Data Science Fundamentals 5

Basic introduction on how to perform typical machine learning tasks with Python.

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Part 3.

In [0]:
```
from sklearn.datasets import make_blobs
from sklearn.model_selection import train_test_split
from sklearn import metrics
from sklearn.mixture import GaussianMixture

from sklearn.cluster import KMeans
from sklearn.metrics import silhouette_score

from matplotlib import  pyplot as plt
import numpy as np
import pandas as pd
from imageio import imread
from time import time as timer
import os

import tensorflow as tf

%matplotlib inline
from matplotlib import animation
from IPython.display import HTML

import umap
from scipy.stats import entropy
```

In [2]:
```
if not os.path.exists('data'):
    path = os.path.abspath('.')+'/colab_material.tgz'
    tf.keras.utils.get_file(path, 'https://github.com/neworldemancer/DSF
5/raw/master/colab_material.tgz')
    !tar -xvzf colab_material.tgz > /dev/null 2>&1
```

```
Downloading data from https://github.com/neworldemancer/DSF5/raw/master/c
olab_material.tgz
98304/96847 [==============================] - 0s 0us/step
```

In [0]:
```
from utils.routines import *
```

1. Clustering

1. K-Means

Theory overview.

Objective: clustering techniques divide the set of data into group of atoms having common features. Each data point p gets assigned a label $l_p \in \{1, .., K\}$. In this presentation the data points are supposed to have D features, i.e. each data point belongs to $\mathbf{R}^D$.

Methods: We call P_k the subset of the data set which gets assigned to class k. K-means aims at minimizing the objective function:

$$L = \sum_k L_k$$

$$L_k = \frac{1}{|P_k|} \sum_{p,p' \in L_k} |\mathbf{x}_p - \mathbf{x}_{p'}|^2$$

One could enumerate all possibilities. The Llyod algorithm is iterative:

- start with an initial guess of the assignements ;
- compute the centroid $\mathbf{c}_k$ for every cluster, defined as:
$$\mathbf{c}_k = \frac{1}{|P_k|} \sum_{p \in L_k} \mathbf{x}_\mathbf{p}$$
- re-assign each data point to the class of the nearest centroid
- re-compute the centroids and iterate till convergence

The Lloyd algorithm finds local minima and may need to be started several times with different initializations.

Terminology and output of a K-means computation:

- *Within-cluster variation* : L_k is called within cluster variation. It can be shown that L_k can be interpreted as the sum os squared variation with respect to the centroid
- *Silhouette score*: K-means clustering fixes the number of clusters a priori. Some tecnhique must be chosen to score the different optimal clusterings for different k. One technique chooses the best *Silouhette score*

Sklearn: implementation and usage of K-means.

We start with a 2D example that can be visualized.

First we load the data-set.

In [0]:
```
points=km_load_th1()
```

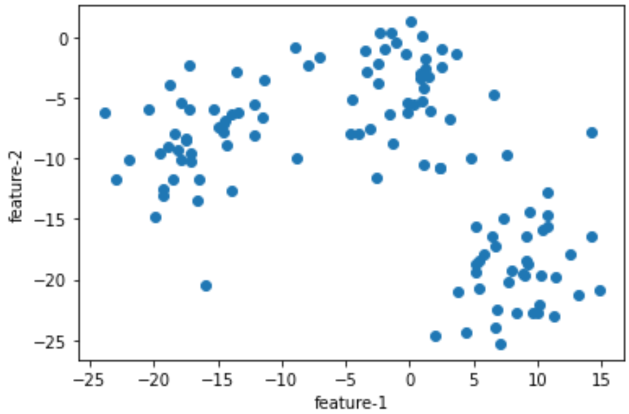
Explore the data-set checking the dataset dimensionality.

In [5]:
```
print(points.shape)
print('We have ', points.shape[0], 'points with two features')
```

```
(120, 2)
We have  120 points with two features
```

In [6]:
```
plt.plot(points[:,0],points[:,1],'o')
plt.xlabel('feature-1')
plt.ylabel('feature-2')
```

Out[6]: Text(0, 0.5, 'feature-2')



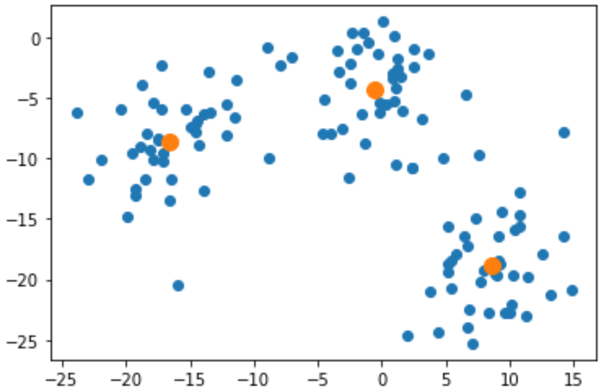
It looks visually that the data set has three clusters. We will cluster them using K-means. As usual, we create a KMeans object. Note that we do not need to initialize it with a data-set.

