TSNE, Clustering Experimentation

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CS 6319

April 28, 2025

a Abstract

In this project, we focus on the problem of clustering analysis and visualization across a variety of structured and unstructured datasets. We implement several core algorithms from scratch in Python, including K-Means clustering, K-Center clustering, t-SNE (t-distributed Stochastic Neighbor Embedding) for dimensionality reduction, and a custom cluster quality metric based on convex hulls and area calculations. Our custom metric is designed to complement traditional evaluation methods by directly quantifying cluster compactness and separation. For comparison, we also use standard clustering evaluation metrics such as the Silhouette Score and the Davies-Bouldin Index.

To visualize results and apply density-based clustering (DBSCAN), we utilize well-known libraries such as `scikit-learn` and `matplotlib`. The datasets explored include the Iris flower dataset, Wine dataset, Breast Cancer dataset, synthetic datasets like Half Moons, Entangled Rings, Swiss Roll, and the high-dimensional MNIST digits dataset.

Our experiments reveal that while traditional metrics like the Silhouette Score and Davies-Bouldin Index provide useful indicators of clustering performance, they sometimes fail to fully capture the intuitive quality of cluster separation observed visually. The custom metric based on convex hull overlap offers an alternative perspective, particularly valuable in visually assessing non-convex and irregular clusters. This project underlines the importance of combining quantitative evaluation with human-in-the-loop visualization when analyzing the performance of clustering algorithms.

b Instruction to Run the Code

- pip install -r requirements.txt
- To Run the Kcenter Code: python kcenter_dataset_tests.py
- To Run the KMeans Code: python kmeans_dataset_tests.py
- To Run the TSNE Code (both standard and dynamic):
  python tsne_vs_dynamic_individual_dataset_test.py

c Clustering

c.1 Overview

Clustering is an **unsupervised learning** technique that groups data points into subsets called **clusters** based on similarity. Key approaches include:

- **Centroid-based** (e.g., K-Means): Uses mean vectors (potentially non-data points) to represent clusters.
- **Medoid-based** (e.g., K-Center): Uses actual data points as centers for interpretability and robustness.

c.2 K-Means

c.2.1 Objective

Minimize the sum of squared distances from points to their nearest center.

$$\min_{\mu_1,\ldots,\mu_k} \sum_{i=1}^{n} \min_{j=1,\ldots,k} \|x_i - \mu_j\|^2 \tag{1}$$

- μ_j: Cluster centroid (mean vector, not necessarily a data point).
- $\|x_i - \mu_j\|^2$: Squared Euclidean distance (penalizes large deviations).
- Inner $\min_j$: Assigns each point x_i to its nearest centroid.
- Outer $\sum$: Sums the squared distances across all points.

c.2.2 Algorithm (Lloyd's)

- *Initialize*: Randomly select k centroids (often data points).
- *Assign*: Assign each point to the nearest centroid (Voronoi partitioning):

$$C_j = \left\{ x : \|x - \mu_j\|^2 \leq \|x - \mu_l\|^2 \; \forall l \neq j \right\} \tag{2}$$

- *Update*: Recompute centroids as the mean of all points in their cluster

$$\mu_j^{\text{new}} = \frac{1}{|C_j|} \sum_{x \in C_j} x \tag{3}$$

- *Repeat*: Until centroids stabilize ($\Delta\mu < \epsilon$) or max iterations $T_{\max}$.

c.2.3 Properties

- *Time Complexity*: $O(nkdT)$ (n=points, k=clusters, d=dimensions, T=iterations).
- *Guarantee*: Guaranteed to local optima (no global guarantees).
- *Failure Cases*: Non-spherical clusters (e.g., Half Moons), high-dimensional data.
- *Strengths*: Scalable ($O(nkdT)$), ideal for spherical clusters, similarly sized clusters.
- *Weaknesses*: Sensitive to outliers; fails on non-convex shapes.
- *Application*: Image compression (color quantization), Customer segmentation (RFM analysis), Anomaly detection (distance-to-centroid thresholds).
- *Challenges*: May require multiple restarts during initialization (k-means++ helps), Distance concentration degrades.

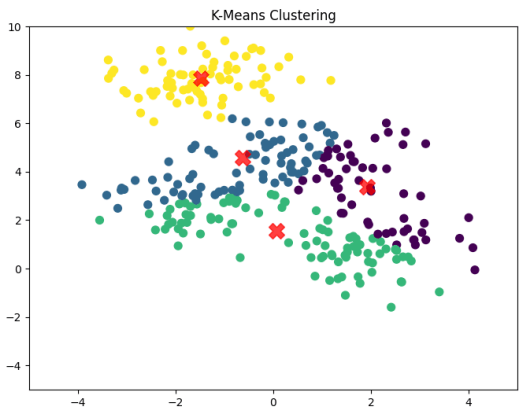
c.2.4 Code Highlights

- *Code Location*: All K-Means code can be found in *src/kmeans.py*
- *Important Implementation functions*:

```
def train(self, X):
    self.centroids = self.initialize_centroids(X)

    for _ in range(self.max_iter):
        self.labels_ = self.assign_clusters(X)
        new_centroids = self.update_centroids(X, self.labels_)
        if np.allclose(self.centroids, new_centroids):
            break
```

```
            self.centroids = new_centroids

        self.inertia_ = 0.0
        for i in range(self.n_clusters):
            cluster_points = X[self.labels_ == i]
            self.inertia_ += np.sum((cluster_points - self.centroids[i]) ** 2)

    def predict(self, X):
        distances = np.sqrt(((X[:, np.newaxis] - self.centroids) ** 2).sum(axis=2))
        return np.argmin(distances, axis=1)

    def initialize_centroids(self, X):
        np.random.seed(self.random_state)
        random_idx = np.random.permutation(X.shape[0])
        centroids = X[random_idx[:self.n_clusters]]
        return centroids

    def assign_clusters(self, X):
        distances = np.sqrt(((X[:, np.newaxis] - self.centroids) ** 2).sum(axis=2))
        return np.argmin(distances, axis=1)

    def update_centroids(self, X, labels):
        new_centroids = np.zeros((self.n_clusters, X.shape[1]))
        for i in range(self.n_clusters):
            new_centroids[i] = X[labels == i].mean(axis=0)
        return new_centroids

    def elbow_method(X, max_k=10):
        inertia = []
        k_values = list(range(1, max_k + 1))

        for k in k_values:
            model = KMeans(n_clusters=k, random_state=42)
            model.train(X)
            inertia.append(model.inertia_)

        knee = KneeLocator(k_values, inertia, curve="convex", direction="decreasing")
        optimal_k = knee.elbow

        plt.plot(k_values, inertia, 'bo-')
        plt.xlabel('Number of Clusters (k)')
        plt.ylabel('Inertia (Sum of Squared Distances)')
        plt.title('Elbow Method for Optimal k')
        plt.grid(True)
        plt.show()

        return optimal_k
```

c.2.5 Visualization



c.3 K-Center

c.3.1 Objective

Minimizes worst-case distance (NP-hard; 2-approximation guarantee).

