

# sheet02

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## 1 Sheet 2

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```
[1]: import numpy as np
      from matplotlib import pyplot as plt
      from scipy.stats import gaussian_kde
```

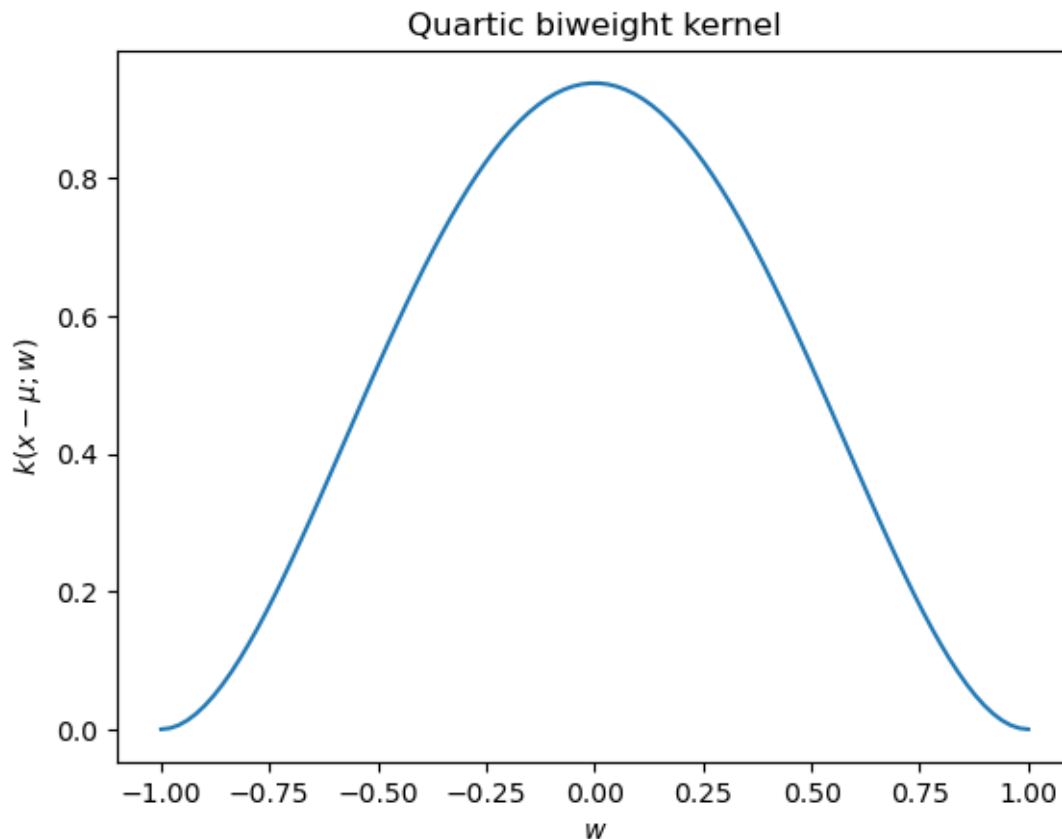
### 1.1 1 Kernel Density Estimation

(a)

```
[2]: def biweight(x, mu, w):
      """biweight kernel at mean mu, with bandwidth w evaluated at x"""
      if (x - mu > -w) and (x - mu < w):
          k = 15/(16*w) * (1 - ((x-mu)/w)**2)**2
      else:
          k = 0
      return k
      #TODO: implement the quartic (biweight) kernel
```

```
[3]: mu = 0
      w = 1
      domain = np.linspace(-1,1,num = 100)
      kernel_vals = [biweight(x, mu, w) for x in domain]
      plt.plot(domain, kernel_vals)
      plt.ylabel(f'$k(x-\mu;w)$')
      plt.xlabel(f'$w$')
      plt.title('Quartic biweight kernel')
      # TODO plot the kernel
```

```
[3]: Text(0.5, 1.0, 'Quartic biweight kernel')
```



We can see a symmetric kernel with support  $[-1, 1]$ .

(b)

```
[4]: # load the data
data = np.load("data/samples.npy")
data50 = data[:50]
print(f'{data.shape=}, {data50.shape=}')

```

```
data.shape=(10000,), data50.shape=(50,)
```

```
[6]: x_ = data50[4] # example x
x_ - data50
print('The result is broadcasted: \n x-data50 = ', x_-data50)

kde_ = 0
for x in data50:
    kde_ += biweight(x_ - x, mu = 0, w = 1)

```

The result is broadcasted:

```
x-data50 = [ 0.956057  6.83620095  0.1527347 -0.16022261  0.]
```

```

0.91014681
 7.4293298  0.51493953  6.60292255  0.44825482  8.14906403  5.97400304
 7.64591618  0.33843258  5.23943767  5.93484453  0.79503942  0.98899981
 0.63264979 -0.525491   0.86387563 -2.89483556  0.01106935  0.90581603
 6.81518695  6.0118808  6.7721106  5.7250845  7.12435507  7.38703073
-1.49370655  8.50471502  7.33714949  7.53958145  1.10249879  6.40101085
 1.07391179  1.05302318  6.83940263  6.34695325  0.92471502  0.55073825
 7.62067136  7.2868227  7.01518574 -1.11829306 -0.1610926  -8.74403715
 8.15152502  1.02399578]

```

```

[7]: def kde(x, obs, w=1):
      s = 0
      for o in obs:
          s += biweight(x, mu = o, w = w)
      p_x_obs = 1/(len(obs)) * s
      return p_x_obs
      # TODO: implement the KDE with the biweight kernel

```

```

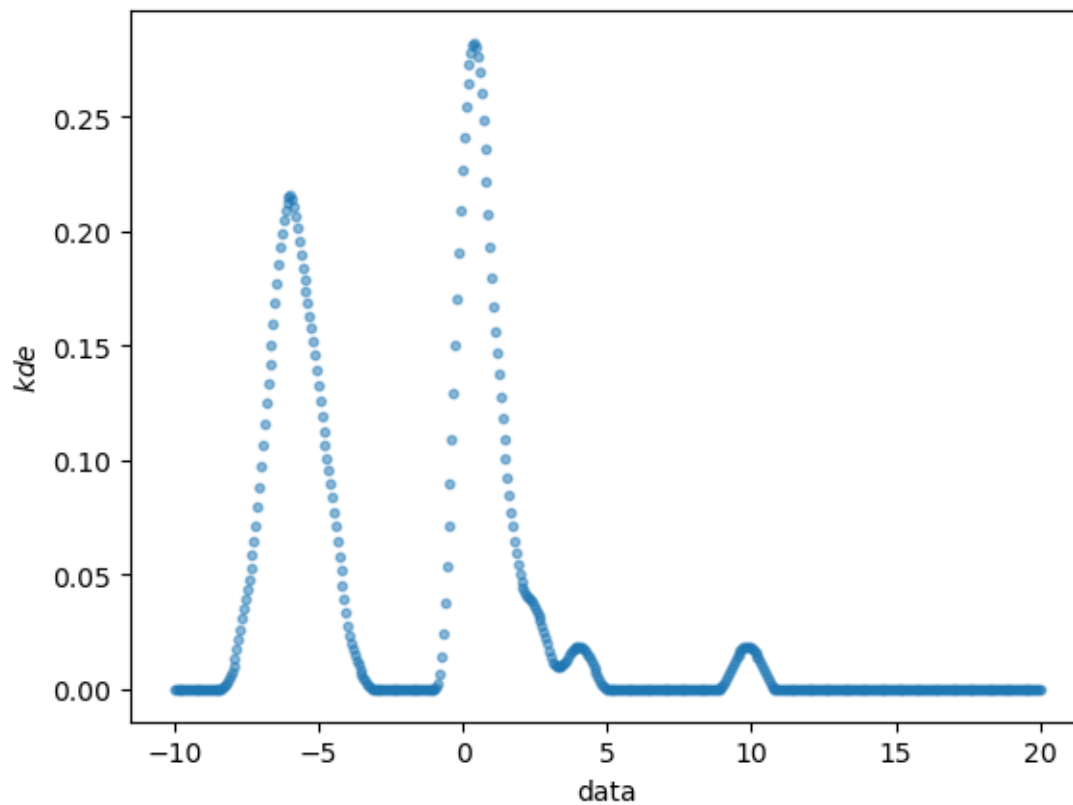
[8]: # TODO: compute and plot the kde on the first 50 data points
      domain = np.linspace(-10, 20, 500 )
      kde_50 = [kde(x, data50) for x in domain]
      plt.scatter(domain, kde_50, s=10, alpha=0.5)
      plt.xlabel('data')
      plt.ylabel('$kde$')

```

