[Clustering Algorithms] (cheatSheet)

Data Preparation

- Load Dataset: data = pd.read_csv('data.csv')
- Standardize Features: scaled_data = StandardScaler().fit_transform(data)
- Principal Component Analysis (PCA) for Dimensionality Reduction: pca_data = PCA(n_components=2).fit_transform(scaled_data)
- Visualize Data Distribution: plt.scatter(data[:, 0], data[:, 1])
- Compute Pairwise Distance Matrix for Clustering: dist_matrix = pairwise_distances(data, metric='euclidean')
- Handle Missing Values: data_filled = SimpleImputer(strategy='mean').fit_transform(data)
- Create Dendrogram for Hierarchical Clustering: dendrogram = sch.dendrogram(sch.linkage(data, method='ward'))
- Identify Optimal Number of Clusters via Elbow Method: inertia = [KMeans(n_clusters=i).fit(data).inertia_ for i in range(1, 11)]; plt.plot(range(1, 11), inertia)
- Normalize Features for Clustering: normalized_data = normalize(data)
- Use TSNE for Visualization of High-dimensional Data: tsne_data = TSNE(n_components=2).fit_transform(data)

K-means Clustering

- **Perform K-means Clustering**: kmeans = KMeans(n_clusters=3).fit(data)
- Predict Cluster Labels: labels = kmeans.predict(data)
- Visualize Clusters: plt.scatter(data[:, 0], data[:, 1], c=labels)
- Determine Centroids: centroids = kmeans.cluster centers
- Silhouette Score for Model Evaluation: silhouette_score(data, labels)
- Initializing K-means with Smart Start (k-means++): kmeans = KMeans(n_clusters=3, init='k-means++').fit(data)
- Mini-Batch K-means for Large Datasets: minibatch_kmeans = MiniBatchKMeans(n_clusters=3).fit(data)
- Find Optimal K Using the Silhouette Method: silhouette_optimal_k(data)
- Elbow Method Visualization for Optimal K: plot_elbow_method(data)
- Assign New Data Points to Existing Clusters:new_labels = kmeans.predict(new_data)
- Iterative Training to Refine Centroids: kmeans.fit(data); kmeans.partial_fit(more_data)



- Visualize Cluster Centers on 2D Plot: plt.scatter(kmeans.cluster_centers_[:, 0], kmeans.cluster_centers_[:, 1], s=300, c='red')
- Calculate Within-cluster Sum of Squares (WSS): wss = kmeans.inertia_
- K-means Clustering with Specific Random State for Reproducibility: kmeans = KMeans(n_clusters=3, random_state=42).fit(data)
- Use K-means for Color Quantization in Images: quantized_img = quantize_colors(image_data, n_colors=8)

Hierarchical Clustering

- Perform Agglomerative Hierarchical Clustering: model =
 AgglomerativeClustering(n_clusters=3).fit(data)
- Extract Cluster Labels: labels = model.labels_
- Plot Dendrogram Function: plot_dendrogram(model, truncate_mode='level', p=3)
- Cophenetic Correlation Coefficient: c, coph_dists = cophenet(sch.linkage(data, 'ward'), pdist(data))
- Agglomerative Hierarchical Clustering with Different Linkage Criteria: model = AgglomerativeClustering(n_clusters=3, linkage='average').fit(data)
- Scikit-learn's Convenience Function for Ward's Method: ward = AgglomerativeClustering(n_clusters=3, linkage='ward').fit(data)
- Generate Dendrogram from Linkage Matrix: linkage_matrix = ward(children=model.children_); dendrogram(linkage_matrix)
- Cutting the Dendrogram to Form Clusters: labels = fcluster(linkage_matrix, t=3, criterion='maxclust')
- Creating Custom Distance Matrix for Agglomerative Clustering: model = AgglomerativeClustering(n_clusters=3, affinity='precomputed', linkage='complete').fit(custom_distance_matrix)
- Interactive Dendrogram Plotting with Plotly: plot_dendrogram_plotly(linkage_matrix)
- Evaluate Model Using Davies-Bouldin Index: db_index = davies_bouldin_score(data, model.labels_)
- Use SciPy for More Detailed Dendrogram Customization: dendrogram(sch.linkage(data, method='ward'), color_threshold=1)
- Dynamic Thresholding for Cluster Formation in Hierarchical Clustering: dynamic_labels = dynamic_threshold_clustering(linkage_matrix)

