practical 6 NAMES

July 13, 2021

1 Practical 6 - Clustering

```
[2]: def stdize(X):
    X_norm = (X - X.mean(axis = 0)) / X.std(axis = 0)
    return X_norm
```

1.1 Task 0: Load data

To explore different clustering algorithms, we generated a toy dataset that consists of 5000 data points from a two dimensional mixture of Gaussian model with seven clusters. Plot the data points with different colors for each cluster and indicated the cluster means.

```
[3]: # load data
with open('data/data_gmms.pkl', 'rb') as f:
    dataset = pickle.load(f)
```

```
[4]: def plot_clustering(data, cluster_ids, means, title):

Plots the (2D) data as scatter plot, with different colors and an extra

⇒symbol for the mean per cluster.

inputs:

data -- (N, n_features)-shaped array of data

cluster_ids -- (N,)-shaped array of integers that hold the cluster

⇒assignment for each data point

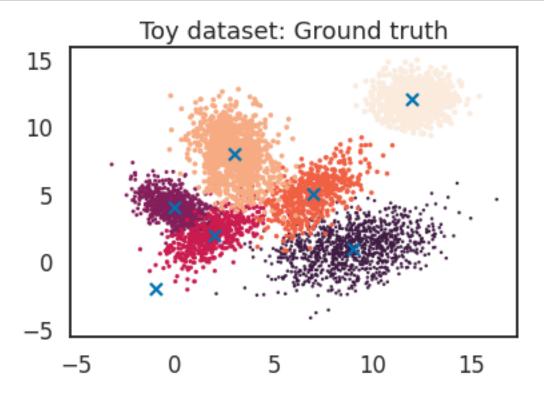
means -- (n_cluster, n_features)-shaped array of mean vectors

title -- string that is added as title
```

```
[5]: toy_data = dataset['data']
toy_cluster_ids_true = dataset['labels']
toy_means = dataset['means']
```

```
[6]: plot_clustering(toy_data, toy_cluster_ids_true, toy_means, 'Toy dataset: Ground_

→truth')
```



1.2 Task 1: Cluster the data using k-Means

First, we will implement k-Means as an example of a simple clustering algorithm and see how it performs on the dataset.

Use the function KMeans provided by sklearn to perform K-Means with different numbers of clusters, for instance 3, 5, 7, 10 and 20.

```
[7]: | \#means = np.array([np.random.uniform(-1.5, 1.5, 2)]) for i in range(7)])
    #distances = [[np.linalq.norm(point - means[k]) for k in range(7)] for point in_{\square}
     \rightarrow toy_norm]
     \#rnk = np.array([distances[i].index(min(distances[i]))) for i in_{\bot}
     \rightarrow range(len(toy_norm))])
    \#means = [sum(toy_norm[rnk == k]) / sum(rnk == k)) for k in range(7)]
[8]: def run_KMeans(data, n_clusters):
         '''Function that performs K-means clustering for a given number of clusters
                data: (n_samples, n_features)-shaped array of data
                number of clusters: int, number of clusters
            output:
                kmeans_result: (n samples,)-shaped array of integers that hold the
     \rightarrow cluster assignment for each data point
         111
        data_norm = stdize(data)
        means = np.array([np.random.uniform(-1.5,1.5,2) for i in range(n_clusters)])
        for i in range(10):
            distances = [[np.linalg.norm(point - means[k]) for k in_
     →range(n_clusters)] for point in data_norm]
            rnk = np.array([distances[i].index(min(distances[i])) for i in_
     →range(len(data norm))])
            means = [sum(data_norm[rnk == k]) / sum(rnk==k) for k in_
     →range(n_clusters)]
        kmeans_result = rnk #, np.array(means)
        # ----- END CODE -----
        return kmeans_result
[9]: # run kmeans with different numbers of clusters
    # ------ INSERT CODE -----
    labels_for_cluster_nr = [run_KMeans(toy_data, i) for i in_
```

 \rightarrow (1,2,3,4,5,6,7,8,9,10,15,20,30)]

----- END CODE -----

<ipython-input-8-507cc6767609>:18: RuntimeWarning: invalid value encountered in

```
long_scalars
  means = [sum(data_norm[rnk == k]) / sum(rnk==k) for k in range(n_clusters)]
```

Plot your results as cluster labels using the "plot_clustering" function and compare it to the original cluster labels. Describe your results.