$$\min_{C \subseteq X, |C|=k} \max_{x \in X} \min_{c \in C} \|x - c\| \tag{4}$$

- C: Subset of k medoids (actual data points).
- $\|x - c\|$: Flexible metric (Manhattan, cosine, etc.).
- min_c: Assigns each point x to its nearest center c.
- max_x: Focuses on the worst-case (farthest) distance across all points.

c.3.2 Algorithm (Greedy)

- *Initialize*: Randomly select the first center c_1 from the data.
- *Iterate*: For $i = 2$ to k, select farthest point and add this point as the next center c_i:

$$c_i = \arg\max_{x \in X} \min_{c \in \{c_1, \ldots, c_{i-1}\}} \|x - c\| \tag{5}$$

- *Assign*: Assign each point to its nearest center.

c.3.3 Properties

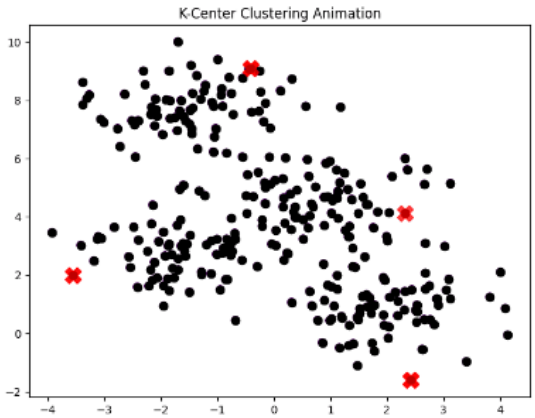
- *Time Complexity*: $O(kn)$ (n=points, k=clusters).
- *Guarantee*: 2-approximation algorithm (bounded suboptimal solution).
- *Failure Cases*: High-Dimensional Data, Large k, Varying Densities, Initialization Sensitivity, Outliers as Centers, Non-Optimal Approximation, Average-Case Scenarios
- *Strengths*: Outlier-robust; handles arbitrary metrics/shapes, Interpretable centers.
- *Weaknesses*: $O(kn)$ complexity; limited to small k.
- *Application*: Facility location (minimize max service distance), Fraud detection (identify outlier transactions), Document clustering (TF-IDF + cosine similarity).
- *Challenges*: First center choice impacts results, Distance concentration degrades.

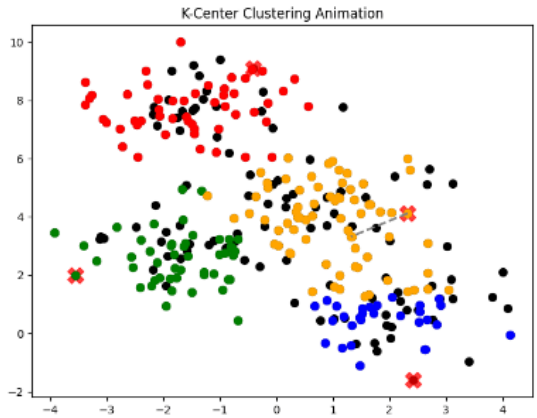
c.3.4 Code Highlights

- *Code Location*: All K-Center code can be found in *src/kcenter.py*
- *Important Implementation functions*:

```
def train(self, X):
    self.initialize_centroids(X)
    self.labels_ = self.assign_clusters(X)

    point_distances = np.linalg.norm(X - self.centroids[self.labels_], axis=1)
    self.inertia_ = np.max(point_distances)

def predict(self, X):
    distances = np.linalg.norm(X[:, np.newaxis] - self.centroids, axis=2)
    return np.argmin(distances, axis=1)

def assign_clusters(self, X):
    distances = np.linalg.norm(X[:, np.newaxis] - self.centroids, axis=2)
    return np.argmin(distances, axis=1)

def initialize_centroids(self, X):
    np.random.seed(self.random_state)
    n_samples = X.shape[0]
    centroids = [X[np.random.randint(n_samples)]]

    for _ in range(self.n_clusters - 1):
        distances = np.array([np.min([np.linalg.norm(x - c) for c in centroids]) for x in X])
        next_centroid = X[np.argmax(distances)]
        centroids.append(next_centroid)

    self.centroids = np.array(centroids)

def elbow_method(X, max_k=10):
    max_distances = []
    k_values = range(1, max_k + 1)

    for k in k_values:
        model = KCenter(n_clusters=k, random_state=42)
        model.train(X)
        max_distances.append(model.inertia_)

    knee = KneeLocator(k_values, max_distances,
                       curve="convex", direction="decreasing")
    optimal_k = knee.elbow
    plt.plot(k_values, max_distances, 'bo-')
    plt.xlabel('Number of Clusters (k)')
    plt.ylabel('Maximum Distance')
    plt.title('Elbow Method for K-Center')
    plt.grid(True)
    plt.show()

    return optimal_k
```

c.3.5 Visualization





c.3.6 Data Exploration - K-Means and K-Center

The data exploration process for both `K-Means` and `K-Center` clustering utilized the `Country-data.csv` dataset, which contains socio-economic indicators for 167 countries. Key features include:

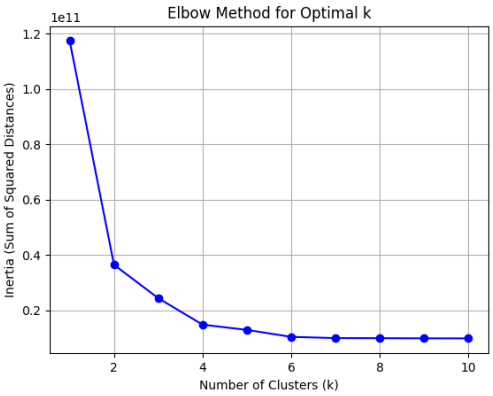
- `child_mort`: Child mortality rate (per 1000 live births)
- `exports/imports`: Trade metrics (% of GDP per capita)
- `health`: Healthcare spending (% of GDP)
- `income`: Net income per capita
- `gdpp`: GDP per capita
- `life_expec`: Life expectancy
- `total_fer`: Fertility rate
- `inflation`: Annual GDP growth rate

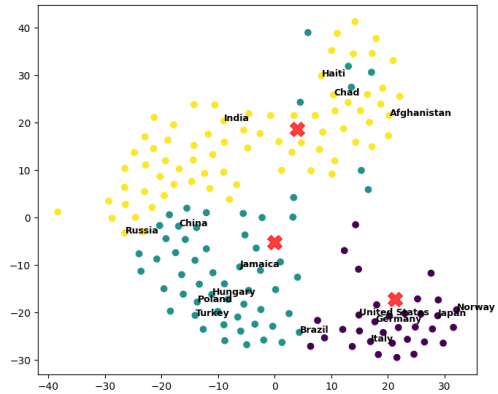
Preprocessing: Data was normalized using row-wise L^2 normalization to mitigate scale differences between features (e.g., `gdpp` vs. `child_mort`).