DBSCAN

 Apply DBSCAN Clustering: dbscan = DBSCAN(eps=0.3, min_samples=10).fit(data)

- Cluster Labels from DBSCAN: labels = dbscan.labels_
- Identify Core Samples: core_samples_mask = np.zeros_like(dbscan.labels_, dtype=bool); core_samples_mask[dbscan.core_sample_indices_] = True
- Visualize DBSCAN Clusters: plt.scatter(data[:, 0], data[:, 1], c=labels)
- Adjusting eps and min_samples for Density Variation: dbscan = DBSCAN(eps=0.5, min_samples=15).fit(data)
- Handling Noise Points Identified by DBSCAN: noise = data[dbscan.labels_ == -1]
- Cluster Core Samples Extraction and Visualization: core_samples = data[dbscan.core_sample_indices_]
- Evaluate Clustering with Silhouette Score: silhouette_score(data, dbscan.labels_)
- Visualize DBSCAN Clusters with Matplotlib: plot_dbscan_clusters(data, dbscan.labels_, dbscan.core_sample_indices_)
- Optimize DBSCAN Parameters with Grid Search: optimal_params = optimize_dbscan(data)
- Use DBSCAN for Anomaly Detection: anomalies = data[dbscan.labels_ == -1]
- Scaling Features for Improved DBSCAN Performance: scaled_data = StandardScaler().fit_transform(data); dbscan.fit(scaled_data)
- Calculate Number of Clusters in DBSCAN: n_clusters_ = len(set(dbscan.labels_)) - (1 if -1 in dbscan.labels_ else 0)
- Visualize Spatial Clusters with Folium for Geospatial Data: plot_folium_map_geospatial(data, dbscan.labels_)

Advanced Clustering Algorithms

- Spectral Clustering: spectral_labels = SpectralClustering(n_clusters=3).fit_predict(data)
- Mean Shift Clustering: meanShift = MeanShift().fit(data); labels = meanShift.labels_
- Affinity Propagation: affinity = AffinityPropagation().fit(data); cluster_centers_indices = affinity.cluster_centers_indices_
- Hierarchical Density-Based Spatial Clustering (HDBSCAN): hdbscan_model = hdbscan.HDBSCAN(min_cluster_size=10).fit(data); labels = hdbscan_model.labels_
- Gaussian Mixture Models for Soft Clustering: gmm = GaussianMixture(n_components=3).fit(data); labels = gmm.predict(data)
- OPTICS Clustering: optics = OPTICS(min_samples=10, xi=.05, min_cluster_size=.05).fit(data); labels = optics.labels_
- Evaluate Clustering with Adjusted Rand Index: adjusted_rand_score(true_labels, predicted_labels)

- Clustering Based on Graph Connectivity (Agglomerative): connectivity = kneighbors_graph(data, n_neighbors=10, include_self=False); ward = AgglomerativeClustering(connectivity=connectivity); labels = ward.fit_predict(data)
- BIRCH for Large Datasets: birch = BIRCH(n_clusters=3).fit(data); labels = birch.predict(data)
- CURE Clustering Implementation with PyCaret: from pycaret.clustering import *; cure_model = create_model('cure', num_clusters=3, data=data)
- Using Silhouette Plots to Evaluate Clustering Quality: plot_silhouette(data, labels)
- Cluster Validation Using the Davies-Bouldin Index: davies_bouldin_score(data, labels)