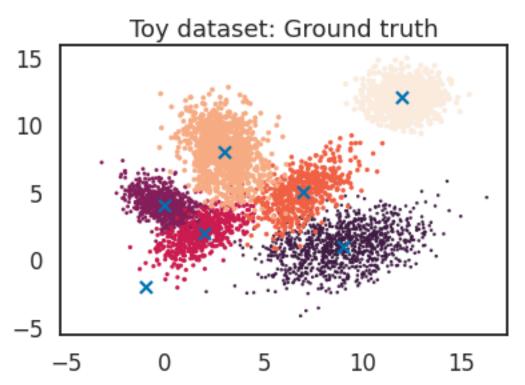
```
[10]: # plot results
                 ---- INSERT CODE -----
     plot_clustering(toy_data, toy_cluster_ids_true, toy_means, 'Toy dataset: Ground_
      plot_clustering(toy_data, labels_for_cluster_nr[5], toy_means, 'Toy dataset:__

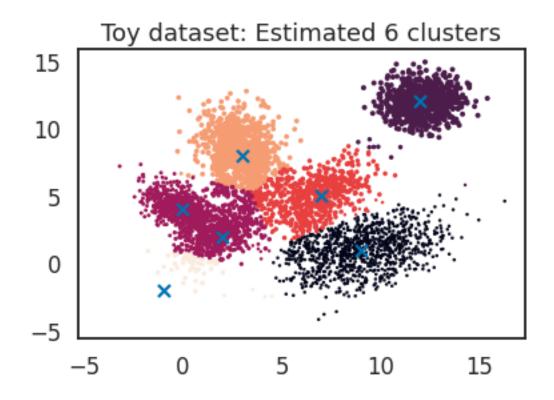
→Estimated 6 clusters')
     plot_clustering(toy_data, labels_for_cluster_nr[6], toy_means, 'Toy dataset:u

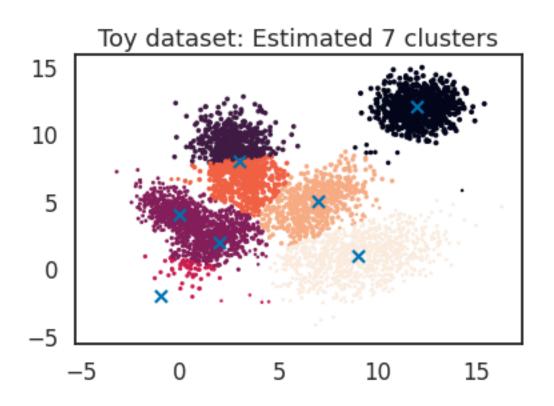
→Estimated 7 clusters')
     plot_clustering(toy_data, labels_for_cluster_nr[3], toy_means, 'Toy dataset:u
      plot_clustering(toy_data, labels_for_cluster_nr[4], toy_means, 'Toy dataset:u

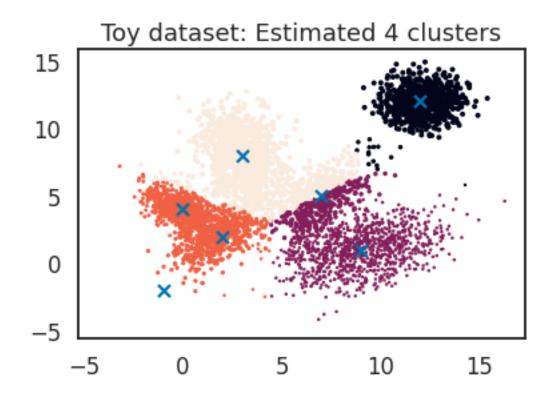
→Estimated 5 clusters')
     plot_clustering(toy_data, labels_for_cluster_nr[10], toy_means, 'Toy dataset:u
      plot_clustering(toy_data, labels_for_cluster_nr[11], toy_means, 'Toy dataset:u
      plot_clustering(toy_data, labels_for_cluster_nr[12], toy_means, 'Toy dataset:__

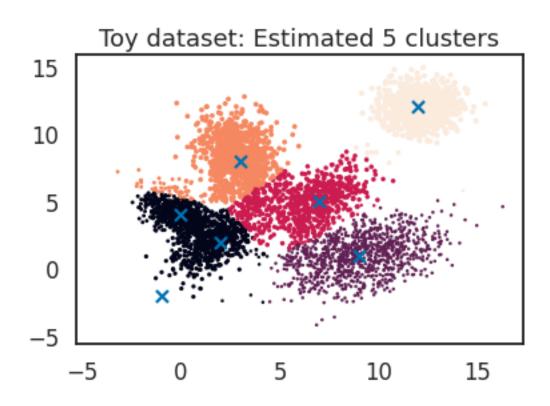
→Estimated 30 clusters')
                    -- END CODE ·
```

