_standardized = scaler.fit_transform(data_filtered)

# Perform PCA
pca = PCA(n_components=4)  # Use 4 principal components
pca.fit(data_standardized)

# Extract the required information
```

```
explained_variance = pca.explained_variance_ratio_
cumulative_variance = explained_variance.cumsum()
standard_deviation = pca.singular_values_ / (len(data_standardized) - 1)**0.

# Create a DataFrame for the output
pca_summary = pd.DataFrame({
    'PC1': [standard_deviation[0], explained_variance[0], cumulative_varianc
    'PC2': [standard_deviation[1], explained_variance[1], cumulative_varianc
    'PC3': [standard_deviation[2], explained_variance[2], cumulative_varianc
    'PC4': [standard_deviation[3], explained_variance[3], cumulative_varianc
}, index=['Standard Deviation', 'Proportion of Variance', 'Cumulative Propor

# Round the numbers for better readability
pca_summary = pca_summary.map(lambda x: f'{x:.4f}')

# Apply styles to the DataFrame
styled_summary = (pca_summary.style
                  .set_caption("PCA Summary")
                  .set_table_styles(
                      [{'selector': 'caption', 'props': [('font-size', '16px
                  )
                  .background_gradient(cmap='coolwarm', axis=None)
                  .set_properties(**{'text-align': 'center'})
)

# Hiding the index column manually (workaround)
styled_summary.set_table_styles({
    'index': [{'selector': '', 'props': 'display:none;'}]  # Hides the index
})

# Display the styled DataFrame
styled_summary
```

Out[ ]:

PCA Summary

	PC1	PC2	PC3	PC4
Standard Deviation	2.3277	1.9574	1.8780	1.6067
Proportion of Variance	0.1548	0.1095	0.1008	0.0738
Cumulative Proportion	0.1548	0.2643	0.3650	0.4388

Binary Mask

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

# Set a random seed for reproducibility
np.random.seed(42)

# Create a sample DataFrame called 'demodata' for demonstration
demodata = pd.DataFrame({
    'column1': [5, 12, 18, 7],
    'column2': [10, 20, 15, 30],
    'column3': [25, 35, 40, 45]
})

# Define the probability of masking (e.g., 0.3 means a 30% chance each eleme
p_m = 0.3

# Convert 'demodata' to a NumPy array for masking
data_array = demodata.values

# Generate a binary mask based on the probability, where 1 = not masked, 0 =
mask = np.random.binomial(1, 1 - p_m, data_array.shape)  # Reverse probabili

# Convert to a DataFrame for easier analysis
binary_mask_df = pd.DataFrame(mask, columns=demodata.columns)

print("Original DataFrame:\n", demodata)
print("\nBinary Mask DataFrame:\n", binary_mask_df)
```

```
Original DataFrame:
    column1  column2  column3
0        5       10       25
1       12       20       35
2       18       15       40
3        7       30       45

Binary Mask DataFrame:
    column1  column2  column3
0        1        0        0
1        1        1        1
2        1        0        1
3        0        1        0
```

Randomly Shuffle

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

# Create a sample DataFrame called 'demodata' for demonstration
demodata = pd.DataFrame({
    'column1': [5, 12, 18, 7],
    'column2': [10, 20, 15, 30],
    'column3': [25, 35, 40, 45]
})

# Shuffle each column in the DataFrame independently
shuffled_demodata = demodata.apply(lambda col: np.random.permutation(col))

print("Original DataFrame:\n", demodata)
print("\nShuffled DataFrame:\n", shuffled_demodata)
```

```
Original DataFrame:
    column1  column2  column3
0         5       10       25
1        12       20       35
2        18       15       40
3         7       30       45

Shuffled DataFrame:
    column1  column2  column3
0         5       10       25
1         7       30       35
2        18       15       45
3        12       20       40
```

Corrupted DataFrame

Formula = (x.values * (1 - m) + x_shuffled.values * m)

In [ ]:

```
import numpy as np
import pandas as pd

# Create a sample DataFrame called 'x' (original data)
x = pd.DataFrame({
    'column1': [5, 12, 18, 7],
    'column2': [10, 20, 15, 30],
    'column3': [25, 35, 40, 45]
})

# Define the probability of masking (e.g., 0.3 means a 30% chance each eleme
p_m = 0.3

# Generate a binary mask matrix 'm'
m = np.random.binomial(1, 1 - p_m, x.shape)
binary_mask_df = pd.DataFrame(m, columns=x.columns)

# Shuffle each column in 'x' independently to create 'x_shuffled'
x_shuffled = x.apply(lambda col: np.random.permutation(col))

# Calculate the corrupted DataFrame 'x_corrupted' using the formula
x_corrupted_array = x.values * (1 - m) + x_shuffled.values * m
x_corrupted = pd.DataFrame(x_corrupted_array, columns=x.columns)

# Display results
print("Original DataFrame (x):\n", x)
print("\nBinary Mask DataFrame (m):\n", binary_mask_df)
print("\nShuffled DataFrame (x_shuffled):\n", x_shuffled)
print("\nCorrupted DataFrame (x_corrupted):\n", x_corrupted)
```

```
Original DataFrame (x):
    column1  column2  column3
0        5       10       25
1       12       20       35
2       18       15       40
3        7       30       45

Binary Mask DataFrame (m):
    column1  column2  column3
0        1        1        0
1        0        1        1
2        1        0        0
3        0        1        1

Shuffled DataFrame (x_shuffled):
    column1  column2  column3
0       12       20       35
1       18       30       40
2        7       15       45
3        5       10       25

Corrupted DataFrame (x_corrupted):
    column1  column2  column3
0       12       20       25
1       12       30       40
2        7       15       40
3        7       10       25
```

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

In [ ]:
```python
import numpy as np
import pandas as pd
from sklearn.preprocessing import StandardScaler

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

# Exclude the specified columns
exclude_columns = ['Event', 'Time', 'Cell_length', 'file_number', 'event_num
data_filtered = data.drop(columns=exclude_columns)

# Set the probability of masking
p_m = 0.3

# Generate a binary mask matrix 'm'
m = np.random.binomial(1, 1 - p_m, data_filtered.shape)
binary_mask_df = pd.DataFrame(m, columns=data_filtered.columns)

# Shuffle each column in 'data_filtered' independently to create 'data_shuff
data_shuffled = data_filtered.apply(lambda col: np.random.permutation(col))