```

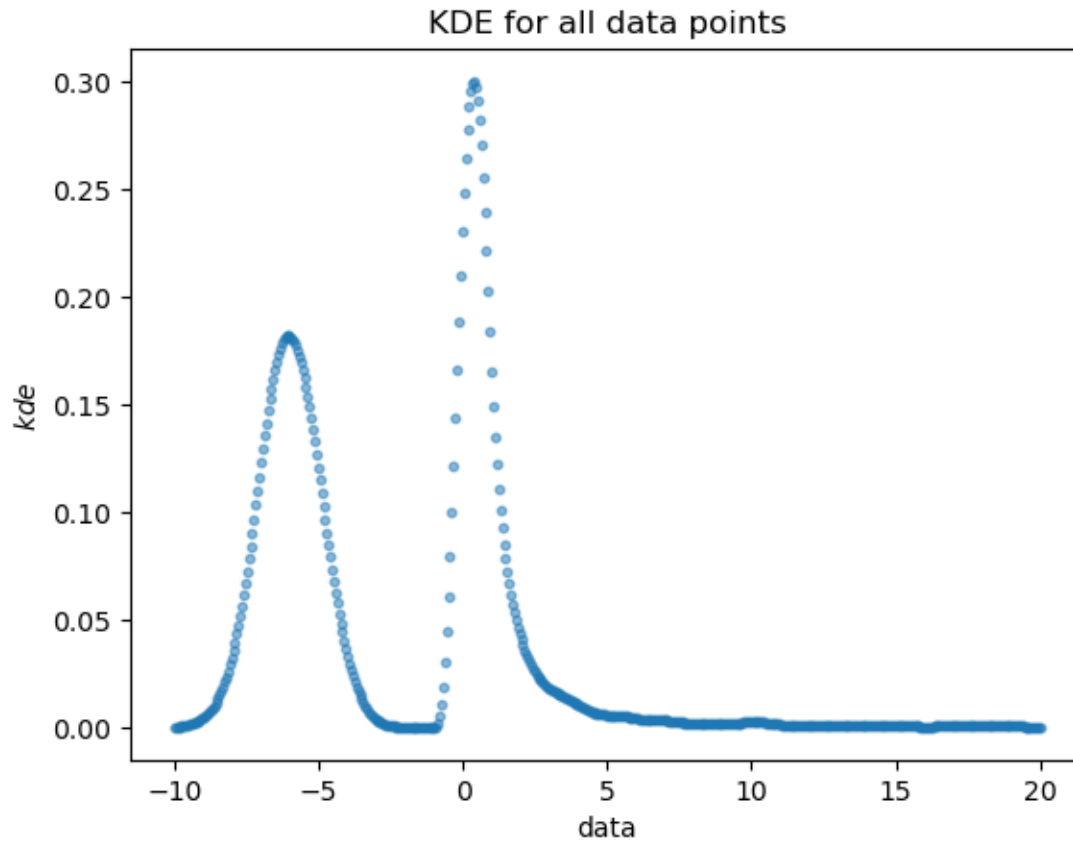
[8]: Text(0, 0.5, '$kde$')

```



```
[9]: # TODO: explore what happens when you increase the number of points
kde_full = [kde(x, data) for x in domain]
plt.scatter(domain, kde_full, s=10, alpha=0.5)
plt.xlabel('data')
plt.ylabel('$kde$')
plt.title('KDE for all data points')
```

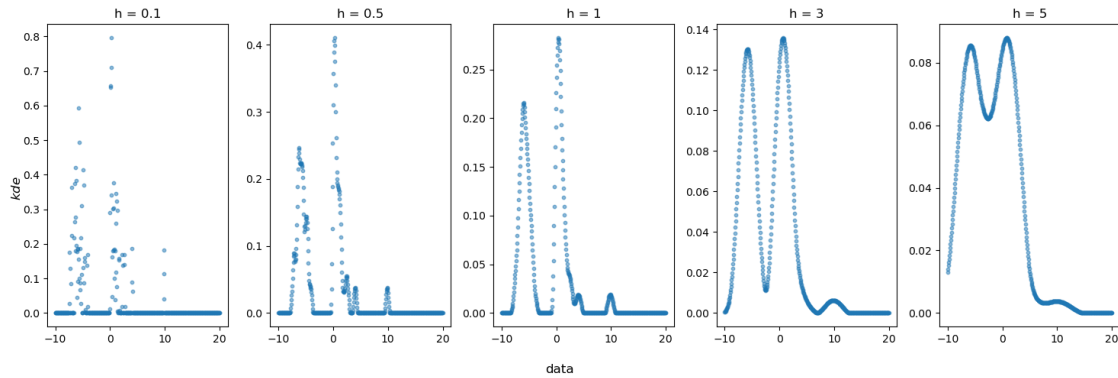
```
[9]: Text(0.5, 1.0, 'KDE for all data points')
```



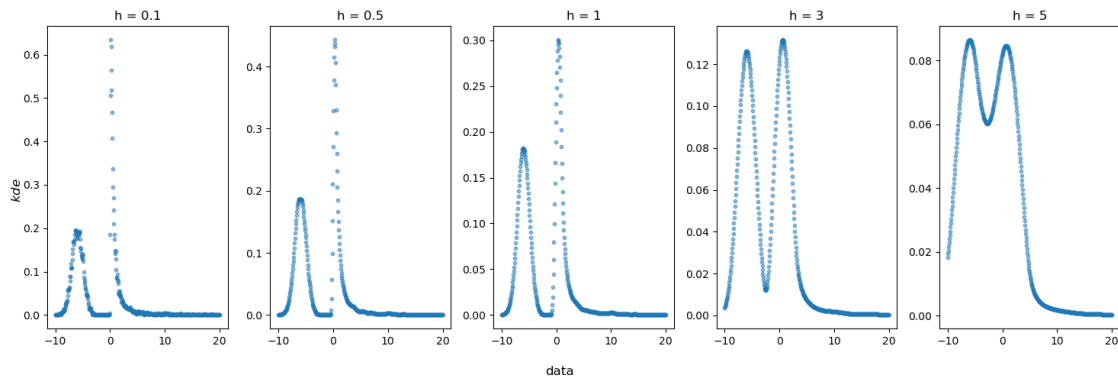
When sampling more data points, we “get rid” of some peaks, that might have been overestimated with less data.

```
[14]: bands = [0.1, 0.5, 1, 3, 5]

fig, axs = plt.subplots(1, 5, figsize=(15,5))
fig.supxlabel('data')
fig.supylabel('$kde$')
for bandw, ax in zip(bands, axs):
    kde_50 = [kde(x, data50, w = bandw) for x in domain]
    ax.scatter(domain, kde_50, s=10, alpha=0.5)
    ax.set_title(f'h = {bandw}')
plt.tight_layout()
```



```
[13]: fig, axs = plt.subplots(1, 5, figsize=(15,5))
fig.supxlabel('data')
fig.supylabel('$kde$')
for bandw, ax in zip(bands, axs):
    kde_list = [kde(x, data, w = bandw) for x in domain]
    ax.scatter(domain, kde_list, s=10, alpha=0.5)
    ax.set_title(f'h = {bandw}')
plt.tight_layout()
```



We see, that with greater bandwidth, the distribution becomes broader and peaks less distinct.

## 1.2 3 Mean-Shift

(b) Bonus

```
[204]: # TODO: implement the update to the local mean
```

```
def mean_shift_step(x, xt, r=1):
    """
```

A single step of mean shift,  
moving every point in `xt` to the local mean of points in `x` within a radius  
of `r`.

#### Parameters

-----

`x : np.ndarray`

Array of points underlying the KDE, shape `(d, N1)`

`xt : np.ndarray`

Current state of the mean shift algorithm, shape `(d, N2)`

`n_components : int, optional`

Number of requested components. By default returns all components.

#### Returns

-----

`np.ndarray`

the points after the mean-shift step

"""

# NOTE: For the exercise you only need to implement this for `d == 1`.

# If you want some extra numpy-practice, implement it for arbitrary

dimension

`assert xt.shape[0] == x.shape[0], f'Shape mismatch: {x.shape[0]}!={xt.shape[0]}'`

# TODO: compute a `N` by `N` matrix 'dist' of distances,

# such that `dists[i, j]` is the distance between `x[i]` and `xt[j]`

`dist = x[:,None] - xt[None, :]`

# TODO: threshold the distances with `r` to get an array of masks for every

data point

`mask = np.abs(dist)<r`

# TODO: compute the number of points in `x` within radius `r` of each `xt`

`num = mask.sum(axis=1)`

# TODO: compute the local means by summing over the neighbors of each

element in `xt`

# and dividing by the number of neighbors

`neighbors = np.where(mask, dist, 0)` # keep the values where the distances

are smaller than 1

# and set to 0 otherwise

`local_means = neighbors.sum(axis=1) / (num + 10e-12)` # to avoid divide by 0

`return local_means`

[231]: `mask = np.abs(dist) < 1`

`num = mask.sum(axis=1)`

```
num # number of distances in the region (the query point itself also counted)
```