In [0]:
```
clusterer = KMeans(n_clusters=3, random_state=10)
```

A call to the fit method computes the cluster centers which can be plotted alongside the data-set. They are accessible from the cluster*centers* attribute:

In [8]:
```
clusterer.fit(points)
plt.plot(points[:,0],points[:,1],'o')
plt.plot(clusterer.cluster_centers_[:,0],clusterer.cluster_centers_[:,
1],'o',markersize=10)
```

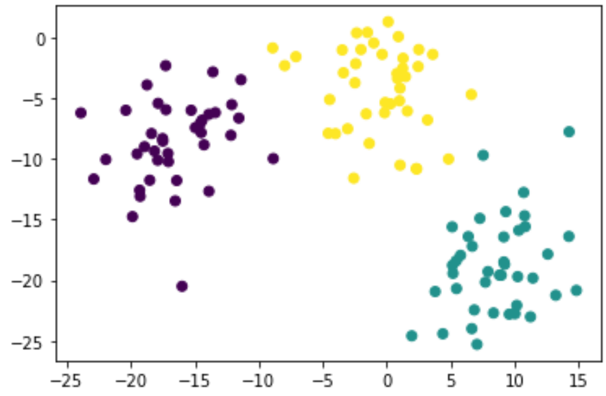
Out[8]: [<matplotlib.lines.Line2D at 0x7fa6eba4e1d0>]



The predict method assigns a new point to the nearest cluster. We can use predict with the training dataset and color the data-set according to the cluster label.

In [9]:
```
cluster_labels=clusterer.predict(points)
plt.scatter(points[:,0],points[:,1],c=cluster_labels)
```

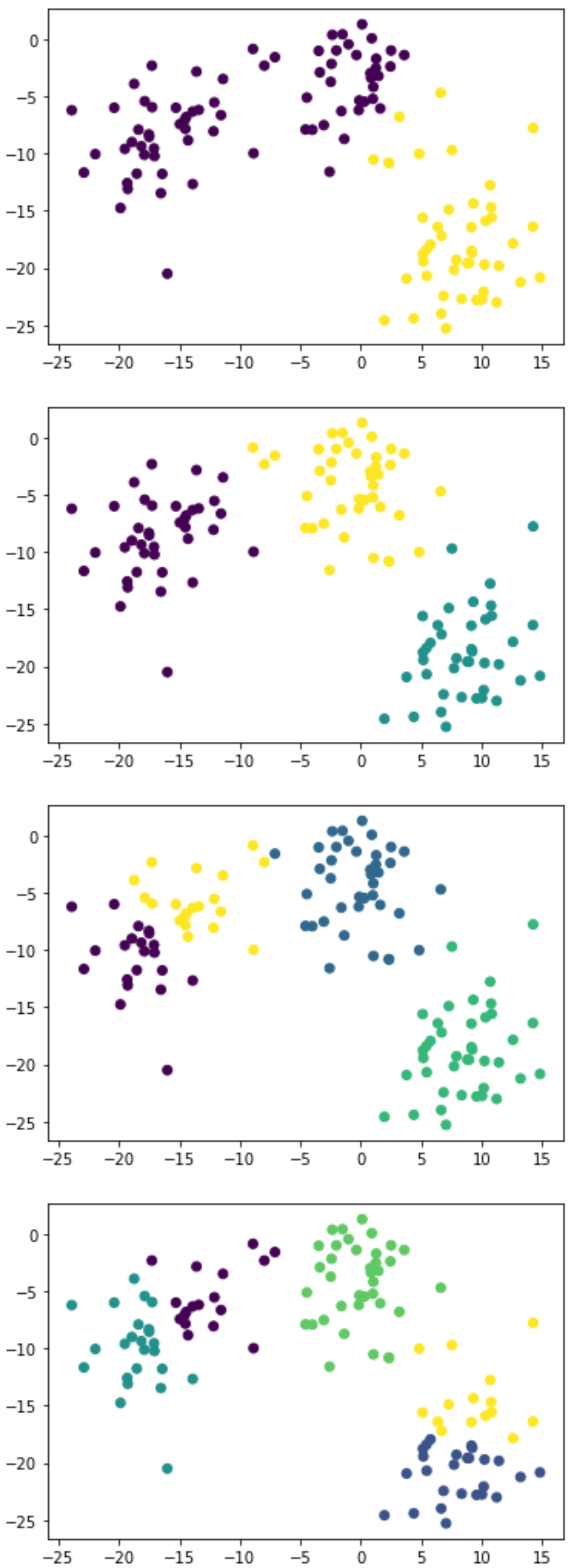
Out[9]: <matplotlib.collections.PathCollection at 0x7fa680121828>

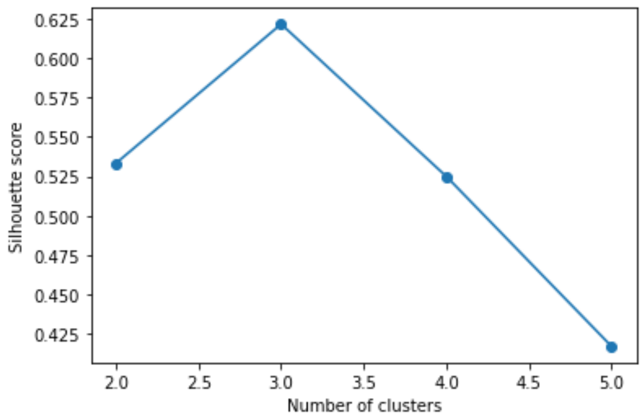


Finally, we can try to vary the number of clusters and score them with the Silhouette score.