# Calculate the corrupted DataFrame 'data_corrupted' using the formula
data_corrupted_array = data_filtered.values * (1 - m) + data_shuffled.values
```

```
data_corrupted = pd.DataFrame(data_corrupted_array, columns=data_filtered.co

# Display results
print("Binary Mask DataFrame (m):\n", binary_mask_df)
print("\nShuffled DataFrame (data_shuffled):\n", data_shuffled)
print("\nCorrupted DataFrame (data_corrupted):\n", data_corrupted)
```

```
Binary Mask DataFrame (m):
         DNA1  DNA2  CD45RA  CD133  CD19  CD22  CD11b  CD4  CD8  CD34  ...  \
0           1     0       0      1     1     0      0    1    1     1  ...
1           1     0       0      1     1     0      1    1    1     1  ...
2           0     0       0      1     1     1      0    0    1     1  ...
3           1     1       1      0     1     1      1    0    1     0  ...
4           1     1       1      1     0     1      1    1    1     1  ...
...       ...   ...     ...    ...   ...   ...    ...  ...  ...   ...  ...
265622      1     1       1      1     1     0      1    1    1     0  ...
265623      1     0       1      1     1     0      1    0    1     1  ...
265624      0     1       0      0     0     0      1    1    1     0  ...
265625      1     0       1      0     1     0      1    1    1     1  ...
265626      1     1       1      1     1     1      0    0    1     1  ...

        CD38  CD13  CD3  CD61  CD117  CD49d  HLA-DR  CD64  CD41  Viability
0          0     0    1     0      1      0       1     1     1          1
1          0     0    1     0      0      1       1     1     1          1
2          1     1    1     1      1      1       0     1     1          1
3          0     1    0     1      0      1       1     1     1          0
4          1     1    1     1      1      1       0     0     0          1
...      ...   ...  ...   ...    ...    ...     ...   ...   ...        ...
265622     1     1    1     0      1      1       1     0     1          1
265623     1     0    1     0      1      1       1     1     1          1
265624     0     1    1     1      0      0       0     1     1          0
265625     1     0    0     0      1      0       1     1     1          1
265626     1     1    1     1      1      1       1     1     0          0

[265627 rows x 35 columns]

Shuffled DataFrame (data_shuffled):
            DNA1      DNA2    CD45RA     CD133      CD19      CD22     CD11
b  \
0       6.786063  4.214412  0.932480 -0.030651 -0.051090 -0.002778 -0.024796
1       3.304212  7.155713  1.322412  0.090728 -0.007041 -0.033089  0.174548
2       4.232708  4.346681  1.713726  0.378271 -0.018368  0.058568  1.044414
3       3.755032  6.724153  0.878355 -0.012575 -0.027815  0.344878  2.169431
4       6.930991  7.020067  0.887629  0.302343  0.265898  0.095072  0.634529
...          ...       ...       ...       ...       ...       ...       ...
265622  4.394648  7.033258  0.237882  0.105213  0.465943  0.350927 -0.010262
265623  3.545460  6.664328  0.784556 -0.021298  0.452340  0.274911 -0.018145
265624  6.721840  7.070103  0.137400  0.046618  0.250286 -0.022243  1.182211
265625  4.143820  4.791909  0.713227 -0.026401  0.264846 -0.030205 -0.012409
265626  3.969794  4.868542  1.126973 -0.021412  2.468656  0.886238  0.119620

             CD4       CD8      CD34  ...      CD38      CD13       CD3  \
0       2.229733  0.380750  0.617069  ... -0.011144  0.570248  0.360248
1      -0.034576  0.028380  0.055998  ...  1.569619  0.157208  4.741579
2       0.176456 -0.023832  0.138957  ...  1.820143  0.401342  0.179631
3       0.046905  0.779659  0.201482  ...  0.335812  0.330737  0.194957
4       0.156090  0.700664 -0.018936  ...  1.498051  0.220634  4.908208
...          ...       ...       ...  ...       ...       ...       ...
265622  0.069230 -0.000519  0.084240  ...  1.209014  0.258038  0.004559
265623 -0.031157  0.167407 -0.020814  ...  2.673337  0.262981  5.468722
265624 -0.032375  2.264701 -0.050539  ...  1.283733  0.761438  4.324525
265625  0.188642  0.009173  1.229125  ...  1.934654  0.065372  0.414364
```

```
265626  0.016725  2.610154 -0.016104  ...  0.837135  0.905025 -0.006939

            CD61     CD117     CD49d    HLA-DR      CD64      CD41  Viabilit
y
0       0.253711  0.025271  0.439650  0.262099  1.541640  0.494105   1.41903
0
1      -0.036119  0.302787  0.529624 -0.019200 -0.039433  0.086273  -0.01077
7
2      -0.014565  0.010527  0.213956  0.396175  0.255850 -0.008803   0.15931
3
3       0.125449  0.232510  0.266171  0.002137  1.904348  0.255121   1.26861
0
4       0.339887  0.167298  0.198912  3.861918  0.219850  1.012320   0.07820
2
...          ...       ...       ...       ...       ...       ...
...
265622  0.775456  0.431145  1.899320  3.525005  0.617201  0.075405   0.67677
1
265623 -0.019933  0.054991 -0.000330 -0.000796 -0.043636  1.289842   1.02400
5
265624  0.019075  0.135054  0.760935 -0.009125  0.624089  0.387557  -0.03445
6
265625  0.046970  0.134328  2.088230 -0.011615  0.078023 -0.007928   0.34438
5
265626  1.335617  0.328452  1.374000  0.111610 -0.037714 -0.021994   1.65772
2

[265627 rows x 35 columns]

Corrupted DataFrame (data_corrupted):
            DNA1      DNA2     CD45RA     CD133      CD19      CD22     CD11
b  \
0       6.786063  4.617262  0.162691 -0.030651 -0.051090  0.066388 -0.009184
1       3.304212  4.816692  0.701349  0.090728 -0.007041  0.074409  0.174548
2       3.838727  4.386369  0.603568  0.378271 -0.018368  0.058568 -0.001881
3       3.755032  6.724153  0.878355 -0.027611 -0.027815  0.344878  2.169431
4       6.930991  7.020067  0.887629  0.302343  0.080423  0.095072  0.634529
...          ...       ...       ...       ...       ...       ...       ...
265622  4.394648  7.033258  0.237882  0.105213  0.465943 -0.007261 -0.010262
265623  3.545460  7.154026  0.784556 -0.021298  0.452340 -0.035158 -0.018145
265624  6.889866  7.070103  0.684921 -0.006264 -0.026111 -0.030837  1.182211
265625  4.143820  7.144353  0.713227 -0.011310  0.264846  0.073983 -0.012409
265626  3.969794  4.868542  1.126973 -0.021412  2.468656  0.886238  3.864711