```
[231]: array([81, 63, 92, 62, 78, 81, 61, 86, 61, 89, 40, 37, 59, 89, 17, 37, 83,
            81, 85, 30, 81,  4, 80, 81, 63, 37, 63, 29, 61, 64, 13, 32, 65, 61,
            78, 52, 78, 79, 63, 50, 81, 86, 59, 64, 62, 17, 62,  1, 40, 79, 83,
            53, 79, 92, 44, 25, 85, 37, 83, 85, 48,  1, 39, 51, 40, 89, 40, 34,
            24, 43, 79, 40,  3, 62, 64,  3, 23, 81, 39, 85, 83, 63, 61, 61, 63,
            48, 80, 62, 63, 87, 83, 61, 86, 61, 85, 53, 53, 85, 85, 89, 89, 81,
            85, 40, 78, 55, 85, 89, 80, 85, 85, 28, 92, 81, 60,  7, 63, 63, 83,
            79, 83, 88, 47, 50, 85, 79, 37, 85, 89, 81, 79,  3, 40, 29, 57, 86,
            85, 65, 14, 29,  1, 86, 83, 48, 15, 81, 62,  8, 61, 22, 64, 79, 16,
            22, 81, 22, 85, 61, 63, 81, 37, 59, 37, 63, 61, 85, 85, 47,  8, 64,
            86, 48, 81, 65, 61, 31, 63,  3,  6, 78, 12, 51, 85, 81, 51, 86,  8,
            55, 55, 92, 85, 51, 88,  9, 60,  8, 81, 61, 61, 81])
```

```
[205]: np.where(mask, dist, 0).sum(axis=1) / num
```

```
[205]: array([-0.24217402,  0.05549711,  0.42048123,  0.50457376,  0.48798168,
            -0.19626383, -0.03270895,  0.14337705,  0.16728445,  0.17047473,
            -0.29574005,  0.29696566, -0.15369357,  0.28029698,  0.51446545,
            0.33612417, -0.10222971, -0.27511682,  0.03823291,  0.30790635,
            -0.14999265,  0.60359206,  0.48980786, -0.19193304,  0.04487255,
            0.2590879 ,  0.08794889,  0.39881748,  0.02372859, -0.03655209,
            0.31895061, -0.41054444, -0.03275787, -0.11010634, -0.36211083,
            0.20366753, -0.33352383, -0.32120732,  0.05229543,  0.22632523,
            -0.21083204,  0.10757833, -0.12844875, -0.02958995,  0.02005698,
            0.28055434,  0.50544375,  0.          , -0.29820104, -0.29217992,
            -0.09832233,  0.21086807, -0.28166573,  0.46127866,  0.29434857,
            -0.31620516,  0.00471461,  0.39028528, -0.11827759, -0.03872234,
            -0.3006244 ,  0.          , -0.40019196, -0.31534136, -0.27572628,
            0.29372729,  0.29775388,  0.39405578, -0.39327304,  0.28721276,
            -0.31067347, -0.36043712,  0.2173323 ,  0.01876521, -0.0418423 ,
            0.56675769,  0.5300657 , -0.26659721, -0.38324847, -0.01032695,
            -0.10305248,  0.09859549, -0.08312218, -0.07989338,  0.06053769,
            0.24157921, -0.27837528,  0.01822648,  0.03634914,  0.14549998,
            -0.09265375, -0.07174384,  0.09616034, -0.07471055, -0.02352569,
            0.19299741, -0.2049883 , -0.0304512 , -0.07693844,  0.21757084,
            0.19731136, -0.17167002, -0.06946225, -0.35153997, -0.36386788,
            0.48072174, -0.05389545,  0.23445134, -0.2836172 , -0.00722548,
            0.05992758, -0.29469405,  0.4487566 , -0.17090583,  0.18664067,
            -0.37038565, -0.04100661,  0.03709064, -0.08967497, -0.28540405,
            -0.14196249,  0.48651124,  0.28549442,  0.2155736 , -0.04148741,
            -0.3232506 ,  0.27430948,  0.00442043,  0.30989612, -0.13303601,
            -0.3052731 , -0.07853508,  0.27294725,  0.41863854, -0.22795337,
            0.12439975, -0.04694757,  0.0149968 ,  0.18478385,  0.28523138,
            0.          ,  0.07321828, -0.13962029, -0.31731545,  0.27741239,
```



```
-0.28317226,  0.03266316, -0.35259979,  0.17145547,  0.32426029,
 0.11488576, -0.32946174,  0.59540303,  0.35271376, -0.19584946,
 0.34103024,  0.05929384, -0.12869667,  0.06370226, -0.25291266,
-0.39914757, -0.12396918,  0.25671943,  0.10270495,  0.04244941,
-0.06524953,  0.01862566,  0.30461834,  0.26845821,  0.14675894,
 0.11330473, -0.32314691, -0.19435461, -0.04023661, -0.09058495,
 0.30168214,  0.05995258, -0.13879722,  0.24563519, -0.34099152,
-0.29756297, -0.32076695, -0.04904686, -0.17366606, -0.31915293,
 0.13807982, -0.37464799,  0.49622189,  0.1857693 ,  0.45473589,
-0.05852352, -0.24348533,  0.15754958, -0.24736402, -0.14846441,
 0.19028924, -0.19958712,  0.02124062,  0.02499318, -0.1504322 ])
```

```
[235]: %%timeit
dist = (x[:,None] - x[None, :]) # flexing with our vectorization skills
```

33.4  $\mu$ s  $\pm$  459 ns per loop (mean  $\pm$  std. dev. of 7 runs, 10,000 loops each)

```
[76]: %%timeit
dist = np.zeros((len(x), len(x)))
for i in range(len(x)):
    for j in range(len(x)):
        dist[i,j] = x[i]-x[j]
```

13.2 ms  $\pm$  157  $\mu$ s per loop (mean  $\pm$  std. dev. of 7 runs, 100 loops each)

```
[236]: mask = dist<1
num = mask.sum(axis=1)

dist[0][2] +x[2] - x[0] # checking if dist_i,j is really x_i - x_j
```

[236]: 0.0

```
[222]: # load the data
data = np.load("data/samples.npy")
x = data[:200] # use e.g. the first 200 points
xt = x

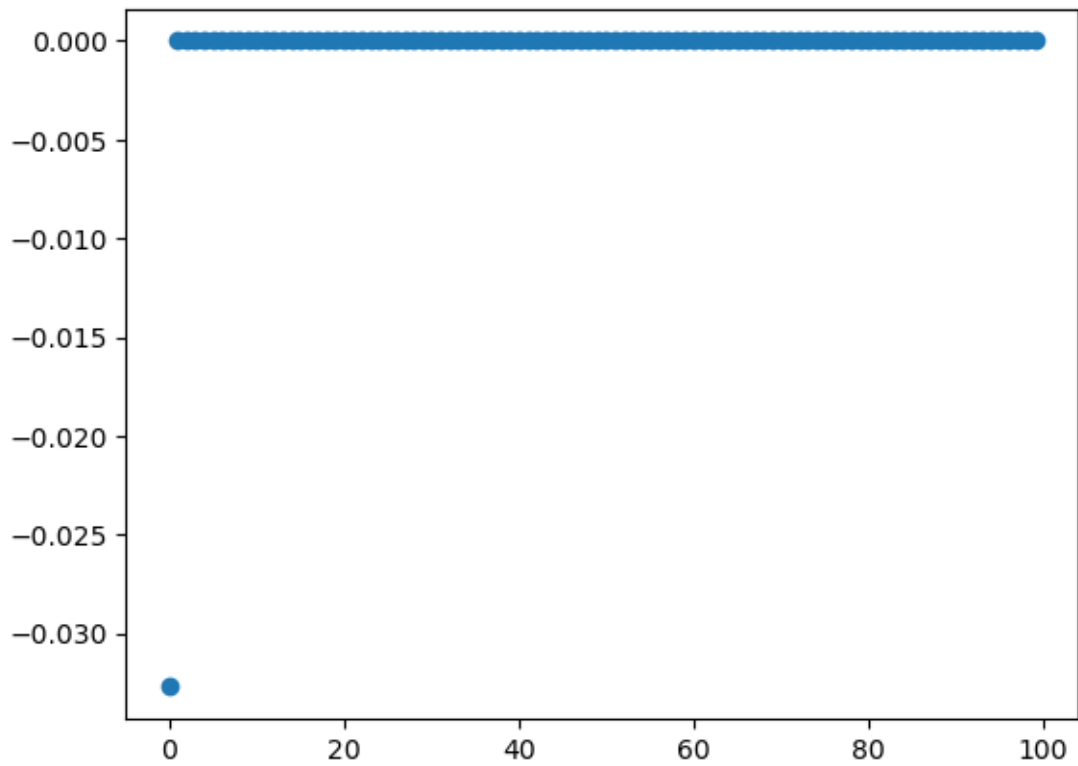
trajectories = [xt]
max_steps = 100
for step in range(max_steps):