In [10]:
```
sil=[]

for iclust in range(2,6):
    clusterer = KMeans(n_clusters=iclust, random_state=10)
    cluster_labels = clusterer.fit_predict(points)
    score=silhouette_score(points,cluster_labels)
    sil.append(score)
    plt.figure()
    plt.scatter(points[:,0],points[:,1],c=cluster_labels)

plt.figure()
plt.xlabel('Number of clusters')
plt.ylabel('Silhouette score')
plt.plot(np.arange(len(sil))+2, sil,'-o')
```

```
Out[10]: [<matplotlib.lines.Line2D at 0x7fa6812c2ac8>]
```





The same techniques can be used on high dimensional data-sets. We use here the famoust MNIST dataset for integer digits, that we are downloading from tensorflow.

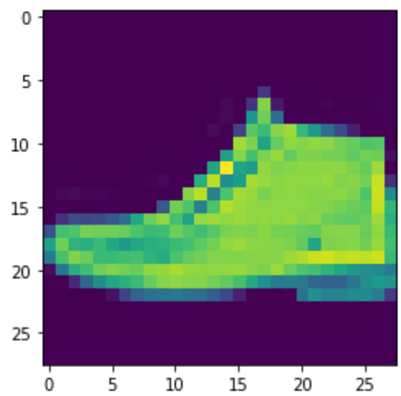
In [11]:
```
fmnist = tf.keras.datasets.fashion_mnist
(train_images, train_labels), (test_images, test_labels) = fmnist.load_d
ata()

X=train_images[:5000,:].reshape(5000,-1)
```

```
Downloading data from https://storage.googleapis.com/tensorflow/tf-keras-
datasets/train-labels-idx1-ubyte.gz
32768/29515 [=================================] - 0s 0us/step
Downloading data from https://storage.googleapis.com/tensorflow/tf-keras-
datasets/train-images-idx3-ubyte.gz
26427392/26421880 [==============================] - 0s 0us/step
Downloading data from https://storage.googleapis.com/tensorflow/tf-keras-
datasets/t10k-labels-idx1-ubyte.gz
8192/5148 [===============================================] - 0s 0us/step
Downloading data from https://storage.googleapis.com/tensorflow/tf-keras-
datasets/t10k-images-idx3-ubyte.gz
4423680/4422102 [==============================] - 0s 0us/step
```

In [12]:
```
print(X.shape)
image=X[1232,:].reshape(28,28)
plt.imshow(image)
```

```
(5000, 784)
```

Out[12]: <matplotlib.image.AxesImage at 0x7fa68175f9b0>

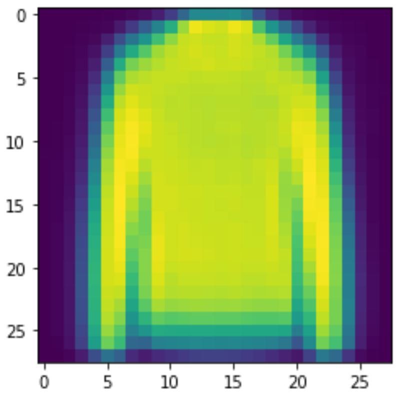


We can cluster the images exactly as we did for the 2d dataset.

In [0]:
```
clusterer = KMeans(n_clusters=10, random_state=10)
cluster_labels = clusterer.fit_predict(X)
```

We can plot the cluster centers (wich are 2D figures!) to see if the clustering is learning correct patterns!

In [14]:
```
for iclust in range(10):
    plt.figure()
    plt.imshow(clusterer.cluster_centers_[iclust].reshape(28,28))
```