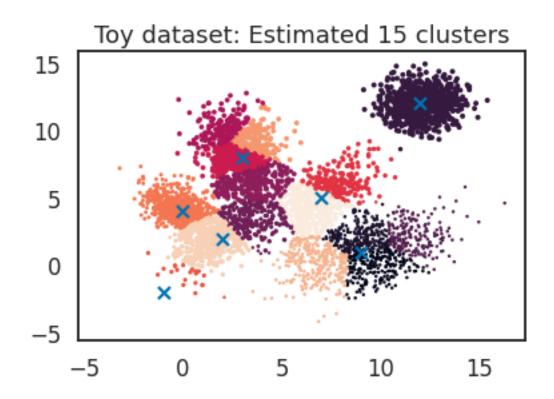


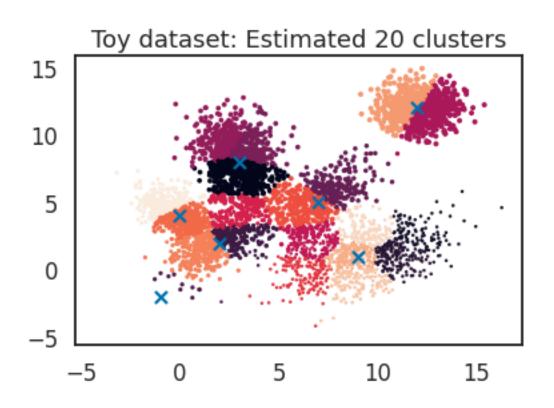


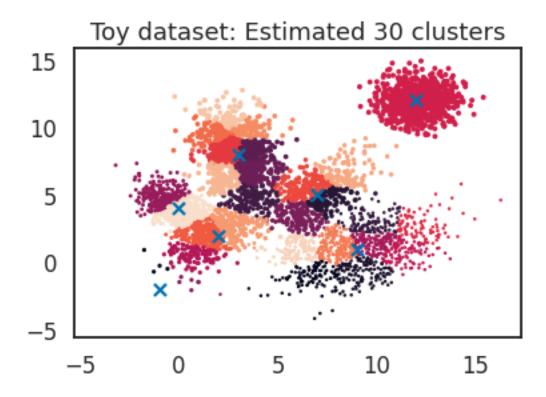












YOUR ANSWER HERE

1.3 Task 2: Clustering using Gaussian Mixture Models

Next, we will implement clustering with Gaussian Mixture models ss discussed in the Bishop in Chapter 9.2.2 pg. 435-439.

Implement the EM algorithm to fit a Gaussian mixture model on the data. Sort the data points by inferring their class labels from your mixture model (by using maximum a-posteriori classification). Fix the seed of the random number generator to ensure deterministic and reproducible behavior.

For this task, it is important to think about a good way to initialize the means, covariances and mixing coefficients. Also, during optimization, covariance matrices can become singular. To prevent this, you can add a small constant (like 10^{-5}) to the diagonal.