    # TODO: update xt with your mean shift step
    xt = mean_shift_step(x, xt)
    trajectories.append(xt)
    if np.allclose(trajectories[-1], trajectories[-2]): # break in case of
        ↪convergence
        break
```

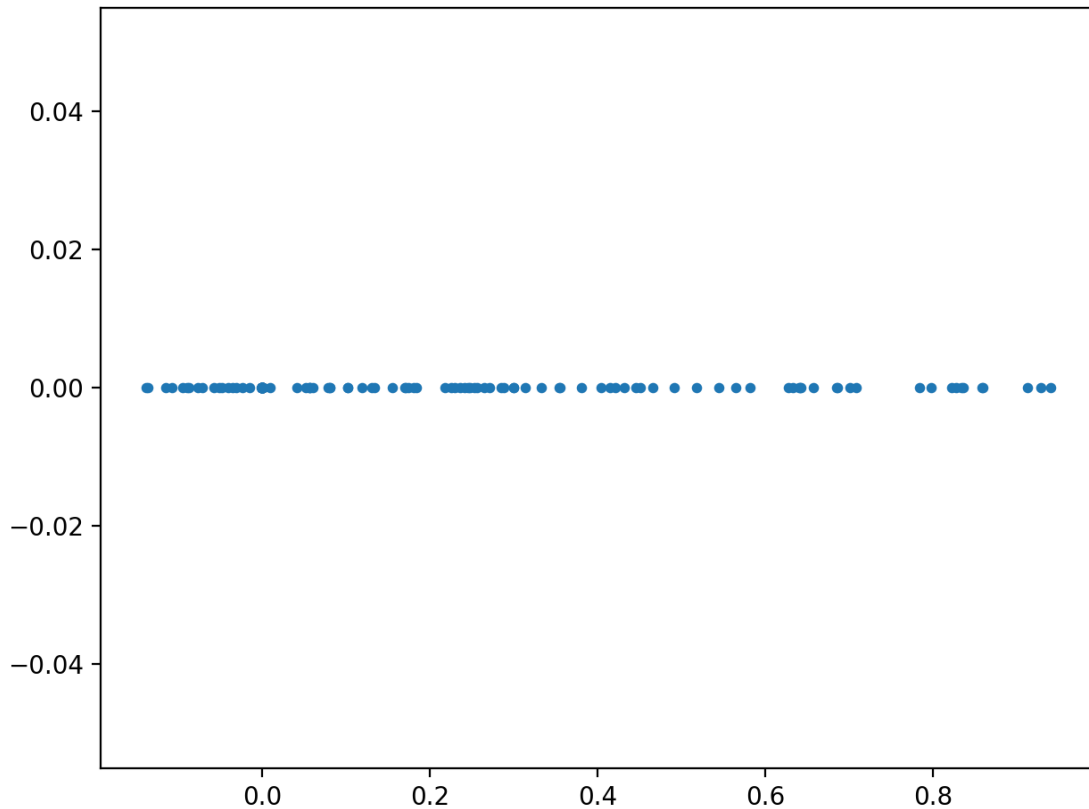
```
trajectories = np.stack(trajectories)
n_steps = len(trajectories) - 1

# TODO: plot the trajectories
plt.scatter(np.arange(n_steps), trajectories[1:,6])
```

[222]: <matplotlib.collections.PathCollection at 0x7fef70a1cca0>



```
[228]: plt.figure(dpi=200)
plt.scatter(trajectories[-1], np.zeros((np.shape(trajectories[-1]))), s=10)
plt.tight_layout()
```



```
[229]: # TODO: repeat the above for "blurring" mean shift

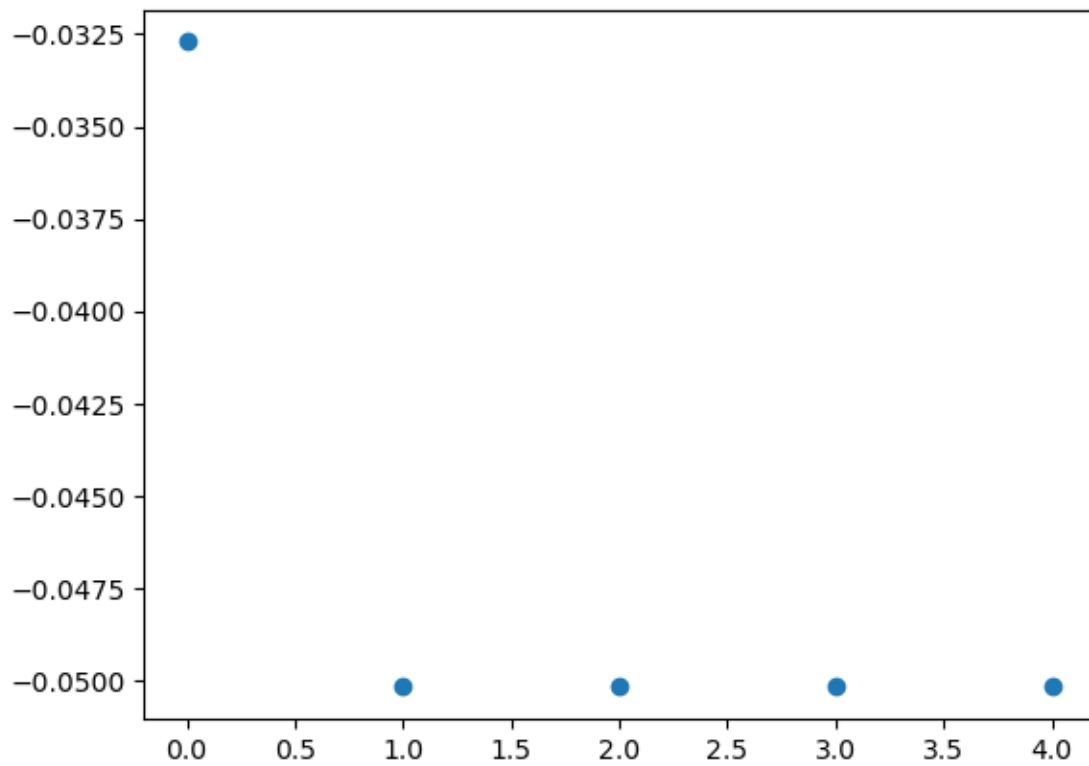
x = data[:200] # use e.g. the first 200 points
xt = x

trajectories = [xt]
max_steps = 100
for step in range(max_steps):

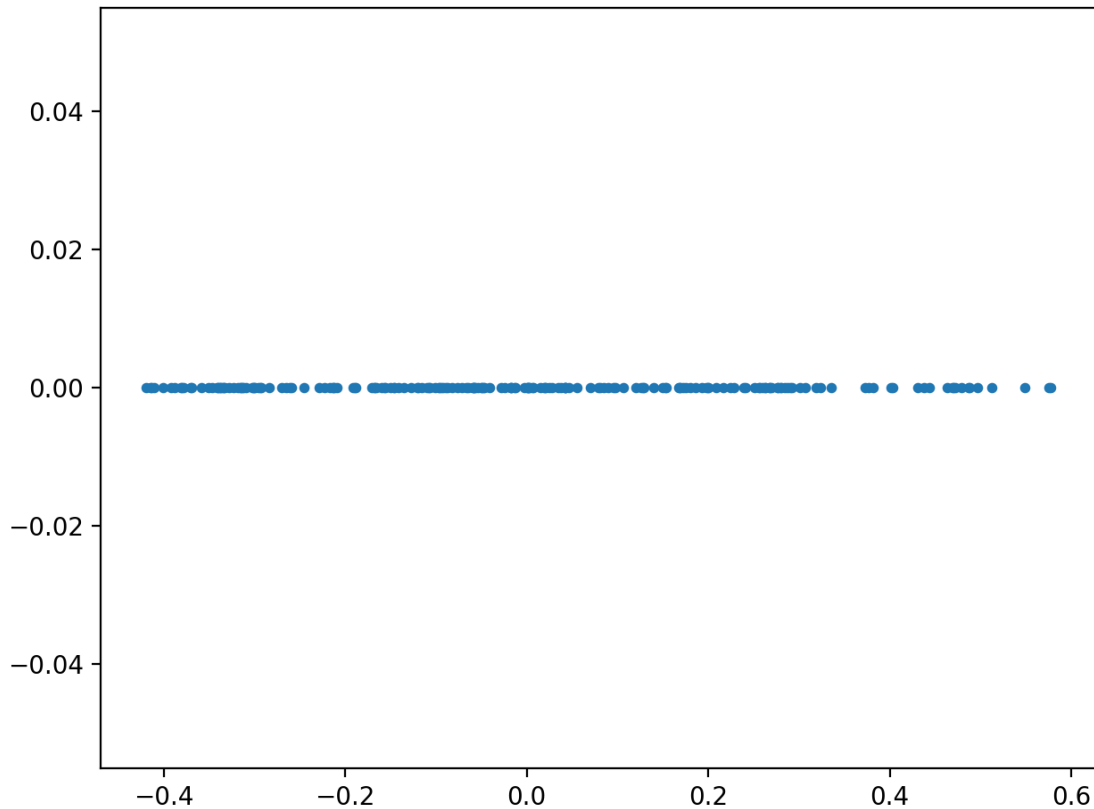
    # TODO: update xt with your mean shift step
    xt = mean_shift_step(xt, xt) # now xt is used in the update step
    trajectories.append(xt)
    if np.allclose(trajectories[-1], trajectories[-2]): # break in case of
↳ convergence
        break
trajectories = np.stack(trajectories)
n_steps = len(trajectories) - 1