0
5
10
15
20
25
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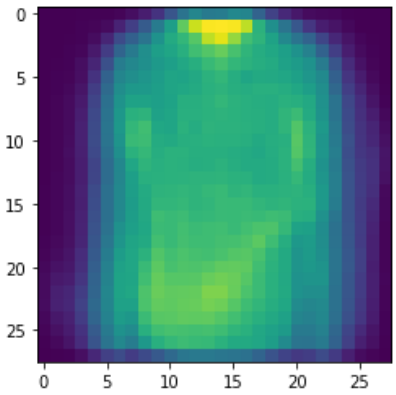
10
15
20
25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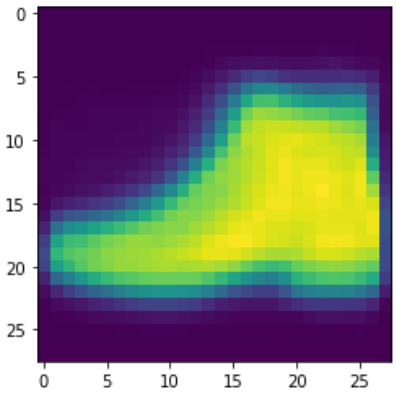
0
5
10
15
20
25
0
5
10
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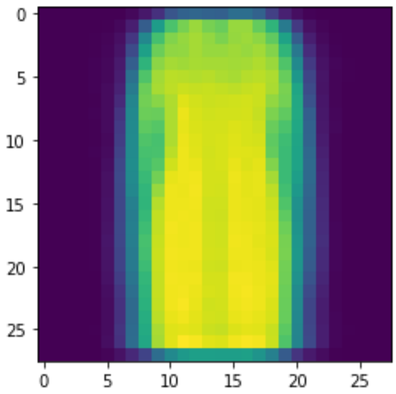
20
25


0
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20
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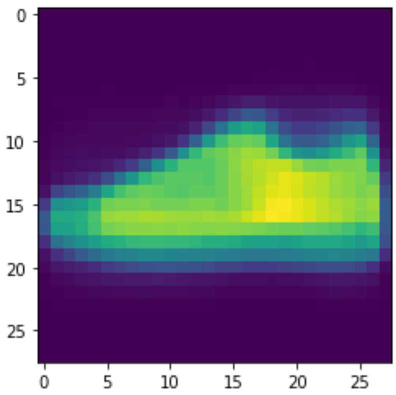
0
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20
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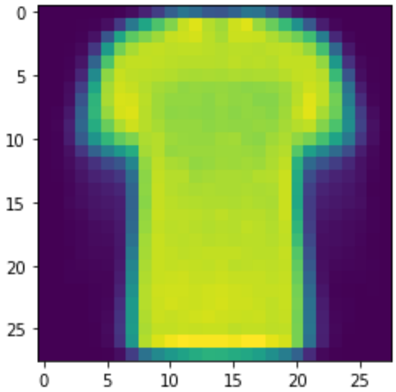
0 5 10 15 20 25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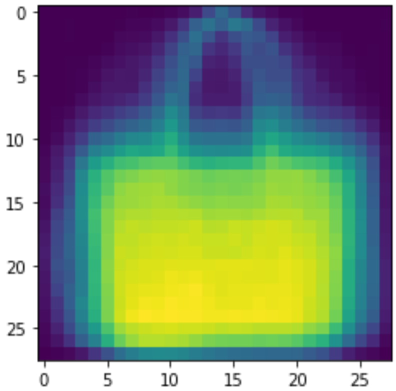
0 5 10 15 20 25


0
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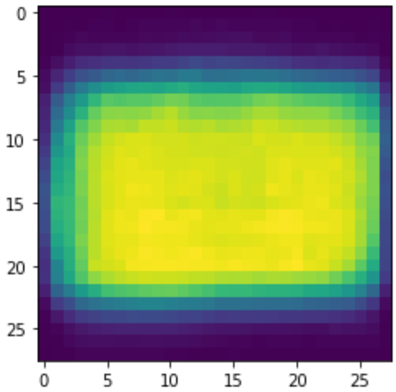
0 5 10 15 20 25


0
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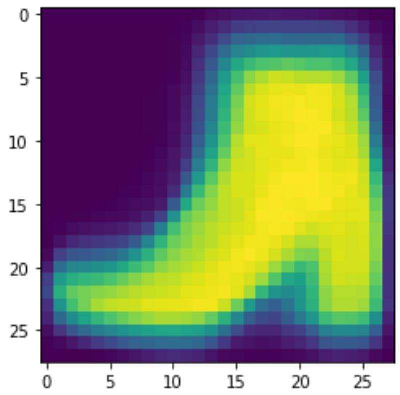
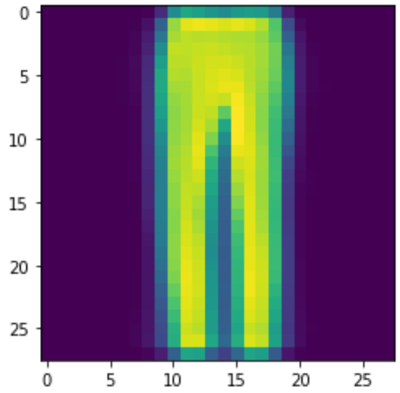
0 5 10 15 20 25





You can see that the model looks to assign one class to the same good. Nevertheless, using the cluster centers and with a further trick, in exercise 2 you will build a digit recognition model !