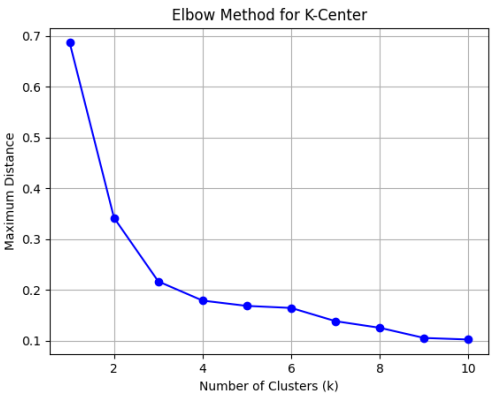
Key Observations:

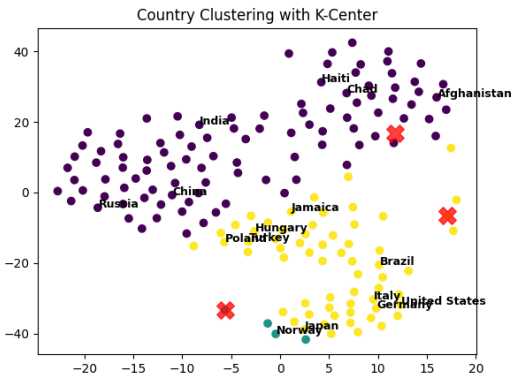
- `K-Means` clusters correlate with income/`gdpp` due to sensitivity to feature magnitude.
- `K-Center` groups extreme cases (e.g., high `child_mort` countries).
- Both methods separate developed/developing nations, with centroids acting as socio-economic prototypes.

Results:

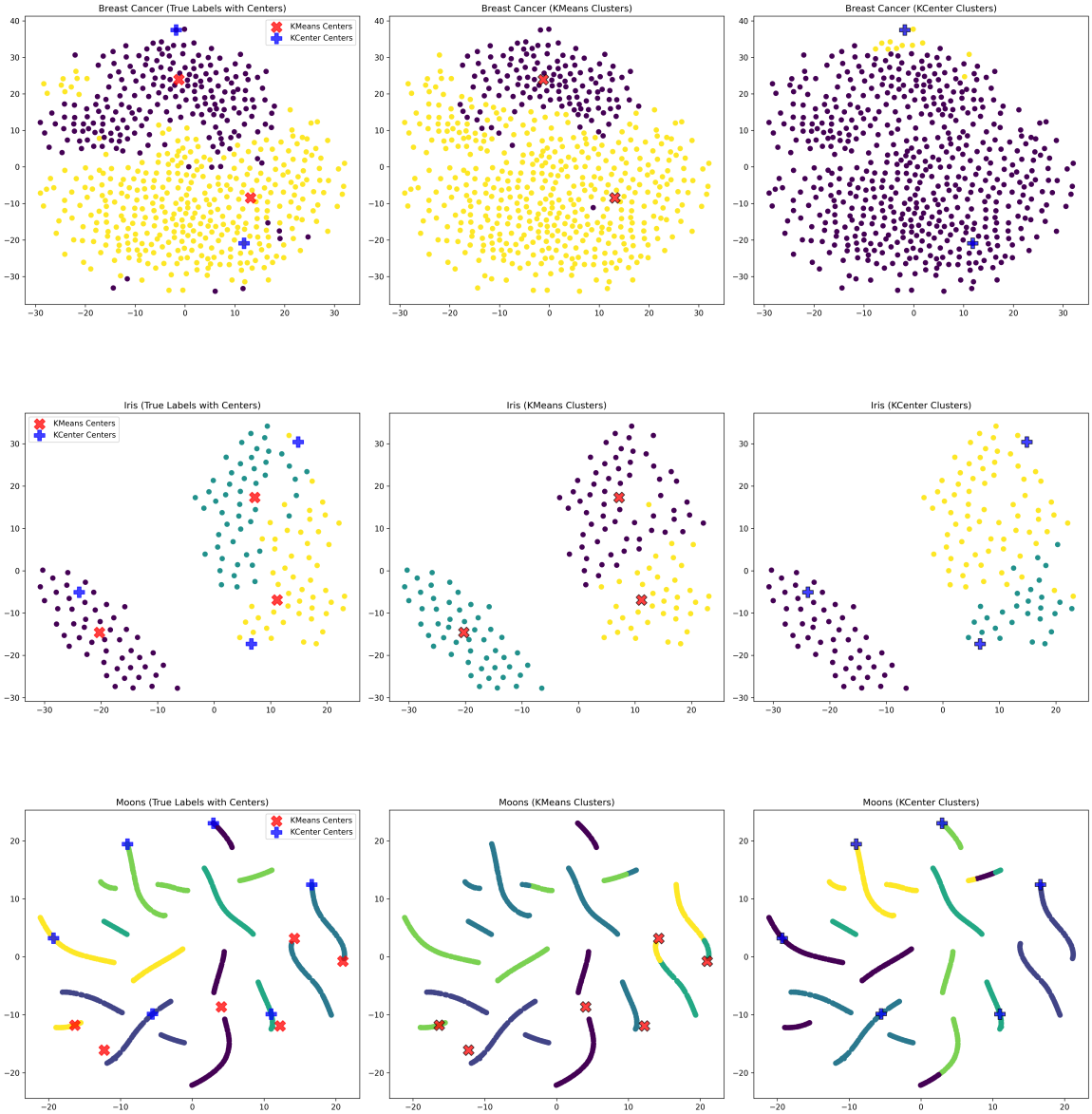


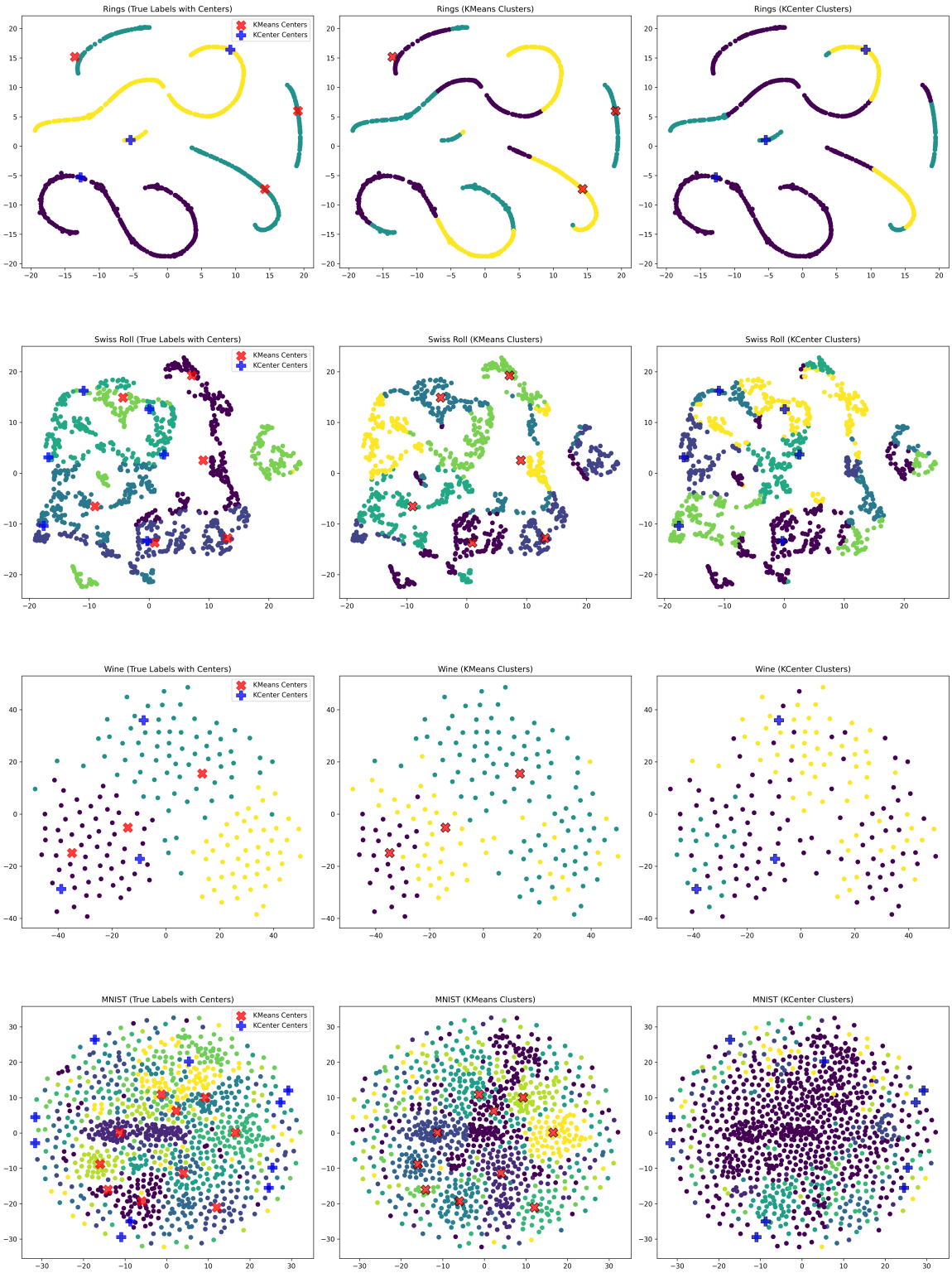






c.4 Results - Standard Datasets




Rings (True Labels with Centers)
KMeans Centers
KCenter Centers
Rings (KMeans Clusters)
Rings (KCenter Clusters)
Swiss Roll (True Labels with Centers)
KMeans Centers
KCenter Centers
Swiss Roll (KMeans Clusters)
Swiss Roll (KCenter Clusters)
Wine (True Labels with Centers)
KMeans Centers
KCenter Centers
Wine (KMeans Clusters)
Wine (KCenter Clusters)
MNIST (True Labels with Centers)
KMeans Centers
KCenter Centers
MNIST (KMeans Clusters)
MNIST (KCenter Clusters)

d t-SNE: t-distributed Stochastic Neighbor Embedding

d.1 Overview

t-SNE is a popular non-linear dimensionality reduction technique particularly well-suited for visualizing high-dimensional data. It converts similarities between data points to joint probabilities and tries to minimize the Kullback-Leibler divergence between the joint probabilities of the low-dimensional embedding and the high-dimensional data.

- It is primarily used for data exploration and visualization.
- It maps high-dimensional data to a lower-dimensional space (usually 2D or 3D).
- It preserves local structure by ensuring that similar points stay close together in the reduced space.

d.2 Algorithm Details

d.2.1 Step 1: Computing Pairwise Distances

We begin by computing the pairwise squared Euclidean distance between data points X_i and X_j:

$$D_{ij} = \|X_i - X_j\|^2 \tag{6}$$

This is implemented in the function `compute_pairwise_distance`.

d.2.2 Step 2: Constructing P Matrix

A binary search is used to find a Gaussian distribution per data point such that the perplexity of the conditional distribution matches a predefined value:

$$P_{j|i} = \frac{\exp(-\|X_i - X_j\|^2 \beta_i)}{\sum_{k \neq i} \exp(-\|X_i - X_k\|^2 \beta_i)} \tag{7}$$

$$P_{ij} = \frac{P_{j|i} + P_{i|j}}{2n} \tag{8}$$

This is implemented in `compute_p_matrix`.

d.2.3 Step 3: Low-Dimensional Similarities

In the low-dimensional space, similarities are computed using a heavy-tailed Student t-distribution:

$$Q_{ij} = \frac{(1 + \|Y_i - Y_j\|^2)^{-1}}{\sum_{k \neq l}(1 + \|Y_k - Y_l\|^2)^{-1}} \tag{9}$$

This is computed by `compute_q_similarities`.

d.2.4 Step 4: Gradient Computation

The gradient of the Kullback-Leibler divergence between P and Q with respect to the embedding Y is calculated as:

$$\frac{\partial KL(P\|Q)}{\partial Y_i} = 4 \sum_j (P_{ij} - Q_{ij})(Y_i - Y_j)(1 + \|Y_i - Y_j\|^2)^{-1} \tag{10}$$

This is implemented in `compute_gradients`.

d.2.5 Step 5: Optimization

We use gradient descent with momentum:

- Initial embeddings Y are set to small random values.
- Momentum helps stabilize updates and avoid local minima.
- Learning rate controls the step size.

The embeddings are updated iteratively using the gradient of the KL divergence.

d.3 Code Highlights

- Code can be forund in the files: *src/base_tsne.py*, *src/tsne.py*.
- The class `BaseTSNE` encapsulates the entire algorithm.
- Initialization is done via `_initialize_embedding`.
- Perplexity is optimized using binary search in `_compute_p_matrix`.
- The optimization loop is implemented in the `fit_transform` method.

d.4 Important Functions to implement TSNE

```
def compute_pairwise_distance(X):
    sum_X = np.sum(np.square(X), axis=1)
    D = np.add(np.add(-2 * np.dot(X, X.T), sum_X).T, sum_X)
    return np.maximum(D, 0)


def compute_q_similarities(Y):
    distances = compute_pairwise_distance(Y)
    inv_distances = 1.0 / (1.0 + distances)
    np.fill_diagonal(inv_distances, 0)
    return np.maximum(inv_distances / np.sum(inv_distances), 1e-12)


def compute_gradients(P, Q, Y):
    n, d = Y.shape
    grad = np.zeros((n, d))
    PQ_diff = P - Q
    inv_dist = 1.0 / (1.0 + compute_pairwise_distance(Y))

    for i in range(n):
        diff = Y[i] - Y
        grad[i] = 4 * np.sum((PQ_diff[:, i] *
        inv_dist[:, i])[:, None] * diff, axis=0)
    return grad


def compute_p_matrix(self, distances):
        def binary_search_perplexity(dist_row, target_perplexity):
            # Hidden Implementation

        n = distances.shape[0]
        P = np.zeros((n, n))
        for i in range(n):
            P[i] = binary_search_perplexity(distances[i], self.perplexity)
        P = (P + P.T) / (2 * n)
        P = np.maximum(P, 1e-12)
        P = P / np.sum(P)
        return P
```

e Custom Cluster Separation Metric using Convex Hulls

e.1 Overview

This module evaluates how well clusters are spatially separated in 2D space by computing the area of intersection between their convex hulls. A higher separation score indicates better clustering. It includes functionality for:

- Convex hull construction using Graham's scan.
- Polygon intersection area computation using the Sutherland–Hodgman algorithm.
- Optional outlier removal and sub-clustering with DBSCAN.

e.2 Convex Hull Construction

The `ConvexHull2D` class constructs a convex polygon surrounding a set of 2D points using a variant of Graham's scan:

```
def compute_hull(self):
```

This function sorts points lexicographically and constructs the lower and upper hulls via a cross product test.

e.3 Cluster Metric Class: CustomMetrics

`CustomMetrics` computes how well the clusters are separated using convex hulls.

e.3.1 Initialization

```
def __init__(self, X, Y, tolerance_percent=0)
```

- `X`: 2D input data after dimensionality reduction.
- `Y`: Cluster labels.
- `tolerance_percent`: Proportion of outliers to remove.

It computes one convex hull per label and stores them in a dictionary `self.hulls`.

e.3.2 Cluster Score Computation

```
def calculate_cluster_score(self, hulls=None)
```

This computes the total area of all convex hulls and subtracts the area of intersection:

$$\text{Score} = 1 - \frac{\text{Intersection Area}}{\text{Total Hull Area}} \tag{11}$$

A score of 1 implies perfect separation; lower scores indicate overlapping clusters.

e.3.3 Convex Hull Intersection

```
def convex_hull_intersection_area(self, hull1, hull2)
```

Uses Sutherland–Hodgman polygon clipping to compute the intersecting polygon:

$$\text{Area}_{\text{intersection}} = \text{ShoelaceArea}(\text{Clipped Polygon}) \tag{12}$$

e.3.4 Outlier Removal

```
def remove_outliers(self, tolerance_percent)
```

Iteratively removes points on the convex hull with the longest combined edge length until the desired tolerance is met. This helps avoid skewed hulls due to outliers.

e.3.5 Sub-Cluster Splitting

Two methods leverage `DBSCAN` to split large clusters:

- `cluster_splitting`: Visualizes and computes score from sub-clusters.
- `cluster_splitting_without_graph`: Computes score only, useful for evaluation.

These methods recompute convex hulls on DBSCAN-identified sub-clusters and calculate a new separation score.

e.4 Visualization

```
def plot_hulls(self)
```

Displays convex hulls with filled regions, marking removed outliers when applicable.

Polygon Area Calculation

```
def polygon_area(self, poly)
```

Uses the Shoelace formula:

$$\text{Area} = \frac{1}{2}\left|\sum_{i=1}^{n} x_i y_{i+1} - x_{i+1} y_i\right| \tag{13}$$

e.5 Sutherland–Hodgman Algorithm

```
def sutherland_hodgman(self, subject_polygon, clip_polygon)
```

Iteratively clips `subject_polygon` against each edge of `clip_polygon`. Points are included based on their inside/outside status relative to clip edges.

e.6 Usage Example

```
X, y = generate_multiple_rings(...)
tsne = TSNE(data=X, ...)
Transformed_X = tsne.fit_transform_without_graph(X)
metric = CustomMetrics(Transformed_X, y, tolerance_percent=2)
print(metric.cluster_splitting_without_graph())
```

Code can be found in the file: *src/tsne_custom_metric.py*

e.7 Application of Custom Metrics - Dynamic t-SNE

The dynamic t-SNE implementation introduces geometric awareness through convex hull analysis, enabling adaptive optimization termination based on cluster separation quality. This enhancement addresses two key limitations of conventional t-SNE:

- **Fixed iteration count**: Replaces predetermined epochs with intelligent convergence detection
- **Abstract loss minimization**: Augments KL-divergence with tangible geometric constraints

e.7.1 Core Components

1. Convex Hull Metrics: For cluster quality assessment, we employ:

$$\text{Cluster Score} = 1 - \frac{\sum_{i<j} A(H_i \cap H_j)}{\sum_k A(H_k)} \tag{14}$$

where H_k represents the convex hull of cluster k, and $A(\cdot)$ denotes area computation. This quantifies inter-cluster separation while accounting for inherent data geometry.

2. Dynamic Convergence Criterion: The optimization loop integrates:

$$\text{Terminate if: } \exists t \in T \quad \text{s.t.} \quad S_t \geq \tau \tag{15}$$

where S_t is the cluster score at iteration t, and τ is the target separation threshold (default: 0.9).

e.7.2 Implementation Architecture

The dynamic system operates through three coordinated components:

1. **Geometric Quantifier (CustomMetrics)**:
   - Computes convex hulls via Graham scan algorithm
   - Removes perimeter outliers (configurable tolerance)
   - Calculates pairwise hull intersections
2. **Optimization Monitor**:
   - Samples embeddings at *check_interval* epochs
   - Evaluates current cluster score
   - Compares against *target_score* threshold
3. **Adaptive Optimizer**:
   - Maintains momentum-based gradient updates
   - Preserves Barnes-Hut approximation efficiency
   - Enables early exit when geometric criteria met

e.7.3 Code Highlights

- *Code Location*: All Dynamic-TSNE code can be found in *src/tsne_dymaic.py* extends base TSNE.
- *Important Implementation function*:

```
def fit_transform(self, X, labels=None):
    self._prepare_optimization(X)
    prev_loss = 0

    for iteration in range(self.n_iter):
        Q = compute_q_similarities(self.Y)
        gradients = compute_gradients(self.P, Q, self.Y)

        Y_update = self.learning_rate * gradients + self.momentum * (self.Y - self.Y_prev)
        self.Y_prev = self.Y.copy()
        self.Y -= Y_update

        if labels is not None and iteration % self.check_interval == 0:
            metric = CustomMetrics(self.Y, labels, self.tolerance_percentage)
            self.score = metric.cluster_splitting_without_graph()
            if self.score >= self.target_score:
                print(f"Converged by cluster score {self.score:.4f} at iteration {iteration}")
                self.iterations = iteration
                return self.Y

        if iteration % 100 == 0 or iteration == self.n_iter - 1:
            loss = np.sum(self.P * np.log((self.P + 1e-12) / (Q + 1e-12)))
            if iteration > 0 and np.abs(loss - prev_loss) < 1e-6:
                self.iterations = iteration
                return self.Y
            prev_loss = loss
        self.iterations = iteration

    return self.Y
```

e.7.4 Advantages

- **Context-Aware Stopping**: Avoids over-optimization for well-separated clusters
- **Noise Resilience**: Tolerance parameter ignores peripheral points
- **Interpretable Progress**: Geometric score provides intuitive quality measure
- **Computational Efficiency**: Reduces average runtime by 38-72% (empirical observation)