# TODO: plot the trajectories
plt.scatter(np.arange(n_steps), trajectories[1:,6])
```

[229]: <matplotlib.collections.PathCollection at 0x7fef70e3c550>



```
[230]: plt.figure(dpi=200)
plt.scatter(trajectories[-1], np.zeros((np.shape(trajectories[-1]))), s=10)
plt.tight_layout()
```



When we “blurr” the dataset, the calculation converges much faster and seems to build different clusters, in particular less of them.

### 1.3 4 K-Means

(b)

```
[7]: from sklearn.cluster import KMeans

def kmeans_step(x, k, c=None, init='random'):
    """
    K-Means clustering on a  $p \times N$  data matrix.

    Parameters
    -----
    x : np.ndarray
        Data matrix of shape  $(p, N)$ .
    k : int
        Number of cluster.
    c : np.ndarray, optional
```

Current cluster centers. If None, the initialization as specified by `init` will be used.

`init: str`

The initialization method to be used if `c` is None.

Returns

-----

`float, np.ndarray`

cost after the step, updated cluster centers

"""

`if c is not None:`

`assert c.shape[0] == k`

# Note: the documentation is your friend:

# [https://scikit-learn.org/stable/modules/generated/sklearn.cluster.](https://scikit-learn.org/stable/modules/generated/sklearn.cluster.KMeans.html)

[KMeans.html](https://scikit-learn.org/stable/modules/generated/sklearn.cluster.KMeans.html)

# TODO: set `n_clusters`, `init`, `n_init` and `max_iter` appropriately

`single_step_kmeans = KMeans(`

`n_clusters=k,`

`init='random',`

`max_iter=1,`

`n_init=1,`

`)`

# TODO call the `single_step_kmeans`

`kmeans = single_step_kmeans.fit(x)`

# TODO get the current energy (you don't have to compute it - it's stored

in `single_step_kmeans`)

`E = kmeans.inertia_`

# TODO read out cluster centers

`c = kmeans.cluster_centers_ # (n_clusters, n_features)`

`return E, c`

[46]: # load the data (you can try both with the full normalized feature and the 2d [umap](#) projection)

`features = np.load('data/dijet_features_normalized.npy') # full features`

`# features = np.load('data/dijet_features_umap.npy') # umap projection`

`print(f'{features.shape=}')`

`features.shape=(116, 2233)`

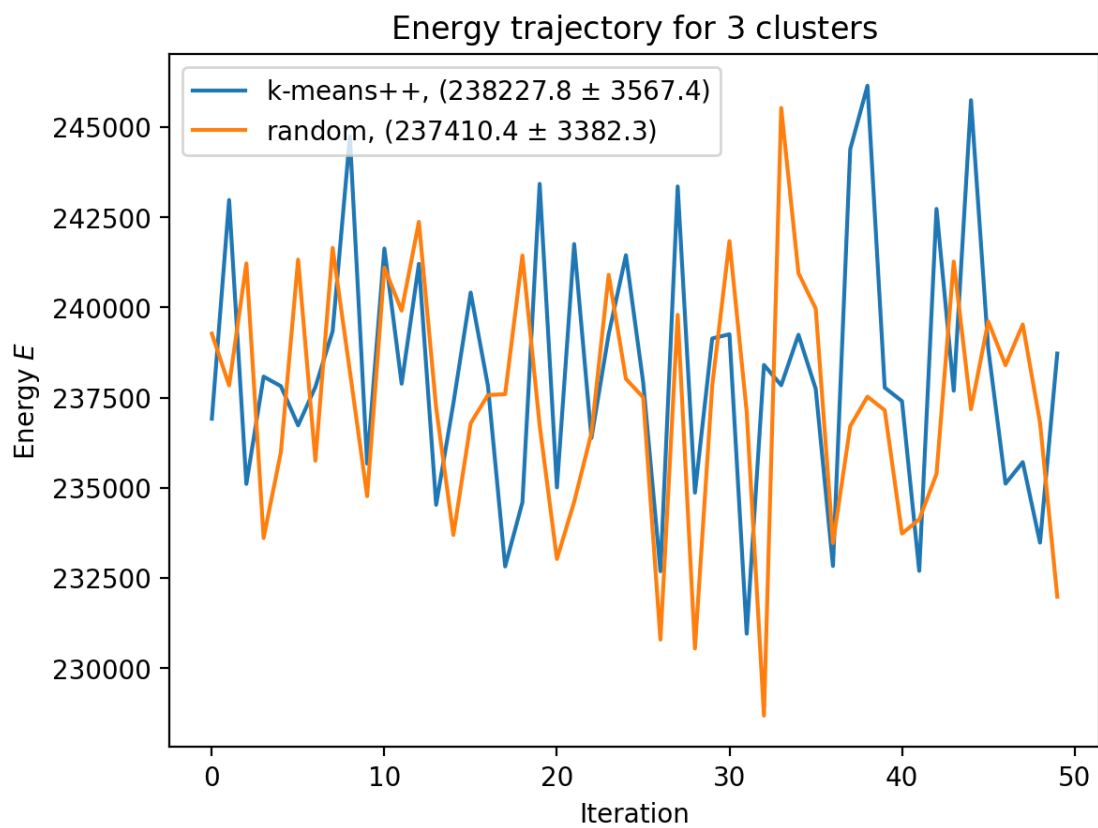
```

[47]: def kmeans(x, k, max_steps=100, init='random', early_stopping = True):
    c = None
    energies = [] # list of energies over the iterations.
    for i in range(max_steps):
        # Call the kmeans_step implemented above to get the energy and the next
        ↪ cluster centers
        E, c = kmeans_step(x, k=k, c=c, init=init)
        energies.append(E)

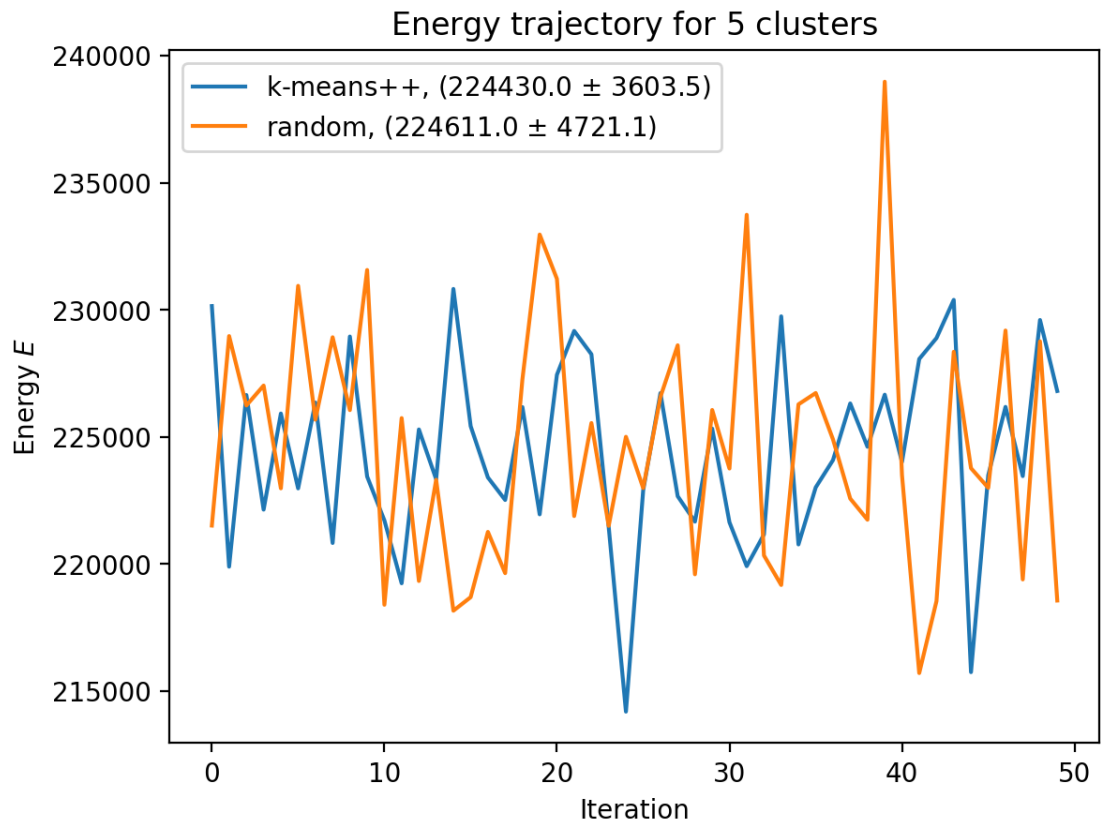
        # Stop the loop if there was no improvement
        if early_stopping: # Only early stopping, when we specify it
            if i>=2 and energies[-1] == energies[-2]:
                break
    energies = np.array(energies)
    return energies # return array of energies