EXERCISE 1: Discover the number of Gaussians

In [0]:
```
### In this exercise you are given the dataset points, consisting of high-dimensional data. It was built taking random
#samples from a number k of multimensional gaussians. The data is therefore made of k clusters but, being
#very high dimensional, you cannot visualize it. Your task it too use K-means combined with the Silouhette
#score to find the number of k.

# 1. Load the data using the function load_ex1_data_clust() , check the dimensionality of the data.

# 2. Fix a number of clusters k and define a KMeans clusterer object. Perform the fitting and compute the Silhouette score.
# Save the results on a list.

# 3. Plot the Silhouette scores as a function ok k? What is the number of clusters ?

# 4. Optional. Check the result that you found via umap.
```

EXERCISE 2: Predict the good using K-Means

In [0]:
```
#In this exercise you are asked to use the clustering performed by K-mea
ns to predict the good in the f-mnist dataset.
#Here we are using the clustering as a preprocessing for a supervised ta
sk. We need therefore the correct labels
#on a training set and #o test the result on a test set:

# 1. Load the dataset.

#fmnist = tf.keras.datasets.fashion_mnist
#(train_images, train_labels), (test_images, test_labels) = fmnist.load_
data()

#X_train=train_images[:5000,:].reshape(5000,-1)
#y_train=train_labels[:5000]

#X_test=test_images[:1000,:].reshape(1000,-1)
#y_test=test_labels[:1000]


# 2. FITTING STEP: The fitting step consists first here in the computati
on of the cluster center, which was done during
# the presentation. Second, to each cluster center we need than to assig
n a good-label, which will be given by the
# majority class of the sample belonging to that cluster.
#
# You can use, if you want, the helper function most_common for this pur
pose.
#
# In detail you should.
# - fix a number of clusters (start with k=10) and define the cluster KM
eans object. fit the model on the training set
# using the fit method
# - call the predict method of the KMeans object you defined on the trai
ning set and compute the cluster labels.
# Call them cluster_labels
# - use the function most_common with arguments (k,y_train, cluster_labe
ls) to compute the assignement list.
#  assignement[i] will be the majority class of the i-cluster

def most_common(nclusters, supervised_labels, cluster_labels):

    """
    Args:
    - nclusters : the number of clusteres
    - supervised_labels : for each sample, the labelling provided by the
training data ( e.g. in y_train or y_test)
    - cluster_labels : for each good, the cluster it was assigned by K-M
eans using the predict method of the Kmeans object

    Returns:
    - a list "assignement" of lengths nclusters, where assignement[i] is
the majority class of the i-cluster
    """

    assignement=[]
    for icluster in range(nclusters):
        indices=list(supervised_labels[cluster_labels==icluster])
        try:
            chosen= max(set(indices), key=indices.count)
        except ValueError :
            print('Em')
            chosen=1
        assignement.append(chosen)

    return assignement


# 3. Using the assignment list and the clusterer, check the performance
```

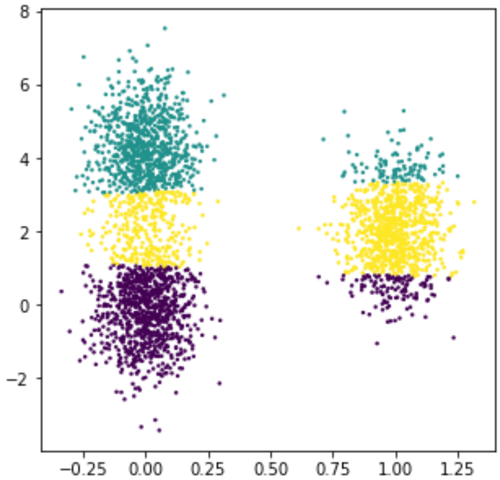
2. Gaussian mixtures

Theory overview.

K-Means is a modelling procedure which is biased towards clusters of circular shape and therefore does not always work perfectly, as the following examples show:

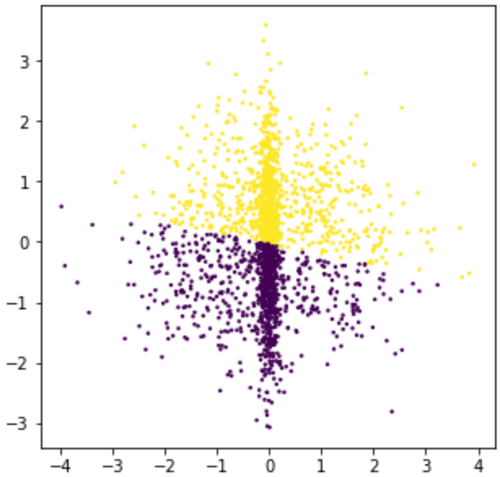
In [19]:
```
points=gm_load_th1()
clusterer = KMeans(n_clusters=3, random_state=10)
cluster_labels=clusterer.fit_predict(points)
plt.figure(figsize=(5,5))
plt.scatter(points[:,0],points[:,1],c=cluster_labels, s=2)
```

