

# Cheat Sheet: Building Unsupervised Learning Models

## Unsupervised learning models

Model Name	Brief Description	Code Syntax
UMAP	<p>UMAP (Uniform Manifold Approximation and Projection) is used for dimensionality reduction.</p> <p><b>Pros:</b> High performance, preserves global structure.</p> <p><b>Cons:</b> Sensitive to parameters.</p> <p><b>Applications:</b> Data visualization, feature extraction.</p> <p><b>Key hyperparameters:</b></p> <ul style="list-style-type: none"><li>• <b>n_neighbors:</b> Controls the local neighborhood size (default = 15).</li><li>• <b>min_dist:</b> Controls the minimum distance between points in the embedded space (default = 0.1).</li><li>• <b>n_components:</b> The dimensionality of the embedding (default = 2).</li></ul>	<pre>from umap.umap_ import UMAP umap = UMAP(n_neighbors=15, min_dist=0.1, n_components=2)</pre>
t-SNE	<p>t-SNE (t-Distributed Stochastic Neighbor Embedding) is a nonlinear dimensionality reduction technique.</p> <p><b>Pros:</b> Good for visualizing high-dimensional data.</p> <p><b>Cons:</b> Computationally expensive, prone to overfitting.</p> <p><b>Applications:</b> Data visualization, anomaly detection.</p> <p><b>Key hyperparameters:</b></p> <ul style="list-style-type: none"><li>• <b>n_components:</b> The number of dimensions for the output (default = 2).</li><li>• <b>perplexity:</b> Balances attention between local and global aspects of the data (default = 30).</li><li>• <b>learning_rate:</b> Controls the step size during optimization (default = 200).</li></ul>	<pre>from sklearn.manifold import TSNE tsne = TSNE(n_components=2, perplexity=30, learning_rate=200)</pre>
PCA	<p>PCA (principal component analysis) is used for linear dimensionality reduction.</p> <p><b>Pros:</b> Easy to interpret, reduces noise.</p> <p><b>Cons:</b> Linear, may lose information in nonlinear data.</p> <p><b>Applications:</b> Feature extraction, compression.</p> <p><b>Key hyperparameters:</b></p> <ul style="list-style-type: none"><li>• <b>n_components:</b> Number of principal components to retain (default = 2).</li><li>• <b>whiten:</b> Whether to scale the components (default = False).</li><li>• <b>svd_solver:</b> The algorithm to compute the components (default = 'auto').</li></ul>	<pre>from sklearn.decomposition import PCA pca = PCA(n_components=2)</pre>
DBSCAN	<p>DBSCAN (Density-Based Spatial Clustering of Applications with Noise) is a density-based clustering algorithm.</p> <p><b>Pros:</b> Identifies outliers, does not require the number of clusters.</p> <p><b>Cons:</b> Difficult with varying density clusters.</p> <p><b>Applications:</b> Anomaly detection, spatial data clustering.</p> <p><b>Key hyperparameters:</b></p> <ul style="list-style-type: none"><li>• <b>eps:</b> The maximum distance between two points to be considered neighbors (default = 0.5).</li><li>• <b>min_samples:</b> Minimum number of samples in a neighborhood to form a cluster (default = 5).</li></ul>	<pre>from sklearn.cluster import DBSCAN dbscan = DBSCAN(eps=0.5, min_samples=5)</pre>
HDBSCAN	<p>HDBSCAN (Hierarchical DBSCAN) improves on DBSCAN by handling varying density clusters.</p> <p><b>Pros:</b> Better handling of varying densities.</p> <p><b>Cons:</b> Can be slower than DBSCAN.</p> <p><b>Applications:</b> Large datasets, complex clustering problems.</p> <p><b>Key hyperparameters:</b></p> <ul style="list-style-type: none"><li>• <b>min_cluster_size:</b> The minimum size of clusters (default = 5).</li><li>• <b>min_samples:</b> Minimum number of samples to form a cluster (default = 10).</li></ul>	<pre>import hdbscan clusterer = hdbscan.HDBSCAN(min_cluster_size=5)</pre>
K-Means clustering	<p>K-Means is a centroid-based clustering algorithm that groups data into k clusters.</p> <p><b>Pros:</b> Efficient, simple to implement.</p> <p><b>Cons:</b> Sensitive to initial cluster centroids.</p>	<pre>from sklearn.cluster import KMeans kmeans = KMeans(n_clusters=3)</pre>

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	<p><b>Applications:</b> Customer segmentation, pattern recognition.</p> <p><b>Key hyperparameters:</b></p> <ul style="list-style-type: none"><li>• <b>n_clusters:</b> Number of clusters (default = 8).</li><li>• <b>init:</b> Method for initializing the centroids ('k-means++' or 'random', default = 'k-means++').</li><li>• <b>n_init:</b> Number of times the algorithm will run with different centroid seeds (default = 10).</li></ul>	

Associated fuctions used

Method	Brief Description	Code Syntax
make_blobs	Generates isotropic Gaussian blobs for clustering.	<pre>from sklearn.datasets import make_blobs X, y = make_blobs(n_samples=100, centers=2, random_state=42)</pre>
multivariate_normal	Generates samples from a multivariate normal distribution.	<pre>from numpy.random import multivariate_normal samples = multivariate_normal(mean=[0, 0], cov=[[1, 0], [0, 1]], size=100)</pre>
plotly.express.scatter_3d	Creates a 3D scatter plot using Plotly Express.	<pre>import plotly.express as px fig = px.scatter_3d(df, x='x', y='y', z='z') fig.show()</pre>
geopandas.GeoDataFrame	Creates a GeoDataFrame from a Pandas DataFrame.	<pre>import geopandas as gpd gdf = gpd.GeoDataFrame(df, geometry='geometry')</pre>
geopandas.to_crs	Transforms the coordinate reference system of a GeoDataFrame.	<pre>gdf = gdf.to_crs(epsg=3857)</pre>
contextily.add_basemap	Adds a basemap to a GeoDataFrame plot for context.	<pre>import contextily as ctx ax = gdf.plot(figsize=(10, 10)) ctx.add_basemap(ax)</pre>

Method	Brief Description	Code Syntax
pca.explained_variance_ratio_	Returns the proportion of variance explained by each principal component.	<pre>from sklearn.decomposition import PCA pca = PCA(n_components=2) pca.fit(X) variance_ratio = pca.explained_variance_ratio_</pre>

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