             CD4       CD8      CD34  ...      CD38      CD13       CD3  \
0       2.229733  0.380750  0.617069  ...  1.395208  0.038552  0.360248
1      -0.034576  0.028380  0.055998  ...  3.448410  1.457326  4.741579
2      -0.008781 -0.023832  0.138957  ...  1.820143  0.401342  0.179631
3      -0.019066  0.779659 -0.027419  ...  4.147996  0.330737  0.060443
4       0.156090  0.700664 -0.018936  ...  1.498051  0.220634  4.908208
...          ...       ...       ...  ...       ...       ...       ...
265622  0.069230 -0.000519 -0.029219  ...  1.209014  0.258038  0.004559
265623  0.970120  0.167407 -0.020814  ...  2.673337  0.408006  5.468722
265624 -0.032375  2.264701  0.107905  ...  1.621310  0.761438  4.324525
265625  0.188642  0.009173  1.229125  ...  1.934654  0.275652 -0.014854
265626  0.792307  2.610154 -0.016104  ...  0.837135  0.905025 -0.006939
```

```
              CD61      CD117      CD49d     HLA-DR       CD64       CD41  Viabilit
y
0        -0.002936  0.025271  0.853505  0.262099  1.541640  0.494105   1.41903
0
1         1.258437  0.089660  0.529624 -0.019200 -0.039433  0.086273  -0.01077
7
2        -0.014565  0.010527  0.213956  1.308337  0.255850 -0.008803   0.15931
3
3         0.125449  0.066470  0.266171  0.002137  1.904348  0.255121  -0.02652
3
4         0.339887  0.167298  0.198912  0.197332  0.076167 -0.040488   0.07820
2
...            ...       ...       ...       ...       ...       ...
...
265622  0.861068  0.431145  1.899320  3.525005 -0.042495  0.075405   0.67677
1
265623  0.565170  0.054991 -0.000330 -0.000796 -0.043636  1.289842   1.02400
5
265624  0.019075  0.087102 -0.055912  0.501536  0.624089  0.387557   0.10720
6
265625 -0.029347  0.134328  0.101955 -0.011615  0.078023 -0.007928   0.34438
5
265626  1.335617  0.328452  1.374000  0.111610 -0.037714 -0.052526   0.31046
6

[265627 rows x 35 columns]
```

New Mask

Formula = (mask_new = 1 * (data_filtered != data_corrupted))

In [ ]:
```python
import numpy as np
import pandas as pd
from sklearn.preprocessing import StandardScaler

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

# Exclude the specified columns
exclude_columns = ['Event', 'Time', 'Cell_length', 'file_number', 'event_num
data_filtered = data.drop(columns=exclude_columns)

# Set the probability of masking
p_m = 0.3

# Generate a binary mask matrix 'm' (changes every run)
m = np.random.binomial(1, 1 - p_m, data_filtered.shape)
binary_mask_df = pd.DataFrame(m, columns=data_filtered.columns)

# Shuffle each column in 'data_filtered' independently to create 'data_shuff
data_shuffled = data_filtered.apply(lambda col: np.random.permutation(col))

# Calculate the corrupted DataFrame 'data_corrupted' using the formula
```

```
data_corrupted_array = data_filtered.values * (1 - m) + data_shuffled.values
data_corrupted = pd.DataFrame(data_corrupted_array, columns=data_filtered.co

# Generate mask_new to indicate differences between original and corrupted d
mask_new = 1 * (data_filtered != data_corrupted)

# Print only the new mask matrix
print("New Mask Matrix (mask_new):\n", mask_new)
```

```
New Mask Matrix (mask_new):
         DNA1  DNA2  CD45RA  CD133  CD19  CD22  CD11b  CD4  CD8  CD34  ...  \
0          1     1       0      0     1     1      1    1    1     1  ...
1          1     1       1      0     1     0      1    1    0     0  ...
2          1     0       1      1     1     0      0    1    1     1  ...
3          0     1       1      1     0     0      0    0    1     0  ...
4          0     1       1      1     1     1      1    0    1     1  ...
...      ...   ...     ...    ...   ...   ...    ...  ...  ...   ...  ...
265622     1     1       1      1     1     0      1    0    1     0  ...
265623     0     1       1      0     1     1      1    1    1     1  ...
265624     1     1       0      1     0     1      1    1    0     1  ...
265625     0     1       0      1     1     1      1    1    1     0  ...
265626     1     1       0      0     1     1      0    1    1     1  ...

        CD38  CD13  CD3  CD61  CD117  CD49d  HLA-DR  CD64  CD41  Viability
0          0     1    1     1      1      0       0     1     1          1
1          1     0    1     1      1      1       0     1     0          1
2          1     1    0     1      1      1       1     1     0          1
3          1     0    1     0      0      1       1     0     1          1
4          1     1    1     0      1      1       0     1     1          1
...      ...   ...  ...   ...    ...    ...     ...   ...   ...        ...
265622     1     0    1     1      0      1       0     1     1          0
265623     1     0    1     0      0      0       1     0     1          1
265624     1     1    0     1      0      1       1     0     1          0
265625     1     1    1     1      1      1       1     1     1          1
265626     0     1    1     1      1      0       0     0     1          1