Out[19]: <matplotlib.collections.PathCollection at 0x7fa67d6ed390>



In [20]:
```
points=gm_load_th2()
clusterer = KMeans(n_clusters=2, random_state=10)
cluster_labels=clusterer.fit_predict(points)
plt.figure(figsize=(5,5))
plt.scatter(points[:,0],points[:,1],c=cluster_labels, s=2)
```

Out[20]: <matplotlib.collections.PathCollection at 0x7fa67bfefef0>



A Gaussian mixture model is able to fit these kinds of clusters. In a Gaussian mixture model each data-set is supposed to be a random point from the distribution:

$$f(\mathbf{x}) = \sum_c \pi_c N(\mu_\mathbf{c}, \mathbf{\Sigma_c})(\mathbf{x})$$

, which is called a Gaussian mixture. The parameters $\{\pi_c, \mu_\mathbf{c}, \mathbf{\Sigma_c}\}$ are fitted from the data using a minimization procedure (maximum likelyhood via the EM algorithm) and N_c is the chosen number of clusters.

Output of a GM computation:

- *Cluster probabilities:* A gaussian mixtures model is an example of soft clustering, where each data point p does not get assigned a unique cluser, but a distribution over clusters $f_p(c), c = 1, \ldots, N_c$.

Given the fitted parameters, $f_p(c)$ is computed as:

$$f_p(c) = \frac{\pi_c N(\mu_\mathbf{c}, \mathbf{\Sigma_c})(\mathbf{x_p})}{\sum_c \pi_c N(\mu_\mathbf{c}, \mathbf{\Sigma_c})(\mathbf{x_p})}, c = 1 \ldots N_c$$

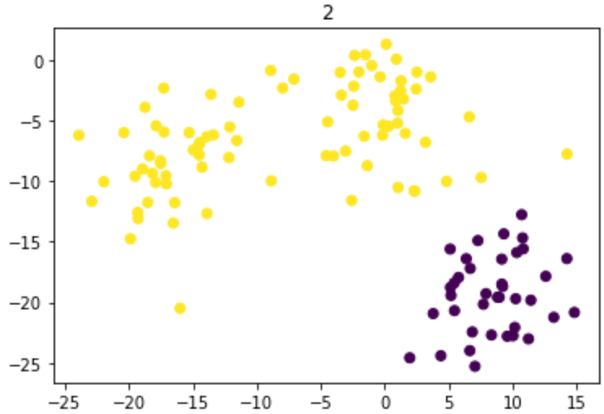
- *AIC/BIC:* after each clustering two numbers are returned. These can be used to select the optimal number of Gaussians to be used, similar to the Silhouette score. (AIC and BIC consider both the likelihood of the data given the parameters and the complexity of the model related to the number of Gaussians used). The lowest AIC or BIC value is an indication of a good fit.

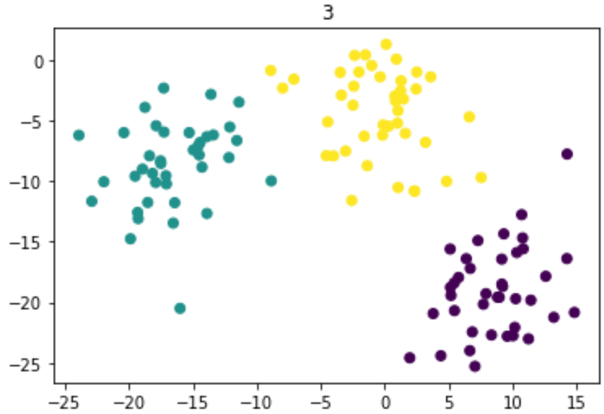
Sklearn: implementation and usage of Gaussian mixtures

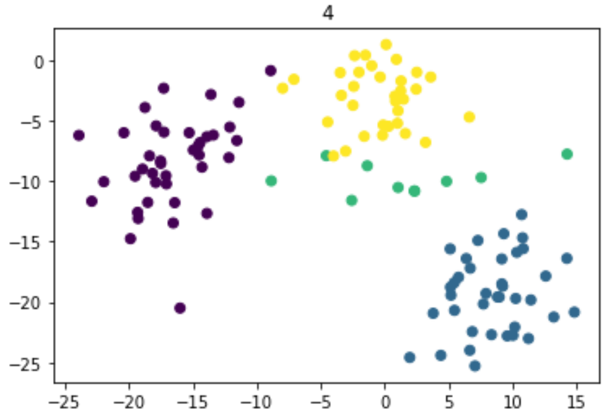
First of all we see how the Gaussian model behaves on our original example:

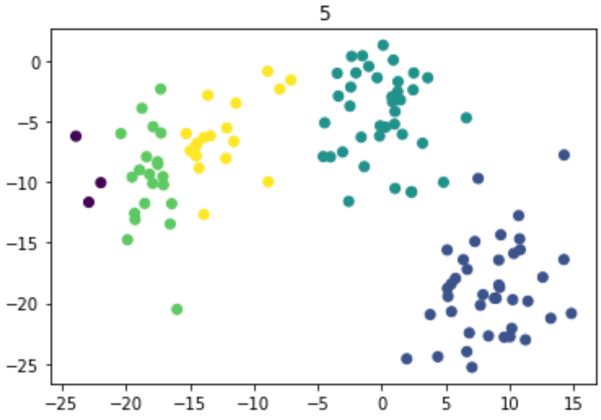
In [21]:
```
points=km_load_th1()

aic=[]
bic=[]
sil=[]

for i_comp in range(2,6):
    plt.figure()
    plt.title(str(i_comp))
    clf = GaussianMixture(n_components=i_comp, covariance_type='full')
    clf.fit(points)
    cluster_labels=clf.predict(points)
    plt.scatter(points[:,0],points[:,1],c=cluster_labels)
    print(i_comp,clf.aic(points),clf.bic(points))
    score=silhouette_score(points,cluster_labels)
    aic.append(clf.aic(points))
    bic.append(clf.bic(points))
    sil.append(score)
```

```
2 1592.1418091070063 1622.804218277609
3 1550.4974051432473 1597.884764770542
4 1553.5290520513045 1617.6413621352915
5 1560.815736563503 1641.6529971041823
```

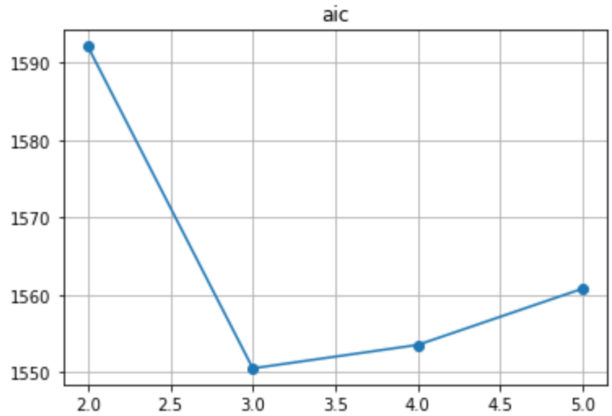


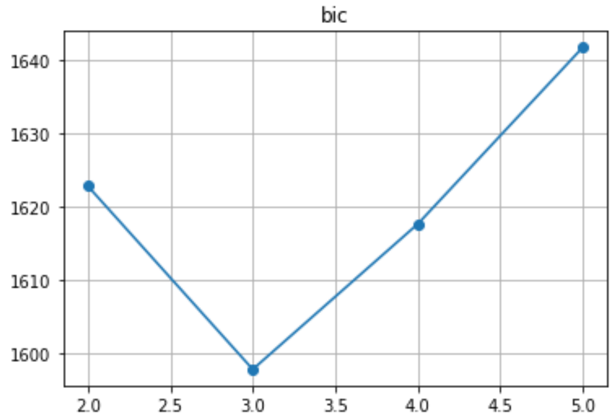


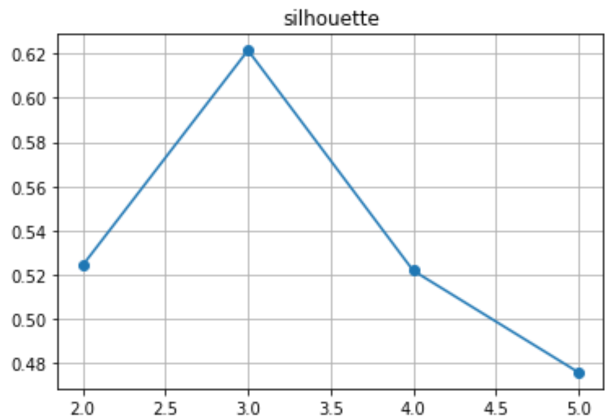



5
0
-5
-10
-15
-20
-25
-25 -20 -15 -10 -5 0 5 10 15

In [22]:
```
plt.plot(np.arange(2,6),aic,'-o')
plt.title('aic')
plt.grid()
plt.figure()
plt.plot(np.arange(2,6),bic,'-o')
plt.title('bic')
plt.grid()
plt.figure()
plt.plot(np.arange(2,6),sil,'-o')
plt.title('silhouette')
plt.grid()
```



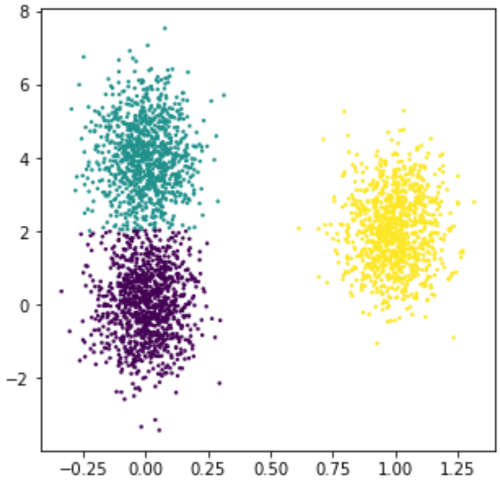




So in this case we get a comparable results, and also the probabilistic tools agree with the Silhouette score ! Let's see how the Gaussian mixtures behave in the examples where K-means was failing.