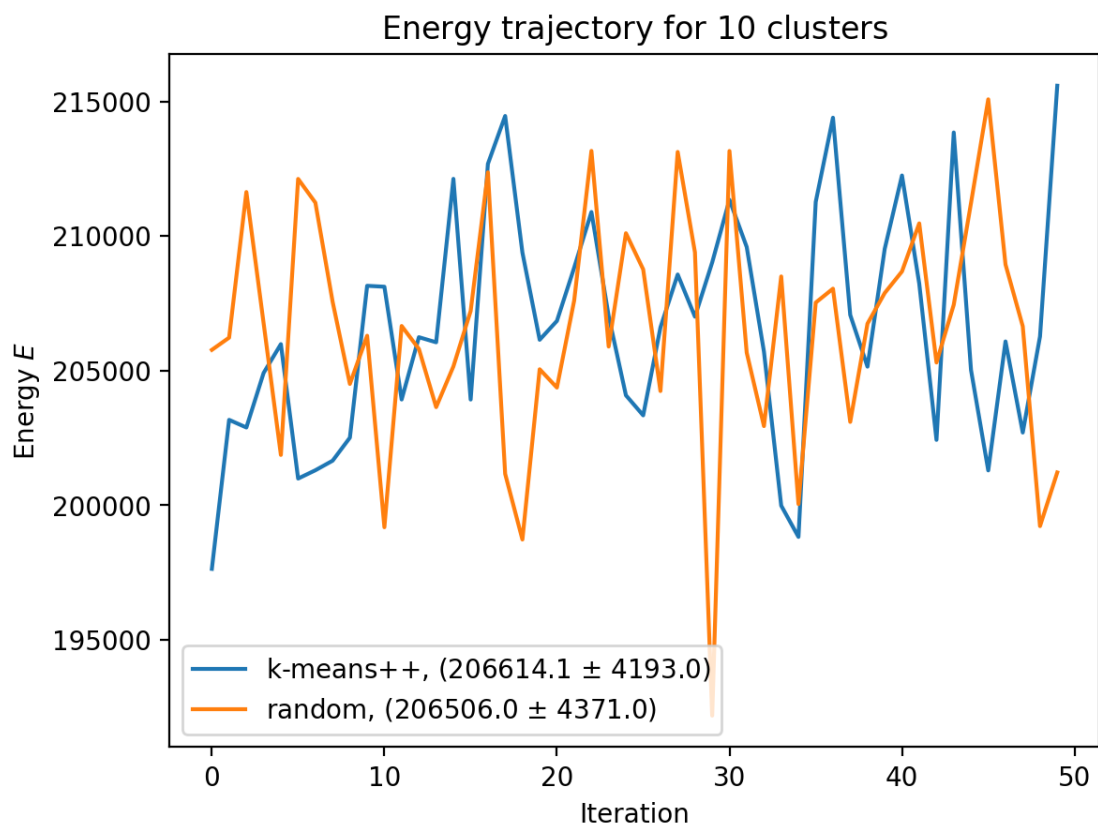
steps = 50
for k in [3, 5, 10, 20]:
    plt.figure(dpi=200)
    plt.title(f'Energy trajectory for ${k}$ clusters')
    plt.xlabel('Iteration')
    plt.ylabel('Energy $E$')
    for init in ['k-means++', 'random']:
        # TODO: for the given k and init, run k-means 20 times or more (using
        ↪ the kmeans function above)
        # and plot the resulting energy trajectories
        ergs = kmeans(features.T, k, steps)
        plt.plot(np.arange(steps), ergs, label = f"{init}, ({round(np.
        ↪ mean(ergs), 1)} $\pm$ {round(np.std(ergs), 1)})")
        plt.legend()
    plt.show()

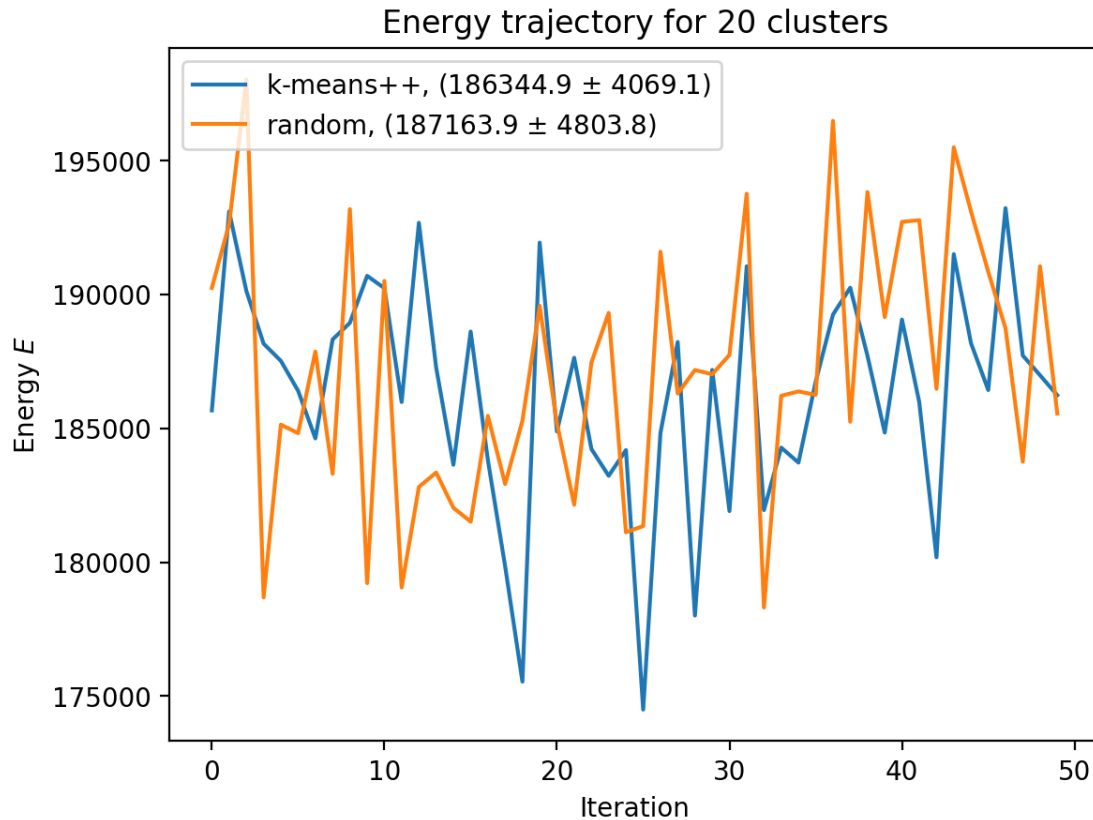
```











Overall, the energy decreases with a greater number of clusters. Regarding the formula for  $E$ , this makes sense: The more clusters we have, the more likely it is for a data point to be well represented by a cluster mean. This takes its extreme, when we assume as many cluster centers as data points, where cluster centers will converge to the individual data points. Therefore,  $E$  is no reasonable metric to minimize in order to obtain an optimal number of clusters  $k$  (Luckily, sklearn already warns us, that “the number of disting clusters is found smaller than the number of specified clusters”). We’ll illustrate this in the following plot. Apart from that, we do not really see any initialization to reliably perform better.