[265627 rows x 35 columns]
```

Split features and labels for unlabeled data

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

# Load the dataset
df = pd.read_csv('/content/drive/MyDrive/Datasets/Levine_32dim.fcs.csv')

# Define the target column used for labeling
label_column = 'label'

# Separate labeled and unlabeled data using label_df
label_df = df[df[label_column].notnull()]  # labeled data
unlabeled_df = df[df[label_column].isnull()]  # unlabeled data

# Split features and labels for labeled data
```

```python
x_labeled = label_df.drop(columns=[label_column])
y_labeled = label_df[label_column]

# Split features and labels for unlabeled data
x_unlabeled = unlabeled_df.drop(columns=[label_column])
y_unlabeled = unlabeled_df[label_column]

# Display results
print("Labeled Features (x_labeled):\n", x_labeled)
print("\nLabeled Labels (y_labeled):\n", y_labeled)
print("\nUnlabeled Features (x_unlabeled):\n", x_unlabeled)
print("\nUnlabeled Labels (y_unlabeled):\n", y_unlabeled)
```

```
Labeled Features (x_labeled):
         Event       Time  Cell_length      DNA1      DNA2    CD45RA  \
0            1    2693.00           22  4.391057  4.617262  0.162691   
1            2    3736.00           35  4.340481  4.816692  0.701349   
2            3    7015.00           32  3.838727  4.386369  0.603568   
3            4    7099.00           29  4.255806  4.830048  0.433747   
4            5    7700.00           25  3.976909  4.506433 -0.008809   
...        ...        ...          ...       ...       ...       ...   
104179  104180  641812.44           58  6.827981  7.249403 -0.000106   
104180  104181  653387.44           55  6.683204  7.166172  0.692668   
104181  104182  671024.44           40  6.911546  7.152603 -0.036795   
104182  104183  680006.44           48  6.700332  7.100771  0.308817   
104183  104184  687494.44           64  6.559460  7.080928  0.519572   

           CD133      CD19      CD22     CD11b  ...      CD61     CD117  \
0      -0.029585 -0.006696  0.066388 -0.009184  ... -0.002936  0.053050   
1      -0.038280 -0.016654  0.074409  0.808031  ...  1.258437  0.089660   
2      -0.032216  0.073855 -0.042977 -0.001881  ...  0.257137  0.046222   
3      -0.027611 -0.017661 -0.044072  0.733698  ... -0.041140  0.066470   
4      -0.030297  0.080423  0.495791  1.107627  ...  0.168609 -0.006223   
...          ...       ...       ...       ...  ...       ...       ...   
104179 -0.030641  1.432347 -0.044946 -0.016534  ...  0.188846 -0.002144   
104180 -0.037335  1.639063  0.286325 -0.036985  ... -0.029213 -0.031301   
104181 -0.014477  1.637975 -0.021794 -0.020169  ... -0.015220 -0.034755   
104182  0.075762  1.455129  0.042576 -0.049737  ... -0.016644 -0.047522   
104183  0.097257  1.346523  0.279473 -0.021585  ... -0.051973 -0.017015   

           CD49d    HLA-DR      CD64      CD41  Viability  file_number  \
0       0.853505  1.664480 -0.005376 -0.001961   0.648429     3.627711   
1       0.197818  0.491592  0.144814  0.868014   0.561384     3.627711   
2       2.586670  1.308337 -0.010961 -0.010413   0.643337     3.627711   
3       1.338669  0.140523 -0.013449 -0.026039  -0.026523     3.627711   
4       0.180924  0.197332  0.076167 -0.040488   0.283287     3.627711   
...          ...       ...       ...       ...        ...          ...   
104179  1.115652  2.373524 -0.004620 -0.051592   0.157816     3.669327   
104180  1.653418  4.367032  0.062683  0.158656   0.025255     3.669327   
104181  1.083173  3.541526  0.110382  0.108349  -0.043739     3.669327   
104182  0.432565  3.882030  0.058852  0.185295   0.204898     3.669327   
104183  0.263008  4.332834 -0.017214  0.130106   0.023135     3.669327   

        event_number  individual  
0                307           1  
1                545           1  
2               1726           1  
3               1766           1  
4               2031           1  
...              ...         ...  
104179        100344           2  
104180        100892           2  
104181        101558           2  
104182        101842           2  
104183        102112           2  

[104184 rows x 41 columns]

Labeled Labels (y_labeled):
 0          1.0
1          1.0
2          1.0
3          1.0
4          1.0
          ...
104179    14.0
104180    14.0
104181    14.0
104182    14.0
104183    14.0
Name: label, Length: 104184, dtype: float64

Unlabeled Features (x_unlabeled):
          Event       Time  Cell_length      DNA1      DNA2    CD45RA  \
104184  104185      40.00           25  4.203073  4.837565  0.095543
104185  104186     176.00           34  4.042991  4.808275  0.035310
104186  104187     189.00           37  4.233125  4.922201  0.415954
104187  104188     193.00           26  3.997143  4.685426 -0.038565
104188  104189     204.00           20  4.115830  4.893428  0.177246
...        ...        ...          ...       ...       ...       ...
265622  265623  707951.44           41  6.826629  7.133022  1.474081
265623  265624  708145.44           45  6.787791  7.154026  0.116755
265624  265625  708398.44           41  6.889866  7.141219  0.684921
265625  265626  708585.44           39  6.865218  7.144353  0.288761
265626  265627  709122.44           41  6.887820  7.127359  0.360753

           CD133      CD19      CD22      CD11b  ...      CD61     CD117  \
104184 -0.027206  0.172384 -0.001950  0.505713  ...  3.029787 -0.010093
104185 -0.013869 -0.043922 -0.001871  0.180261  ... -0.017628  0.346248
104186  0.412757  0.431715 -0.025619  0.491190  ...  0.000544  0.691393
104187  0.125894  0.191383 -0.026497  0.342190  ... -0.012887  0.033096
104188  0.171916  0.028568 -0.029751  2.480689  ... -0.015719 -0.043689
...          ...       ...       ...       ...  ...       ...       ...
265622 -0.019174 -0.055620 -0.007261  0.063395  ...  0.861068 -0.011105
265623 -0.056213 -0.008864 -0.035158 -0.041845  ...  0.565170  0.143869
265624 -0.006264 -0.026111 -0.030837 -0.034641  ... -0.008680  0.087102
265625 -0.011310 -0.048786  0.073983 -0.031787  ... -0.029347 -0.047971
265626  0.128604 -0.006934  0.109846  3.864711  ... -0.023831  0.080195

           CD49d    HLA-DR      CD64      CD41  Viability  file_number  \
104184  0.387121  2.859639  2.709532  1.208795   0.102978     3.627711
104185  0.089940 -0.017702  0.045091 -0.022009   0.092770     3.627711
104186  2.996583  5.812406  1.713608  0.479122   1.888485     3.627711
104187 -0.029722 -0.031126 -0.020739 -0.014693   0.067437     3.627711
104188  0.027586  2.543139  3.323810 -0.002918   0.109243     3.627711
...          ...       ...       ...       ...        ...          ...
265622  0.533736  0.123758 -0.042495 -0.027971   0.236957     3.669327
265623  1.269464  0.047215 -0.008000 -0.025811  -0.003500     3.669327
265624 -0.055912  0.501536  0.053884 -0.042602   0.107206     3.669327
265625  0.101955  6.200001  0.296877  0.192786   0.620872     3.669327
265626  0.037962  3.675123 -0.000878 -0.052526   0.310466     3.669327

        event_number  individual
104184             1           1
104185             6           1
```

```
104186              7           1
104187              8           1
104188              9           1
...               ...         ...
265622         102686           2
265623         102690           2
265624         102701           2
265625         102706           2
265626         102720           2

[161443 rows x 41 columns]

Unlabeled Labels (y_unlabeled):
 104184   NaN
104185   NaN
104186   NaN
104187   NaN
104188   NaN
          ..
265622   NaN
265623   NaN
265624   NaN
265625   NaN
265626   NaN
Name: label, Length: 161443, dtype: float64
```

