sklearn.cluster.MeanShift

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class `sklearn.cluster.`**`MeanShift`**(*bandwidth=None*, *seeds=None*, *bin_seeding=False*, *min_bin_freq=1*, *cluster_all=True*, *n_jobs=1*) [source]

Mean shift clustering using a flat kernel.

Mean shift clustering aims to discover “blobs” in a smooth density of samples. It is a centroid-based algorithm, which works by updating candidates for centroids to be the mean of the points within a given region. These candidates are then filtered in a post-processing stage to eliminate near-duplicates to form the final set of centroids.

Seeding is performed using a binning technique for scalability.

Read more in the User Guide.

Parameters: **bandwidth** : float, optional

Bandwidth used in the RBF kernel.

If not given, the bandwidth is estimated using sklearn.cluster.estimate_bandwidth; see the documentation for that function for hints on scalability (see also the Notes, below).

seeds : array, shape=[n_samples, n_features], optional

Seeds used to initialize kernels. If not set, the seeds are calculated by clustering.get_bin_seeds with bandwidth as the grid size and default values for other parameters.

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bin_seeding : boolean, optional

> If true, initial kernel locations are not locations of all points, but rather the location of the discretized version of points, where points are binned onto a grid whose coarseness corresponds to the bandwidth. Setting this option to True will speed up the algorithm because fewer seeds will be initialized. default value: False Ignored if seeds argument is not None.

min_bin_freq : int, optional

> To speed up the algorithm, accept only those bins with at least min_bin_freq points as seeds. If not defined, set to 1.

cluster_all : boolean, default True

> If true, then all points are clustered, even those orphans that are not within any kernel. Orphans are assigned to the nearest kernel. If false, then orphans are given cluster label -1.

n_jobs : int

> The number of jobs to use for the computation. This works by computing each of the n_init runs in parallel.
>
> If -1 all CPUs are used. If 1 is given, no parallel computing code is used at all, which is useful for debugging. For n_jobs below -1, (n_cpus + 1 + n_jobs) are used. Thus for n_jobs = -2, all CPUs but one are used.

Previous

Attributes:	**cluster_centers_** : array, [n_clusters, n_features]
	Coordinates of cluster centers.
	labels_ : :
	Labels of each point.

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Notes

Scalability:

Because this implementation uses a flat kernel and a Ball Tree to look up members of each kernel, the complexity will tend towards O(T*n*log(n)) in lower dimensions, with n the number of samples and T the number of points. In higher dimensions the complexity will tend towards O(T*n^2).

Scalability can be boosted by using fewer seeds, for example by using a higher value of min_bin_freq in the get_bin_seeds function.

Note that the estimate_bandwidth function is much less scalable than the mean shift algorithm and will be the bottleneck if it is used.

References

Dorin Comaniciu and Peter Meer, “Mean Shift: A robust approach toward feature space analysis”. IEEE Transactions on Pattern Analysis and Machine Intelligence. 2002. pp. 603-619.

Methods

`fit`(X[, y])	Perform clustering.
`fit_predict`(X[, y])	Performs clustering on X and returns cluster labels.
`get_params`([deep])	Get parameters for this estimator.
`predict`(X)	Predict the closest cluster each sample in X belongs to.
`set_params`(**params)	Set the parameters of this estimator.

`__init__`(*bandwidth=None*, *seeds=None*, *bin_seeding=False*, *min_bin_freq=1*, *cluster_all=True*, *n_jobs=1*) [source]

Previous

`fit`(*X*, *y=None*) [source]

Perform clustering.

Parameters:	**X** : array-like, shape=[n_samples, n_features] Samples to cluster. **y** : Ignored

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`fit_predict`(*X*, *y=None*) [source]

Performs clustering on X and returns cluster labels.

Parameters:	**X** : ndarray, shape (n_samples, n_features) Input data.
Returns:	**y** : ndarray, shape (n_samples,) cluster labels

`get_params`(*deep=True*) [source]

Get parameters for this estimator.

Parameters:	**deep** : boolean, optional If True, will return the parameters for this estimator and contained subobjects that are estimators.
Returns:	**params** : mapping of string to any Parameter names mapped to their values.

`predict`(*X*) [source]

Predict the closest cluster each sample in X belongs to.

Previous

Parameters:	**X** : {array-like, sparse matrix}, shape= [n_samples, n_features] New data to predict.
Returns:	**labels** : array, shape [n_samples,] Index of the cluster each sample belongs to.

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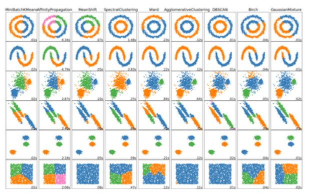
`set_params`(***params*) [source]

Set the parameters of this estimator.

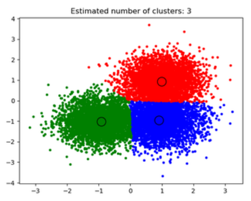
The method works on simple estimators as well as on nested objects (such as pipelines). The latter have parameters of the form `<component>__<parameter>` so that it's possible to update each component of a nested object.

Returns:	**self** :

Examples using `sklearn.cluster.MeanShift`



Comparing different clustering algorithms on toy datasets



A demo of the mean-shift clustering algorithm

Previous **Next**