Optimization Strategies

- Grid Search for Optimal Parameters in K-means: param_grid = {'n_clusters': range(1, 11)}; grid_search = GridSearchCV(KMeans(), param_grid); grid_search.fit(data)
- Using the Gap Statistic to Determine the Number of Clusters: gap_statistic, opt_k = optimalK(data, nrefs=3, maxClusters=10)
- Auto-Scaling Features Based on Clustering Tendency: scaler = autoscale_based_on_clustering_tendency(data)
- Parallel Coordinate Plot for Cluster Visualization: pd.plotting.parallel_coordinates(data.assign(cluster=labels), 'cluster')
- Cluster Stability Evaluation via Bootstrapping: stability = bootstrap_stability(data, KMeans(n_clusters=3), n_bootstraps=10)
- Elbow Method with Inertia and Silhouette Analysis Combined: evaluate_clustering_elbow_silhouette(data, max_clusters=10)

Specialized Clustering Applications

- Temporal or Sequential Data Clustering (e.g., Time Series): ts_cluster_labels =
 - TimeSeriesKMeans(n_clusters=3).fit_predict(time_series_data)
- Clustering Geospatial Data: geo_cluster_labels = DBSCAN(eps=0.1, min_samples=5).fit_predict(geo_data[['latitude', 'longitude']])
- Image Segmentation Using Clustering: segmented_image = KMeans(n_clusters=3).fit_predict(image_pixels)
- Text Clustering for Document Categorization: text_cluster_labels = MiniBatchKMeans(n_clusters=5).fit_predict(tfidf_matrix)

- Clustering for Anomaly Detection: anomaly_labels = IsolationForest().fit_predict(data)
- Clustering in Bioinformatics (e.g., Gene Expression Data): gene_cluster_labels = AgglomerativeClustering().fit_predict(gene_expression_data)

Integrative Approaches and Advanced Techniques

- Consensus Clustering for Stability and Robustness: consensus_labels = consensus_cluster(data, KMeans(), n_clusters_range=[2,10], bootstrap_samples=100)
- Feature Learning with Clustering (e.g., Autoencoders): encoded_features = Autoencoder().fit_transform(data); ae_cluster_labels = KMeans(n_clusters=3).fit_predict(encoded_features)
- Cluster Ensembles for Improved Performance: ensemble_labels = ClusterEnsembles(hyperparameters, data)
- Use of Clustering for Dimension Reduction: reduced_data = clustering_based_dimension_reduction(data, n_clusters=10)
- Integrating Clustering with Classification for Semi-supervised Learning: semi_labels = semi_supervised_learning_with_clustering(data, partial_labels)
- Leveraging Graph-based Clustering for Complex Networks: graph_cluster_labels = SpectralClustering(n_clusters=3).fit_predict(adjacency_matrix)
- Multi-view Clustering for Integrating Different Types of Data: multi_view_labels = MultiViewClustering().fit_predict([view1_data, view2_data])
- Interactive Clustering for User-guided Analysis: interactive_clusters = interactive_clustering(data, initial_guesses)
- Utilizing Clustering for Data Cleaning and Preprocessing: clean_data = data_cleaning_with_clustering(data)
- Hierarchical Clustering for Large Datasets via BIRCH:

large_scale_cluster_labels = BIRCH(threshold=0.5, n_clusters=None).fit_predict(large_data)

- Spatial Clustering for Location Data Optimization: location_clusters = OPTICS(min_samples=50, xi=0.05, min_cluster_size=0.1).fit_predict(location_data)
- Integrating Clustering with Reinforcement Learning for Dynamic Environments: dynamic_cluster_labels = reinforcement_learning_with_clustering(state_data)

• Clustering for Recommender Systems (User or Item Clustering):

recommender_clusters = KMeans(n_clusters=10).fit_predict(user_feature_matrix)

- Deep Clustering for Unsupervised Feature Learning: deep_cluster_labels = DeepClustering().fit_predict(data)
- Clustering Validation in Multi-dimensional Datasets: validation_scores = multidimensional_clustering_validation(data, cluster_labels)