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

In [ ]:

```python
import numpy as np
import pandas as pd
from sklearn.model_selection import train_test_split

# Load the dataset
df = pd.read_csv('/content/drive/MyDrive/Datasets/Levine_32dim.fcs.csv')

# Define the target column used for labeling
label_column = 'label'

# Separate labeled data
label_df = df[df[label_column].notnull()]

# Split features and labels for labeled data
x_labeled = label_df.drop(columns=[label_column])
y_labeled = label_df[label_column]

# Split labeled data into training and testing sets (70%-30% split)
x_train, x_test, y_train, y_test = train_test_split(x_labeled, y_labeled, te

# Display results
print("Training Features (x_train):\n", x_train)
print("\nTesting Features (x_test):\n", x_test)
print("\nTraining Labels (y_train):\n", y_train)
print("\nTesting Labels (y_test):\n", y_test)
```

```
Training Features (x_train):
          Event       Time  Cell_length      DNA1      DNA2    CD45RA  \
64113     64114  401196.00           25  3.899656  4.594272  0.976652
82744     82745  502826.44           31  6.592998  6.901888  0.431481
24294     24295  488377.00           41  3.543583  4.467671  0.377192
7820       7821  225689.00           38  4.305227  4.881685  0.199351
43295     43296  153333.00           26  4.159271  4.861015  0.831285
...         ...        ...          ...       ...       ...       ...
54886     54887   93991.00           15  4.074604  4.747052  0.431805
76820     76821   46189.00           33  6.584427  6.882117  0.640424
103694   103695  574005.44           43  6.719895  7.080995  0.306443
860         861  516979.00           26  3.886782  4.886936  0.060176
15795     15796  225860.00           25  3.523293  4.289820  0.646288

           CD133      CD19      CD22     CD11b  ...      CD61     CD117  \
64113   0.302811  0.154761 -0.011676  3.180236  ...  0.051464 -0.003680
82744  -0.052898 -0.037690 -0.029715 -0.040846  ... -0.036430  0.021689
24294   0.219081  0.245478  0.193328  0.075123  ...  1.003383  0.406137
7820    0.100678 -0.025812 -0.002898  1.437247  ... -0.007282  1.421540
43295   0.191518  2.002712  3.387782  0.179219  ... -0.040754  0.060944
...          ...       ...       ...       ...  ...       ...       ...
54886   0.228761 -0.011434 -0.017082  1.379518  ... -0.029607 -0.039425
76820  -0.044057 -0.013737 -0.030704 -0.009781  ... -0.038000  0.190509
103694 -0.026339  2.074008  0.052549  0.167479  ...  0.054690  0.011329
860     0.233401 -0.020592 -0.007786  1.090780  ... -0.001868 -0.046200
15795  -0.028126  0.184879  0.214664  0.224471  ...  0.089666  0.343049

           CD49d    HLA-DR      CD64      CD41  Viability  file_number  \
64113   1.260410  0.700093  2.355886  0.125409   0.840205     3.627711
82744   0.034946 -0.055651 -0.023248 -0.054842  -0.009329     3.669327
24294   1.928676 -0.046849  0.229309  0.937020   1.231347     3.627711
7820    1.443145  2.461705  0.528679  0.072205   0.892480     3.627711
43295   1.294561  3.085858 -0.014128  0.479256   2.269233     3.627711
...          ...       ...       ...       ...        ...          ...
54886   0.036619  2.424191  1.080756 -0.014481   0.190138     3.627711
76820   0.204920 -0.004600  0.135288 -0.042874  -0.023160     3.669327
103694  0.267845  4.060155  0.123218  0.006991  -0.026324     3.669327
860     1.016980  0.000744 -0.030356 -0.033473   0.371143     3.627711
15795   0.784416  0.064465  0.088172 -0.013586   0.153918     3.627711

        event_number  individual
64113         318320           1
82744          80934           2
24294         366690           1
7820          203131           1
43295         152117           1
...              ...         ...
54886          96894           1
76820           8563           2
103694         94148           2
860           378748           1
15795         203230           1

[72928 rows x 41 columns]

Testing Features (x_test):
        Event      Time  Cell_length      DNA1      DNA2    CD45RA     CD133
\
60544  60545  278003.0           49  3.618797  4.144135  0.198186  0.000282
50673  50674  490341.0           27  3.660988  4.497041  1.272625  0.129642
50682  50683  490912.0           23  3.854865  4.663734  1.527763  0.151383
1761    1762  170466.0           17  3.716473  4.465312  0.375236 -0.037150
98760  98761  423490.0           32  6.826030  7.007709  0.223441 -0.048813
...      ...       ...          ...       ...       ...       ...       ...
20510  20511  370777.0           63  3.260559  3.934633  0.448954  0.219533
11540  11541   99635.0           37  3.204839  3.422136  0.088893  0.359100
30042  30043  145367.0           57  3.351777  4.185945  1.148632  0.383412
40569  40570   45221.0           50  4.010990  4.529642  1.211406  1.121462
93618  93619  289293.0           37  6.732461  6.913152  1.734362  0.126751

           CD19      CD22     CD11b  ...      CD61     CD117     CD49d  \
60544  0.253703 -0.018972  2.665005  ...  0.307357  0.208639  2.039954
50673  3.054480  2.493220  0.189975  ...  0.084448  0.033192  0.004637
50682  2.361353  2.281009  0.528589  ... -0.041903 -0.026017  0.109363
1761  -0.035385  0.127904  0.415204  ... -0.001024 -0.017034  0.023385
98760 -0.018816 -0.045954  4.067125  ... -0.029816 -0.046020  0.140410
...         ...       ...       ...  ...       ...       ...       ...
20510  0.105799  0.093621 -0.006647  ...  0.599577  0.376384  2.196247
11540 -0.001227  0.128556  0.008345  ...  0.908547  0.001992  0.464461
30042 -0.037390  0.229479  0.005238  ...  0.596622  0.055177  0.761682
40569  1.185200  0.905587  0.254603  ...  0.120182 -0.007947  1.649371
93618  1.406384  1.672294  0.082506  ... -0.033528 -0.011614  0.134475

         HLA-DR      CD64      CD41  Viability  file_number  event_number  \
60544  2.847283  2.798986  1.090235   1.005784     3.627711        237532
50673  4.488360  0.866820 -0.002174   0.917810     3.627711        367731
50682  2.328828 -0.008223 -0.018680   1.091297     3.627711        367970
1761   0.120367  0.472159 -0.014919   0.620643     3.627711        164637
98760  0.735830  1.011186 -0.044875   0.149759     3.669327         62492
...         ...       ...       ...        ...          ...           ...
20510  0.342656  0.235691  0.128557   1.251073     3.627711        298390
11540 -0.011717  0.331829  0.804992   1.791590     3.627711        103618
30042  0.194395  0.496897  1.122718   0.614461     3.627711        146117
40569  3.598308  0.521024  0.592218   1.099637     3.627711         37211
93618  1.677873  0.355002 -0.013528  -0.017024     3.669327         56333

       individual
60544           1
50673           1
50682           1
1761            1
98760           2
...           ...
20510           1
11540           1
30042           1
40569           1
93618           2

[31256 rows x 41 columns]

Training Labels (y_train):
 64113     10.0
82744      7.0
24294      7.0
7820       6.0
43295      9.0
          ...
54886     10.0
76820      7.0
103694    13.0
860        1.0
15795      7.0
Name: label, Length: 72928, dtype: float64

Testing Labels (y_test):
 60544    10.0
50673     9.0
50682     9.0
1761      2.0
98760    10.0
         ...
20510     7.0
11540     7.0
30042     8.0
40569     9.0
93618     9.0
Name: label, Length: 31256, dtype: float64
```