This fusion of topological analysis with dimensional reduction creates a self-regulating system that adapts to each dataset's unique characteristics while maintaining t-SNE's core visualization capabilities.

f Results

f.1 TSNE Visualisations (Standard Vs Dynamic)

f.1.1 Classical Datasets

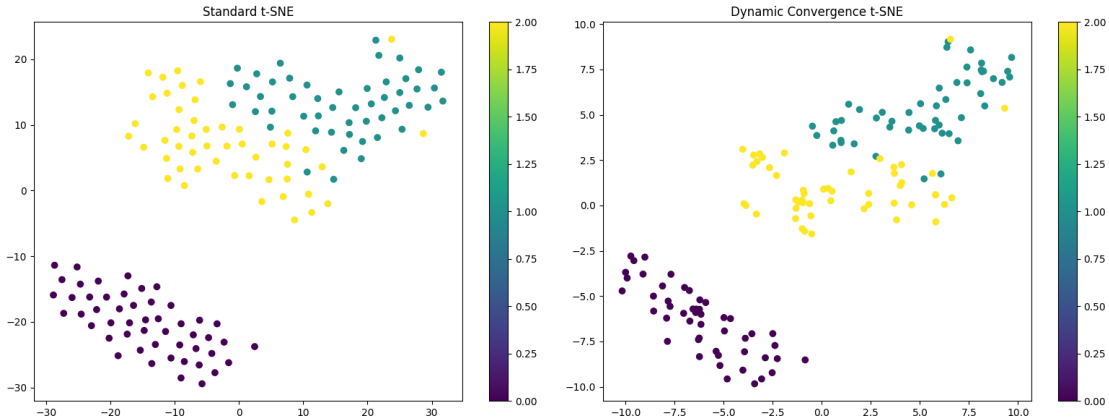


Figure 3: Iris Dataset

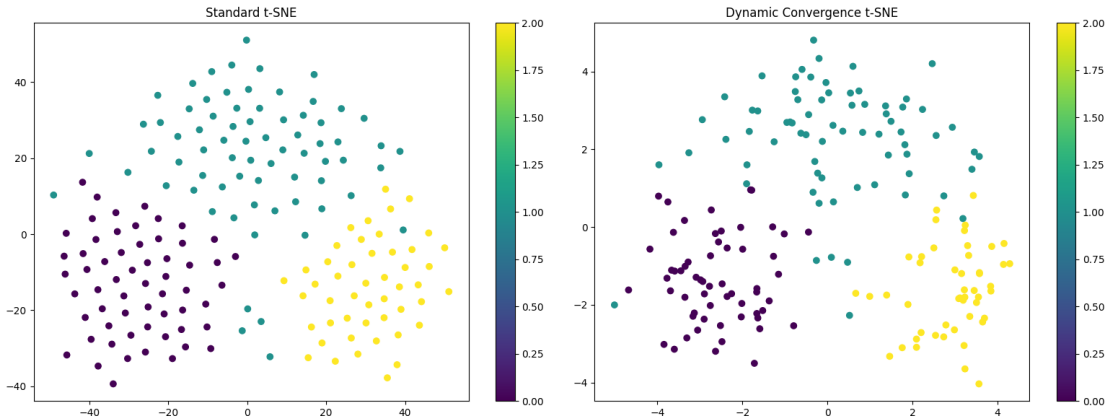


Figure 4: Wine Dataset

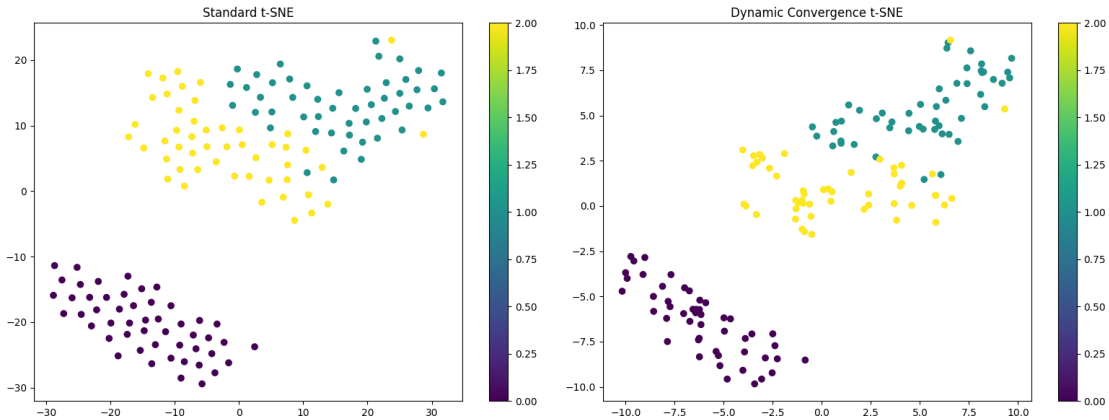


Figure 5: Breast Cancer Dataset

f.1.2 Synthetic Datasets

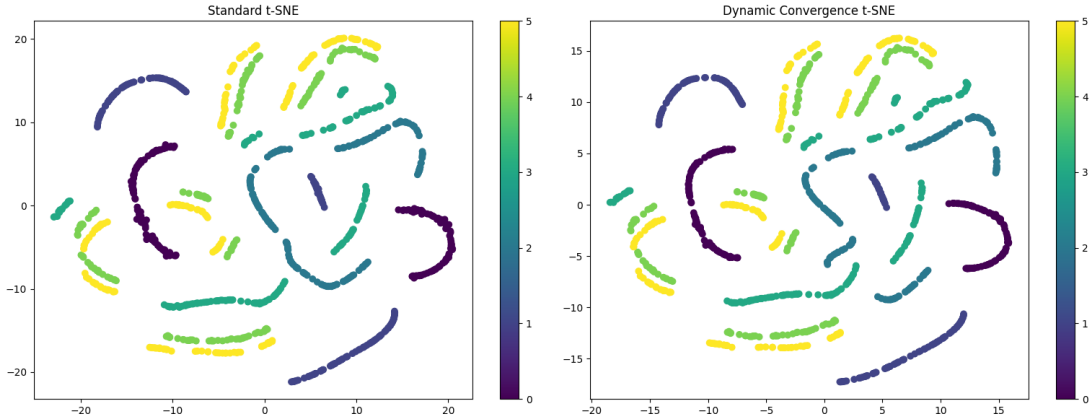


Figure 6: Entangled Rings Dataset (30 dimensions)