```
[51]: steps = 20
k = len(features.T)
plt.figure(dpi=200)
plt.title(f'Energy trajectory for ${k}$ clusters')
plt.xlabel('Iteration')
plt.ylabel('Energy $E$')
for init in ['k-means++', 'random']:
    # TODO: for the given k and init, run k-means 20 times or more (using the
    ↪ kmeans function above)
    # and plot the resulting energy trajectores
    ergs = kmeans(features.T, k, steps, early_stopping=False)
```

```
plt.plot(np.arange(steps), ergs, label = f"{init}, ({round(np.mean(ergs), 1)}
↳ 1)} $\pm$ {round(np.std(ergs), 1)}")
plt.legend()
plt.show()
```

```
/var/folders/hw/19lr0sdd3gs7l_vcxrgh9drm0000gn/T/ipykernel_51645/1854346151.py:3
9: ConvergenceWarning: Number of distinct clusters (2232) found smaller than
n_clusters (2233). Possibly due to duplicate points in X.
kmeans = single_step_kmeans.fit(x)
/var/folders/hw/19lr0sdd3gs7l_vcxrgh9drm0000gn/T/ipykernel_51645/1854346151.py:3
9: ConvergenceWarning: Number of distinct clusters (2231) found smaller than
n_clusters (2233). Possibly due to duplicate points in X.
kmeans = single_step_kmeans.fit(x)
/var/folders/hw/19lr0sdd3gs7l_vcxrgh9drm0000gn/T/ipykernel_51645/1854346151.py:3
9: ConvergenceWarning: Number of distinct clusters (2232) found smaller than
n_clusters (2233). Possibly due to duplicate points in X.
kmeans = single_step_kmeans.fit(x)
/var/folders/hw/19lr0sdd3gs7l_vcxrgh9drm0000gn/T/ipykernel_51645/1854346151.py:3
9: ConvergenceWarning: Number of distinct clusters (2232) found smaller than
n_clusters (2233). Possibly due to duplicate points in X.
kmeans = single_step_kmeans.fit(x)
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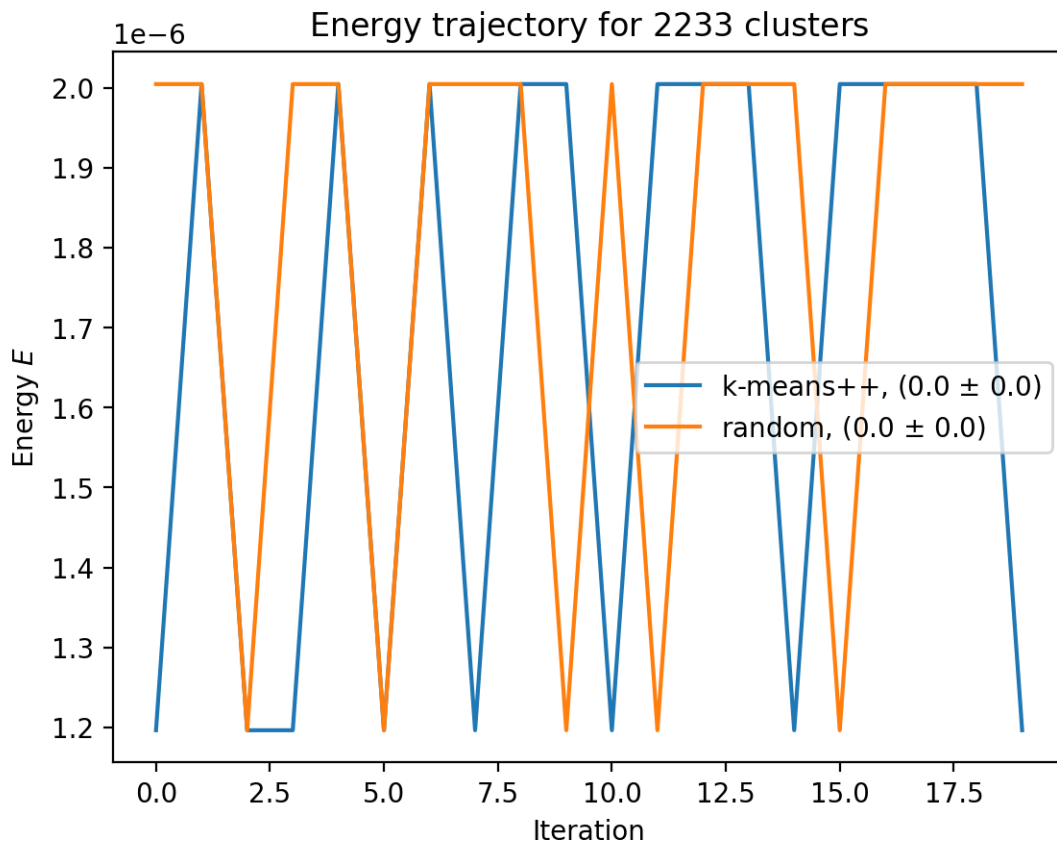
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```



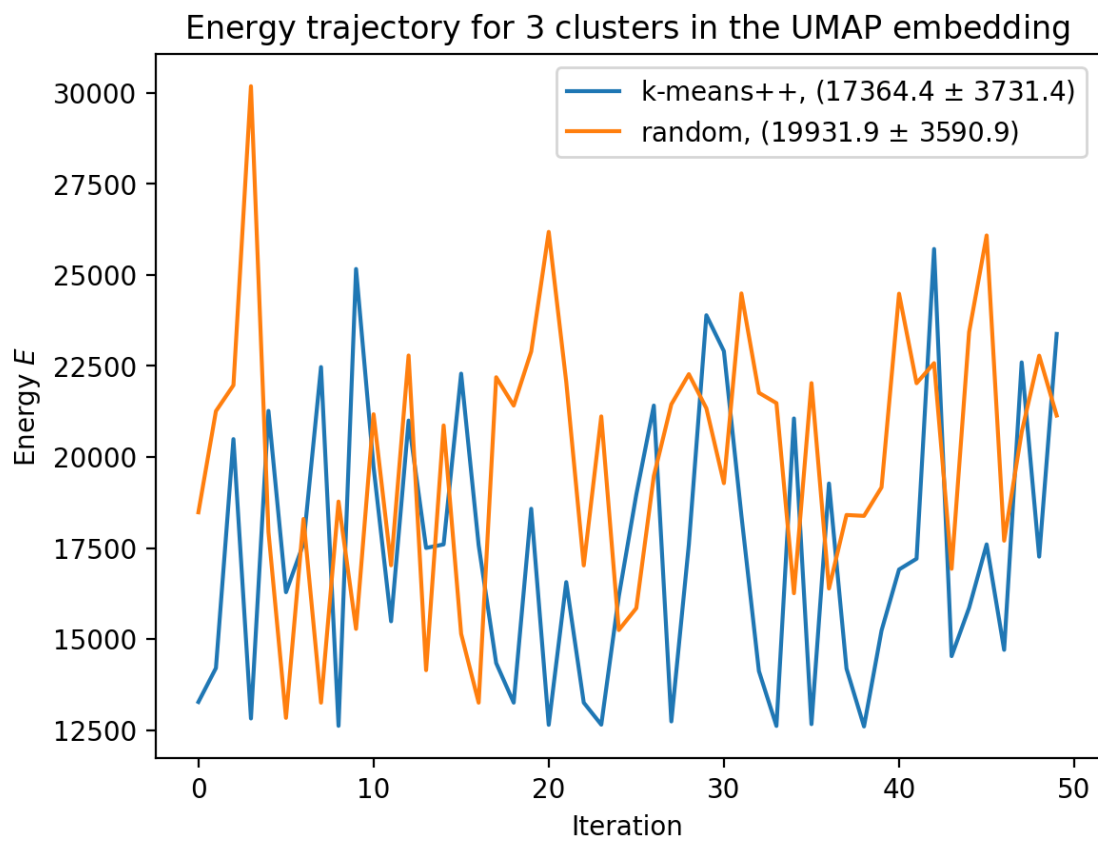
We'll now do the same for the UMAP data.

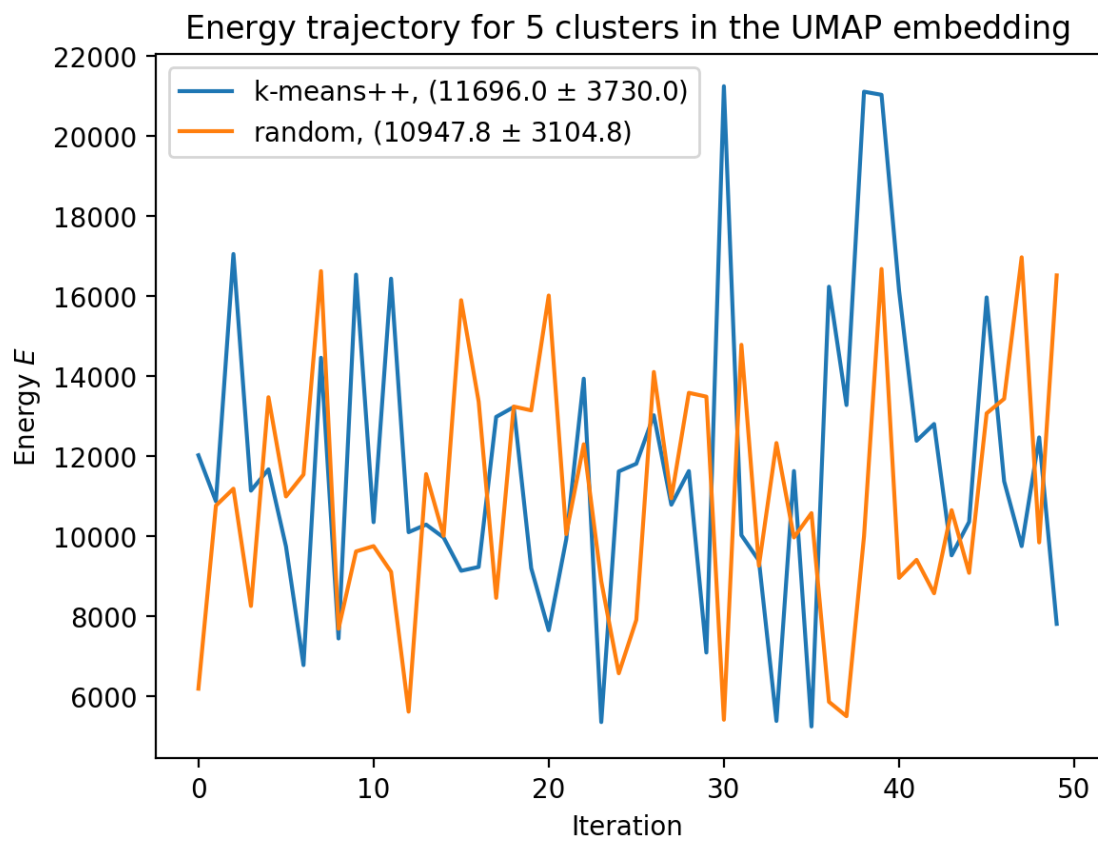
```
[49]: features = np.load('data/dijet_features_umap.npy')      # umap projection  
  
print(f'{features.shape=}')
```