Logistic regression and Xgboost

In [20]:
```python
import numpy as np
import pandas as pd
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from xgboost import XGBClassifier
from sklearn.preprocessing import LabelEncoder, StandardScaler

# Load the dataset
df = pd.read_csv('/content/drive/MyDrive/Datasets/Levine_32dim.fcs.csv')

# Define the target column used for labeling
label_column = 'label'

# Separate labeled data
label_df = df[df[label_column].notnull()]

# Split features and labels for labeled data
x_labeled = label_df.drop(columns=[label_column])
y_labeled = label_df[label_column]

# Encode labels if necessary (e.g., for non-numeric labels)
label_encoder = LabelEncoder()
y_labeled = label_encoder.fit_transform(y_labeled)

# Split labeled data into training and testing sets (70%-30% split)
x_train, x_test, y_train, y_test = train_test_split(x_labeled, y_labeled, te
# Scale features for Logistic Regression and XGBoost
scaler = StandardScaler()
x_train_scaled = scaler.fit_transform(x_train)
x_test_scaled = scaler.transform(x_test)

# Logistic Regression Model with increased max_iter and scaled data
logistic_model = LogisticRegression(max_iter=2000)
logistic_model.fit(x_train_scaled, y_train)
y_test_hat_logistic = logistic_model.predict_proba(x_test_scaled)

# XGBoost Model (using scaled data)
xgb_model = XGBClassifier(eval_metric='mlogloss')
xgb_model.fit(x_train_scaled, y_train)  # Use scaled data for training
y_test_hat_xgb = xgb_model.predict_proba(x_test_scaled)  # Use scaled test c

# Display the predicted probabilities for Logistic Regression and XGBoost
print("Logistic Regression Predicted Probabilities:\n", y_test_hat_logistic)
print("\nXGBoost Predicted Probabilities:\n", y_test_hat_xgb)
```

```
Logistic Regression Predicted Probabilities:
 [[8.71532016e-11 7.15777514e-16 5.86413815e-12 ... 3.71679135e-10
  2.57615663e-08 2.92952487e-08]
 [3.89684389e-14 5.45734530e-13 1.08967360e-13 ... 9.25120232e-10
  3.73081988e-05 6.16167181e-09]
 [1.84225273e-11 5.90550517e-10 1.12355888e-11 ... 1.59113271e-11
  1.62867175e-05 6.66716712e-10]
 ...
 [5.05774251e-10 1.66206209e-05 5.93223532e-09 ... 3.54583852e-09
  3.57005966e-11 9.95221511e-09]
 [6.94828817e-11 7.05048241e-10 2.51660858e-10 ... 1.19779551e-11
  1.34185137e-06 2.54193720e-06]
 [3.32647158e-10 1.39746320e-06 5.84840148e-10 ... 1.09125625e-13
  1.93385444e-05 1.73713000e-10]]

XGBoost Predicted Probabilities:
 [[8.8804103e-07 8.2875789e-07 5.7034327e-07 ... 1.1134865e-06
  7.0003387e-07 9.7590839e-07]
 [7.1397778e-07 7.8185877e-07 5.3256036e-07 ... 1.1057809e-06
  6.3680345e-06 1.2659862e-06]
 [8.2513844e-07 9.2658485e-07 6.4014063e-07 ... 9.4035636e-07
  2.3140719e-06 1.1265030e-06]
 ...
 [4.7537603e-07 1.6399291e-06 4.6528021e-07 ... 5.1612403e-07
  4.0387292e-07 4.1018055e-07]
 [3.5595222e-06 3.8425301e-06 3.3242245e-06 ... 4.7351091e-06
  7.2303219e-06 2.1757294e-05]
 [1.9763070e-06 1.7193395e-06 1.8571778e-06 ... 2.2942536e-06
  3.7291477e-06 2.6302241e-06]]
```