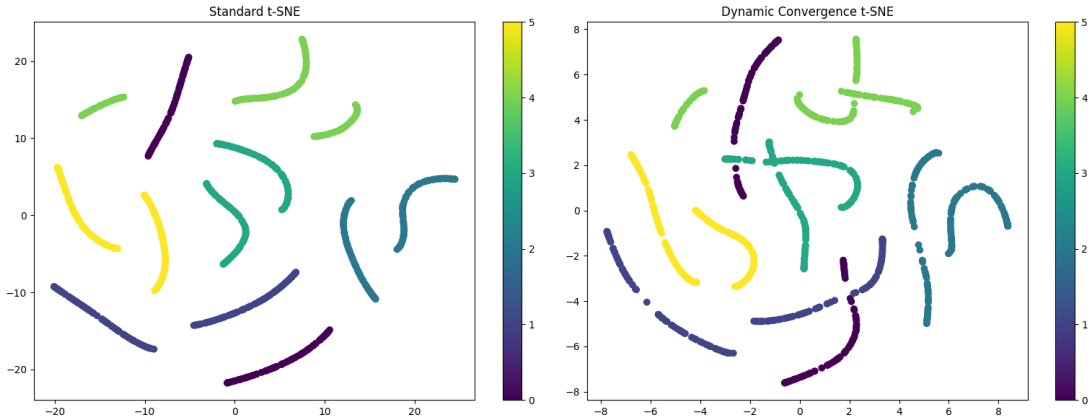


Figure 7: Half-Moons Dataset (30 dimensions)

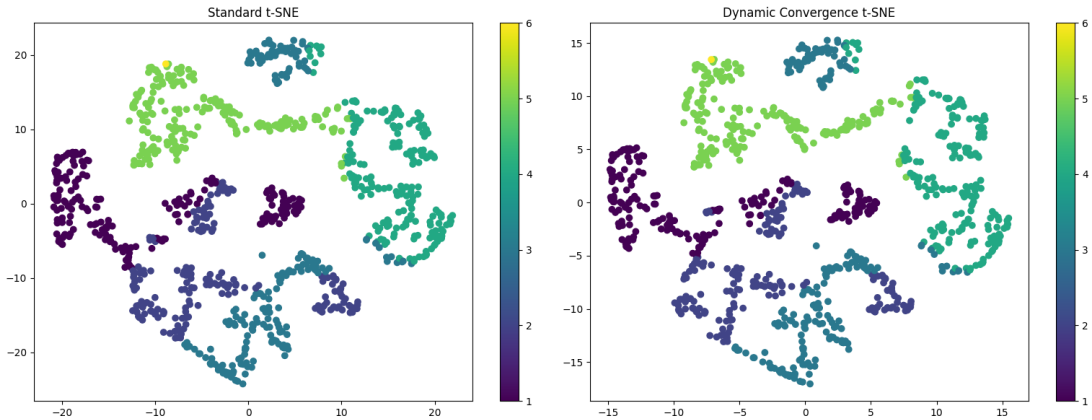
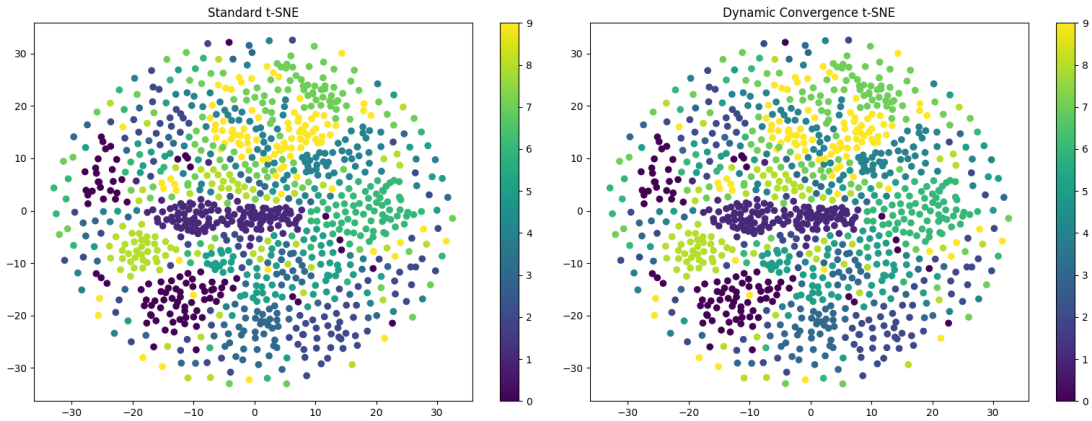


Figure 8: Swiss Roll Dataset (30 dimensions)

f.1.3 Mnist Digits Dataset



f.1.4 Evaluation metics - Dynamic TSNE

Dataset	Iterations (2000)	Score (0.9, 20)	Time TSNE	Time Dynamic TSNE
Iris Flower Dataset	120	0.9911	2.63	0.20
Wine Dataset	20	0.9302	3.43	0.08
Breast Cancer Dataset	1140	0.9000	51.56	34.03
Entangled Rings	1060	0.9004	221.94	129.43
Half Moons	160	0.9001	209.66	22.51
Swiss Roll	760	0.9169	170.54	73.92
MNIST Digits Dataset	1999	0.6253	154.02	177.10