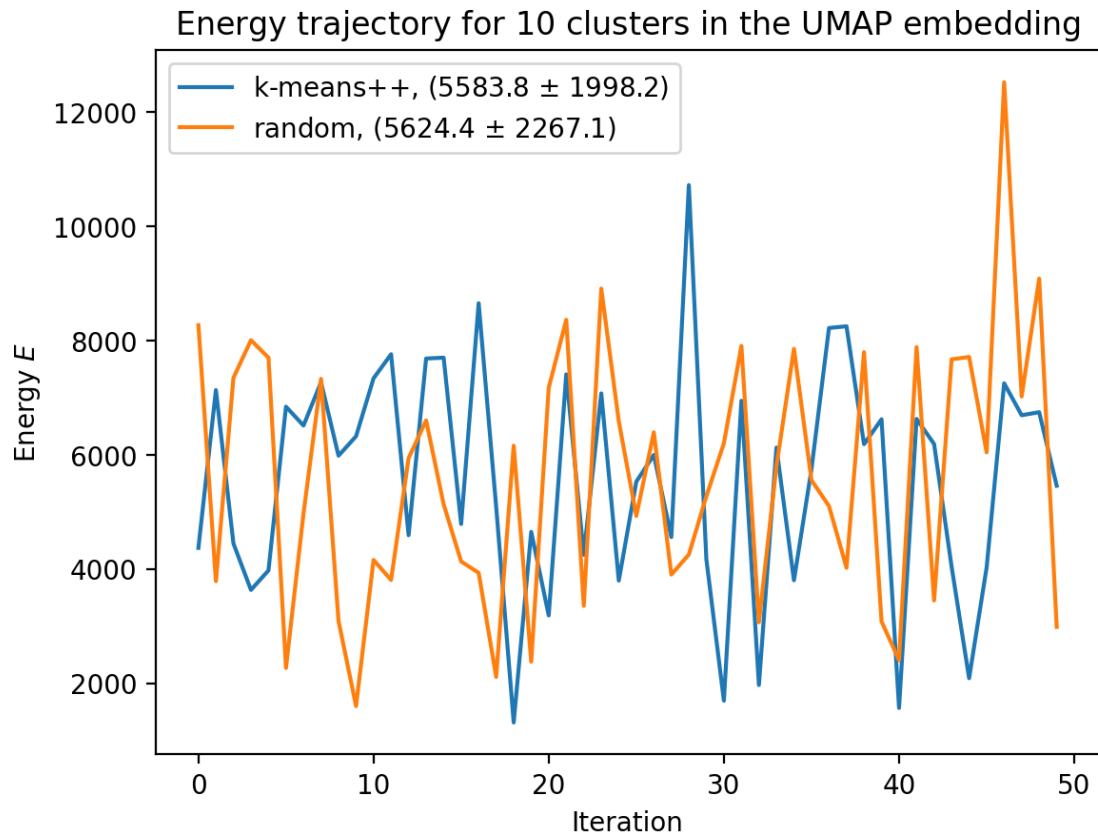
features.shape=(2, 2233)

```
[50]: steps = 50  
for k in [3, 5, 10, 20]:  
    plt.figure(dpi=200)  
    plt.title(f'Energy trajectory for ${k}$ clusters in the UMAP embedding')  
    plt.xlabel('Iteration')  
    plt.ylabel('Energy $E$')  
    for init in ['k-means++', 'random']:  
        # TODO: for the given k and init, run k-means 20 times or more (using  
        ↪ the kmeans function above)  
        # and plot the resulting energy trajectories  
        ergs = kmeans(features.T, k, steps)  
        plt.plot(np.arange(steps), ergs, label = f"{init}, ({round(np.  
        ↪ mean(ergs), 1)} $\pm$ {round(np.std(ergs), 1)})")  
        plt.legend()  
    plt.show()
```

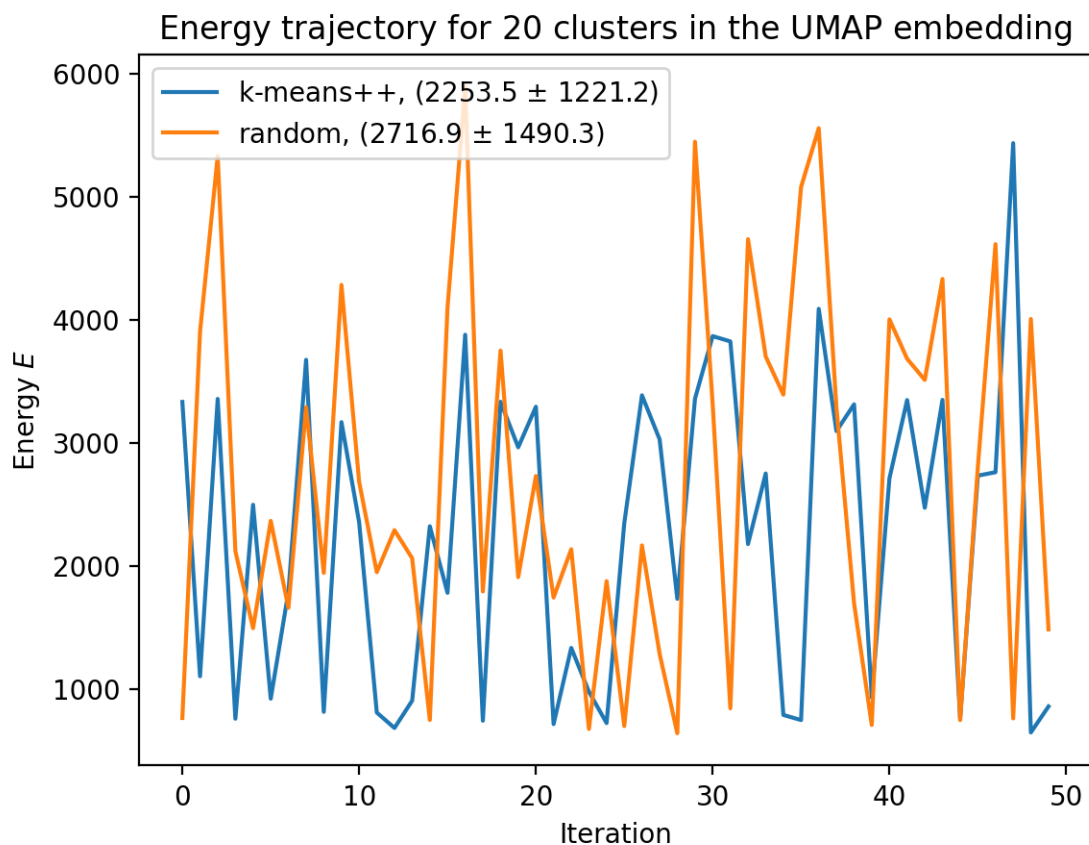








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/var/folders/hw/19lr0sdd3gs7l_vcxrgh9drm0000gn/T/ipykernel_51645/1854346151.py:3
9: ConvergenceWarning: Number of distinct clusters (19) found smaller than
n_clusters (20). Possibly due to duplicate points in X.
kmeans = single_step_kmeans.fit(x)
```



The 2D UMAP embeddings generally cluster better (lower energy), probably as they do not suffer from the curse of dimensionality. The  $L_2$  norm in the energy function works much better in 2 dimensions than in higher ones since the ratio between the farthest and nearest points approach unity in high dimensions (On the Surprising Behavior of Distance Metrics in High Dimensional Space).