Logistic Regression Log Loss

In [39]:
```
from sklearn.metrics import log_loss

# Calculate log loss for Logistic Regression
```

```
logistic_loss = log_loss(y_test, y_test_hat_logistic)
print("Logistic Regression Log Loss:", logistic_loss)
```

```
Logistic Regression Log Loss: 0.007401566937746702
```

XGBoost Log Loss

In [40]:
```
from sklearn.metrics import log_loss


# Calculate log loss for XGBoost
xgb_loss = log_loss(y_test, y_test_hat_xgb)
print("XGBoost Log Loss:", xgb_loss)
```

```
XGBoost Log Loss: 0.0014473331046161019
```

CLASSWORK

In [7]:
```
from keras.layers import Input, Dense
from keras.models import Model
import numpy as np

def binary_mask(p_m, data):
    """Generates a binary mask with probability p_m."""
    return np.random.binomial(1, 1 - p_m, data.shape)

def corruption(mask, data):
    num_samples, num_features = data.shape
    shuffled_data = np.zeros([num_samples, num_features])

    for feature_idx in range(num_features):
        shuffled_indices = np.random.permutation(num_samples)
        shuffled_data[:, feature_idx] = data[shuffled_indices, feature_idx]

    data_corrupted = data * (1 - mask) + shuffled_data * mask
    mask_new = (data != data_corrupted).astype(int)

    return mask_new, data_corrupted

def self_supervised(x_unlabeled, p_m, alpha, parameters):
    epochs = parameters['epochs']
    batch_size = parameters['batch_size']
    _, dimension = x_unlabeled.shape

    # Define model architecture
    input_layer = Input(shape=(dimension,))
    h = Dense(int(dimension), activation='relu')(input_layer)

    output1 = Dense(int(dimension), activation='sigmoid', name='mask_estimat
    output2 = Dense(int(dimension), activation='sigmoid', name='feature_esti

    model = Model(inputs=input_layer, outputs=[output1, output2])
    # Compile model with appropriate loss functions and weights
    model.compile(
        optimizer="rmsprop",
        loss={'mask_estimation': 'binary_crossentropy', 'feature_estimation'
        loss_weights={'mask_estimation': 1.0, 'feature_estimation': float(al
    )

    # Generate corrupted input and mask labels
    corruption_binary_mask = binary_mask(p_m, x_unlabeled)
    x_unlabeled_corrupted,mask_label = corruption(corruption_binary_mask, x_

    assert x_unlabeled_corrupted.shape == mask_label.shape


    # Train model
    model.fit(x_unlabeled_corrupted, {'mask_estimation': mask_label, 'featur
              epochs=epochs, batch_size=batch_size)

    # Display model summary (this will print the model's parameters)
    model.summary()

    # Define encoder
    name_of_layer = model.layers[1].name
    layer_output = model.get_layer(name_of_layer).output
    encoder = Model(inputs=model.input, outputs=layer_output)

    return encoder
```