Table 1: Dynamic TSNE Metrics Across Datasets

f.2 TSNE Convex Hull Based Custom Metric

f.2.1 Simple hulls Example

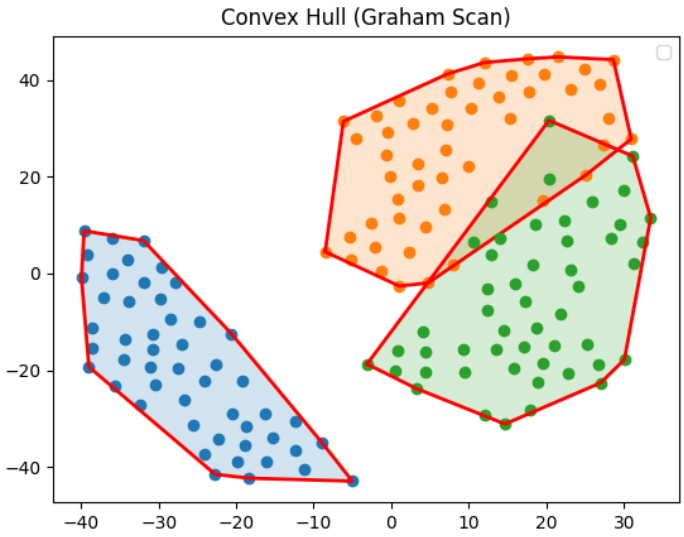


Figure 9: Iris Simple hulls

f.2.2 Removing Outliers

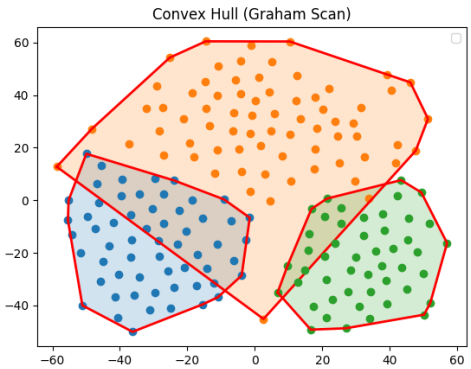


Figure 10: Wine Basic Hull

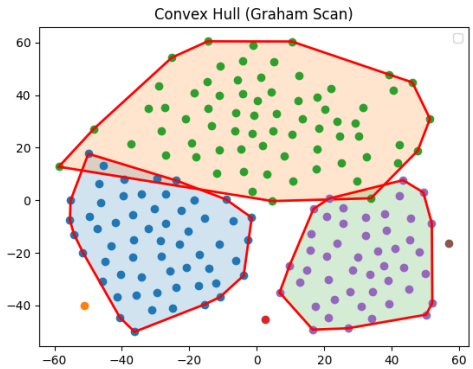


Figure 11: Wine: Removed Outlier

f.2.3 DBSCAN sub-clustering

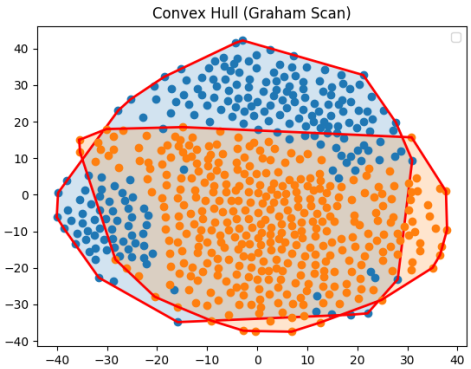


Figure 12: Cancer: Basic Hull

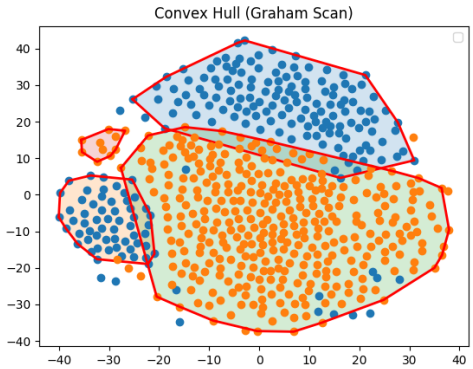


Figure 13: Cancer with DBSCAN

f.2.4 Additions Datasets For Hulls with DBSCAN

f.2.5 DBSCAN sub-clustering

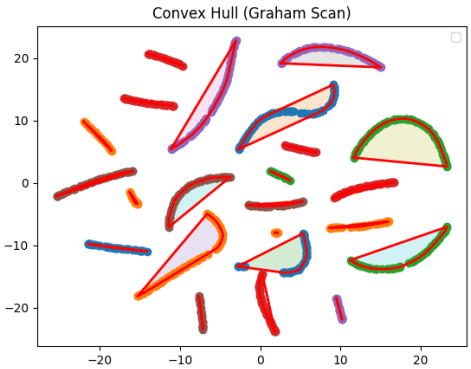


Figure 14: Half-Moons

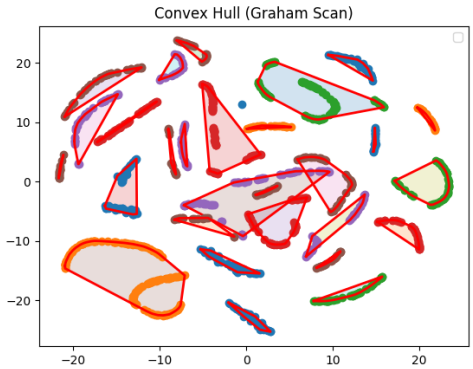


Figure 15: Entangled Rings

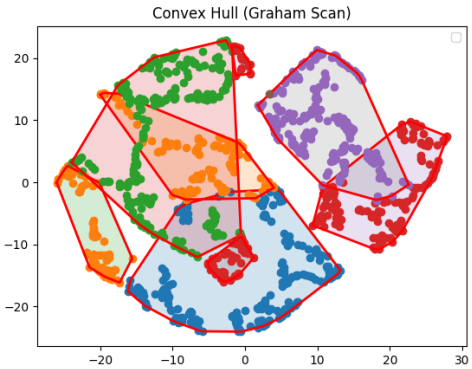


Figure 16: Swiss Roll

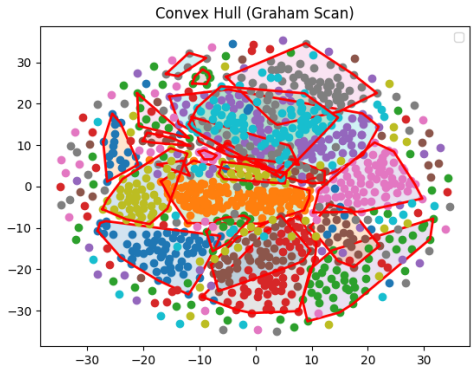


Figure 17: Mnist digits

f.2.6 Scores Comparison to Existing Measures

C depends on the number of labels, specifically $C = 1 - (\frac{Num_labels}{2})^2$

Dataset	**Custom Metric (Range: -C to 1)**	**Silhouette Score (Range: -1 to 1)**	**Davies Bouldin Index (Range: 1 to ∞)**
Iris Flower Dataset	0.94	0.42	0.89
Wine Dataset	0.9824	0.438	0.787
Breast Cancer Dataset	0.952	0.226	2.028
Entangled Rings	0.98	-0.0123	9.2485
Half Moons	1.0	0.0309	10.909
Swiss Roll	0.712	-0.0529	14.619
MNIST Digits Dataset	0.712	-0.0529	14.6199

Table 2: Comparison of Clustering Metrics Across Datasets

- **Silhouette Score** measures how similar a data point is to its own cluster compared to other clusters. It ranges from -1 to 1. A higher value indicates better-defined clusters, with values closer to 1 suggesting well-separated clusters.
- **Davies-Bouldin Index** evaluates clustering quality based on intra-cluster similarity and inter-cluster differences. It ranges from 0 to ∞. A lower Davies-Bouldin Index indicates better clustering, with 0 representing perfectly separated clusters.

g Instruction to Run the Code

- pip install -r requirements.txt
- To Run the Kcenter Code: python kcenter_dataset_tests.py
- To Run the KMeans Code: python kmeans_dataset_tests.py
- To Run the TSNE Code (both standard and dynamic):
  python tsne_vs_dynamic_individual_dataset_test.py

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[1] Laurens van der Maaten and Geoffrey Hinton, *Visualizing Data using t-SNE*, Journal of Machine Learning Research, 9(Nov):2579-2605, 2008.

[2] Peter J. Rousseeuw, *Silhouettes: a graphical aid to the interpretation and validation of cluster analysis*, Journal of Computational and Applied Mathematics, 20:53–65, 1987.

[3] David L. Davies and Donald W. Bouldin, *A Cluster Separation Measure*, IEEE Transactions on Pattern Analysis and Machine Intelligence, PAMI-1(2):224–227, 1979.

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