In order to speed up the computation, define a convergence criterion that stops the algorithm after convergence.

```
[11]: # cov update old very tough bottleneck!!!
#samples = N_total
#clusters = 7
#helper_list = [0] * samples
#for i in range(samples):
```

```
# for j in range(clusters):
# centered_x = toy_data[i:i+1] - means[j:j+1]
# helper_list[i] = responsibilities[i,j] * centered_x.T @ centered_x
# covs[j] = 1/N_groups[j] * sum(helper_list)
```

```
[12]: def gmm(data, n_clusters, verbose=True, max_iter=1000,__
       '''Function that fits a mixture of gaussians to data.
              inputs:
                               -- (n_samples, n_features)-shaped array of data points
                  data
                  n\_clusters
                                -- int, number of clusters / mixture components
                  verbose -- bool, if True, print current likelihood after each ⊔
       \hookrightarrow EM iteration
                               -- maximum number of EM iterations
                  convergence_threshold -- stop algorithm if change in_
       \rightarrow log-lieklihood is below the treshold
              outputs:
                  cluster_ids -- (N,)-shaped array of integers that hold the cluster_
       \rightarrow assignment for each data point
                  means
                              -- (n_clusters, n_features)-shaped array of fit mean_
       \rightarrow vectors
                              -- (n_features, n_features, n_cluster)-shaped array of
                  covs
       \hookrightarrow fit covariance matrices
                           -- (n_cluster)-shaped arrays of fit priors / mixing_
                  priors
       \hookrightarrow coefficients
              111
          # ----- INSERT CODE -----
          from scipy.stats import multivariate_normal
          n_samples, n_features = data.shape
          data_norm = stdize(data)
          ### INITIALIZATION ###
          means = np.array([np.random.uniform(-1.5,1.5,n_features) for i in_
       →range(n_clusters)])
          covs = [np.eye(n_features)] * n_clusters
          priors = np.random.uniform(0,1,n_clusters)
          ### ALTERNATE BETWEEN E & M STEP ###
          for loop_count in range(2):
```

```
### E-STEP ###
       denominator_matrix = np.array(
           [ [priors[j] * multivariate normal.pdf(datapoint, mean=means[j],_
→cov=covs[j]) for j in range(n_clusters)]
            for datapoint in data_norm])
       #divide denominator matrix by its rowSums via transposing-trick
       responsibilities = (denominator_matrix.T/denominator_matrix.
\rightarrowsum(axis=1)).T
       ### M-STEP ###
       N groups = responsibilities.sum(axis = 0)
       priors = N_groups/n_samples
       means = [1/N_groups[k] * sum([responsibilities.T[k][i] * data_norm[i]_

→for i in range(len(data_norm))]) for k in range(n_clusters)]
       #update covariance matrix
       weighted_demeaned_obs = [[responsibilities[i,j] * (data_norm[i:
\rightarrowi+1]-means[j:j+1]).T @ (data_norm[i:i+1]-means[j:j+1]) for j inu
→range(n_clusters)] for i in range(n_samples)]
       colsums = np.array(weighted demeaned obs).sum(axis = 0)
       covs = [1/N_groups[k] * colsums[k] for k in range(n_clusters)]
       ### CHECK FOR CONVERGENCE/ PRINT LOG_LIKELIHOOD if VERBOSE ###
       loglik_contribs = np.array([[
           \verb|sum(multivariate_normal.pdf(datapoint, mean=means[k], cov=covs[k])_{\sqcup}|
→for k in range(n_clusters))
           ] for datapoint in data_norm])
       loglik = sum(np.log(loglik_contribs))
       if verbose == True:
           print('Iteration: {}'.format(loop_count+1))
           print('Loglik: {}'.format(loglik))
   ### ASSIGN CLUSTER LABELS ###
   cluster_ids = [resp_row.index(min(resp_row)) for resp_row in_
→responsibilities.tolist()]
   # ----- END CODE -----
   return (cluster_ids, means, covs, priors)
```

Explore the results of GMM using different numbers of clusters and initialization strategies.

```
[13]: # fit GMM
cluster_ids, means, covs, priors = gmm(toy_data, 7, verbose=True,
    →max_iter=1000, convergence_threshold=1e-4)
```

Iteration: 1

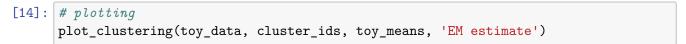
Loglik: [-3606.54520882]

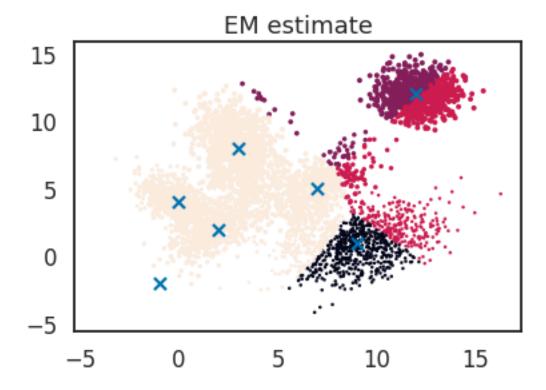
Iteration: 2

Loglik: [-3337.67419538]

Plot the data points from the toy dataset and indicate in color the cluster each point was assigned to by your model. How does the assignment compare to ground truth? How does it compare to the k-Means solution? Plot ground truth, k-Means and GMM cluster assignment side-by-side to compare them.

If you run the algorithm multiple times, you will notice that some solutions provide suboptimal clustering solutions - depending on your initialization strategy.





YOUR ANSWER HERE