In [8]:
```
import pandas as pd
import numpy as np
from sklearn.preprocessing import StandardScaler

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

# Exclude specified columns
exclude_columns = ['Event', 'Time', 'Cell_length', 'file_number', 'event_num
data_filtered = data.drop(columns=exclude_columns)

# Standardize the data
scaler = StandardScaler()
x_unlabeled_scaled = scaler.fit_transform(data_filtered)  # Now x_unlabeled_

# Define other parameters
p_m = 0.3
alpha = 2.0
parameters = {
    'batch_size': 128,
    'epochs': 50,
}

# Run the self_supervised function with the scaled data
encoder_model = self_supervised(x_unlabeled_scaled, p_m, alpha, parameters)
```

```
Epoch 1/50
2076/2076 ━━━━━━━━━━━━━━━━━━━━ 5s 2ms/step - loss: 2.0832
Epoch 2/50
2076/2076 ━━━━━━━━━━━━━━━━━━━━ 6s 3ms/step - loss: 1.9925
Epoch 3/50
2076/2076 ━━━━━━━━━━━━━━━━━━━━ 4s 2ms/step - loss: 1.9959
Epoch 4/50
2076/2076 ━━━━━━━━━━━━━━━━━━━━ 4s 2ms/step - loss: 1.9581
Epoch 5/50
2076/2076 ━━━━━━━━━━━━━━━━━━━━ 8s 3ms/step - loss: 1.8994
Epoch 6/50
2076/2076 ━━━━━━━━━━━━━━━━━━━━ 4s 2ms/step - loss: 1.8662
Epoch 7/50
2076/2076 ━━━━━━━━━━━━━━━━━━━━ 4s 2ms/step - loss: 1.8019
Epoch 8/50
2076/2076 ━━━━━━━━━━━━━━━━━━━━ 6s 3ms/step - loss: 1.9000
Epoch 9/50
2076/2076 ━━━━━━━━━━━━━━━━━━━━ 8s 2ms/step - loss: 1.7035
Epoch 10/50
2076/2076 ━━━━━━━━━━━━━━━━━━━━ 4s 2ms/step - loss: 1.3959
Epoch 11/50
2076/2076 ━━━━━━━━━━━━━━━━━━━━ 6s 3ms/step - loss: 1.5150
Epoch 12/50
2076/2076 ━━━━━━━━━━━━━━━━━━━━ 4s 2ms/step - loss: 1.3383
Epoch 13/50
2076/2076 ━━━━━━━━━━━━━━━━━━━━ 4s 2ms/step - loss: 1.2883
Epoch 14/50
2076/2076 ━━━━━━━━━━━━━━━━━━━━ 8s 3ms/step - loss: 1.2600
Epoch 15/50
2076/2076 ━━━━━━━━━━━━━━━━━━━━ 4s 2ms/step - loss: 1.0581
Epoch 16/50
2076/2076 ━━━━━━━━━━━━━━━━━━━━ 6s 2ms/step - loss: 0.7630
Epoch 17/50
2076/2076 ━━━━━━━━━━━━━━━━━━━━ 5s 2ms/step - loss: 0.3620
Epoch 18/50
2076/2076 ━━━━━━━━━━━━━━━━━━━━ 4s 2ms/step - loss: 0.2985
Epoch 19/50
2076/2076 ━━━━━━━━━━━━━━━━━━━━ 4s 2ms/step - loss: 0.7215
Epoch 20/50
2076/2076 ━━━━━━━━━━━━━━━━━━━━ 6s 3ms/step - loss: -0.1579
Epoch 21/50
2076/2076 ━━━━━━━━━━━━━━━━━━━━ 8s 2ms/step - loss: -0.0397
Epoch 22/50
2076/2076 ━━━━━━━━━━━━━━━━━━━━ 7s 3ms/step - loss: 0.3407
Epoch 23/50
2076/2076 ━━━━━━━━━━━━━━━━━━━━ 9s 2ms/step - loss: 0.2010
Epoch 24/50
2076/2076 ━━━━━━━━━━━━━━━━━━━━ 6s 3ms/step - loss: -1.1176
Epoch 25/50
2076/2076 ━━━━━━━━━━━━━━━━━━━━ 8s 2ms/step - loss: 0.1148
Epoch 26/50
2076/2076 ━━━━━━━━━━━━━━━━━━━━ 7s 3ms/step - loss: -1.3213
Epoch 27/50
2076/2076 ━━━━━━━━━━━━━━━━━━━━ 4s 2ms/step - loss: -3.8500
Epoch 28/50
2076/2076 ━━━━━━━━━━━━━━━━━━━━ 4s 2ms/step - loss: -1.2900
```

```
 Epoch 29/50
 2076/2076 ━━━━━━━━━━━━━━━━━━━━ 7s 3ms/step - loss: -1.3041
 Epoch 30/50
 2076/2076 ━━━━━━━━━━━━━━━━━━━━ 8s 2ms/step - loss: -3.6426
 Epoch 31/50
 2076/2076 ━━━━━━━━━━━━━━━━━━━━ 5s 3ms/step - loss: -1.6354
 Epoch 32/50
 2076/2076 ━━━━━━━━━━━━━━━━━━━━ 9s 2ms/step - loss: -3.9099
 Epoch 33/50
 2076/2076 ━━━━━━━━━━━━━━━━━━━━ 5s 2ms/step - loss: -2.4034
 Epoch 34/50
 2076/2076 ━━━━━━━━━━━━━━━━━━━━ 5s 2ms/step - loss: -2.3920
 Epoch 35/50
 2076/2076 ━━━━━━━━━━━━━━━━━━━━ 4s 2ms/step - loss: -1.1857
 Epoch 36/50
 2076/2076 ━━━━━━━━━━━━━━━━━━━━ 6s 2ms/step - loss: -4.3850
 Epoch 37/50
 2076/2076 ━━━━━━━━━━━━━━━━━━━━ 5s 2ms/step - loss: -4.6088
 Epoch 38/50
 2076/2076 ━━━━━━━━━━━━━━━━━━━━ 5s 3ms/step - loss: -6.8267
 Epoch 39/50
 2076/2076 ━━━━━━━━━━━━━━━━━━━━ 10s 2ms/step - loss: -7.7914
 Epoch 40/50
 2076/2076 ━━━━━━━━━━━━━━━━━━━━ 4s 2ms/step - loss: -7.1373
 Epoch 41/50
 2076/2076 ━━━━━━━━━━━━━━━━━━━━ 6s 3ms/step - loss: -5.6402
 Epoch 42/50
 2076/2076 ━━━━━━━━━━━━━━━━━━━━ 9s 2ms/step - loss: -9.3524
 Epoch 43/50
 2076/2076 ━━━━━━━━━━━━━━━━━━━━ 7s 3ms/step - loss: -9.3948
 Epoch 44/50
 2076/2076 ━━━━━━━━━━━━━━━━━━━━ 8s 2ms/step - loss: -11.3782
 Epoch 45/50
 2076/2076 ━━━━━━━━━━━━━━━━━━━━ 7s 3ms/step - loss: -11.6957
 Epoch 46/50
 2076/2076 ━━━━━━━━━━━━━━━━━━━━ 8s 2ms/step - loss: -6.5291
 Epoch 47/50
 2076/2076 ━━━━━━━━━━━━━━━━━━━━ 7s 3ms/step - loss: -8.5328
 Epoch 48/50
 2076/2076 ━━━━━━━━━━━━━━━━━━━━ 4s 2ms/step - loss: -8.4592
 Epoch 49/50
 2076/2076 ━━━━━━━━━━━━━━━━━━━━ 5s 2ms/step - loss: -5.3708
 Epoch 50/50
 2076/2076 ━━━━━━━━━━━━━━━━━━━━ 7s 3ms/step - loss: -16.0661
Model: "functional"
```

Layer (type)	Output Shape	Param #
input_layer (InputLayer)	(None, 35)	0
dense (Dense)	(None, 35)	1,260
mask_estimation (Dense)	(None, 35)	1,260
feature_estimation (Dense)	(None, 35)	1,260

Total params: 7,562 (29.54 KB)

Trainable params: 3,780 (14.77 KB)

Non-trainable params: 0 (0.00 B)

Optimizer params: 3,782 (14.78 KB)

In [10]:
```
encoder_path = "/content/encoder_model.keras"


encoder_model.save(encoder_path)
```

In [11]:
```
from keras.models import load_model
encoder_model = load_model(encoder_path)
```

In [38]:
```
X_train_scaled_encoded = encoder_model.predict(x_train_scaled)
X_test_scaled_encoded = encoder_model.predict(x_test_scaled)

logistic_model = LogisticRegression(max_iter=2000)
logistic_model.fit(X_train_scaled_encoded, y_train)
y_encoded = logistic_model.predict_proba(X_test_scaled_encoded)

from sklearn.metrics import log_loss
print("Logistic Regression Log Loss:", log_loss(y_test, y_encoded))

xgb_model = XGBClassifier(eval_metric='mlogloss')
xgb_model.fit(X_train_scaled_encoded, y_train)
y_encoded_xgb = xgb_model.predict_proba(X_test_scaled_encoded)

print("XGBoost Log Loss:", log_loss(y_test, y_encoded_xgb))
```

```
2279/2279 ━━━━━━━━━━━━━━━━━━━━ 7s 3ms/step
977/977 ━━━━━━━━━━━━━━━━━━━━ 1s 1ms/step
Logistic Regression Log Loss: 0.04272104968091639
XGBoost Log Loss: 0.047771756718024666
```