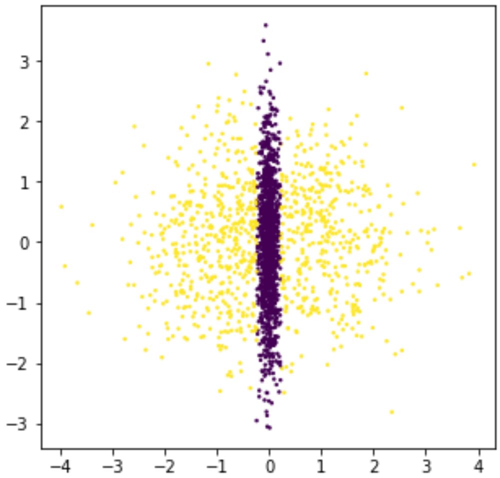
In [23]:
```
points=gm_load_th1()
clf = GaussianMixture(n_components=3, covariance_type='full')
clf.fit(points)
cluster_labels=clf.predict(points)
plt.figure(figsize=(5,5))
plt.scatter(points[:,0],points[:,1],c=cluster_labels, s=2)
```

Out[23]: `<matplotlib.collections.PathCollection at 0x7fa67bfc72e8>`



In [24]:
```
points=gm_load_th2()
clf = GaussianMixture(n_components=2, covariance_type='full')
clf.fit(points)
cluster_labels=clf.predict(points)
plt.figure(figsize=(5,5))
plt.scatter(points[:,0],points[:,1],c=cluster_labels, s=2)
```

Out[24]: `<matplotlib.collections.PathCollection at 0x7fa67bacf3c8>`



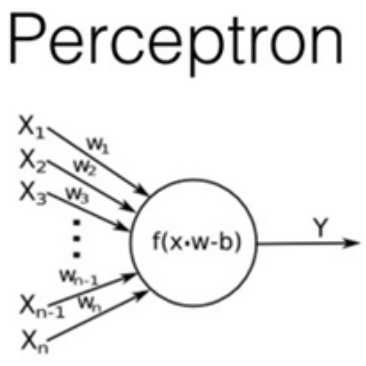
EXERCISE 3 : Find the prediction uncertainty

In [0]:
```
#In this exercise you need to load the dataset used to present K-means (
def km_load_th1() ) or the one used to discuss
# the Gaussian mixtures model ( def km_load_th1() ).
#As discussed, applying a fitting based on gaussian mixtures you can not
only predict the cluster label for each point,
#but also a probability distribution over the clusters.

#From this probability distribution, you can compute for each point the
entropy of the corresponging
#distribution (using for example scipy.stats.entropy) as an estimation o
f the undertainty of the prediction.
#Your task is to plot the data-cloud with a color proportional to the un
certainty of the cluster assignement.

# In detail you shoud:
# 1. Instantiate a GaussianMixture object with the number of clusters th
at you expect
# 2. fit the object on the dataset with the fit method
# 3. compute the cluster probabilities using the method predict_proba. T
his will return a matrix of dimension
# npoints x nclusters
# 4. use the entropy function ( from scipy.stats import entropy ) to eva
luate for each point the uncertainty of the prediction
# 5. Plot the points colored accordingly to their uncertanty. You can us
e for example the code

#cm = plt.cm.get_cmap('RdYlBu')
#plt.scatter(x, y, c=colors, cmap=cm)
#plt.colorbar(sc)

# where colors is the list of entropies computed.
```

2. Neural Networks Introduction

1. Perceptron

(Artificial) Neural network consists of layers of neurons. Artificial neuron, or perceptron, is in fact inspired by a biological neuron.



Such neuron first calculates the linear transformation of the input vector $\bar{x}$:

$$z = \bar{W} \cdot \bar{x} + b = \sum W_i x_i + b$$

where $\bar{W}$ is vector of weights and b - bias.

2. Nonlinearity

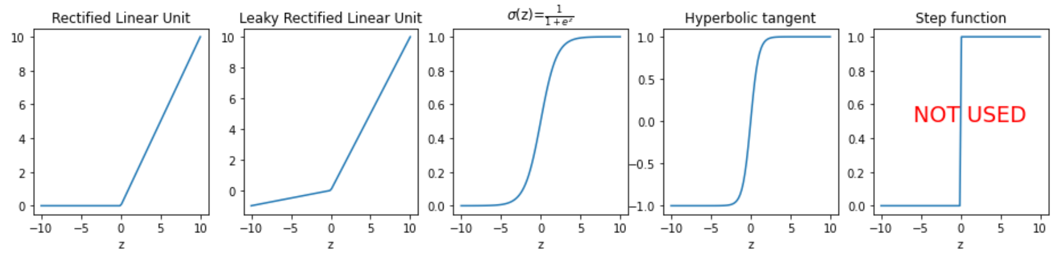
Combining multiple of such objects performing linear transformation would not bring any additional benefit, as the combined output would still be a linear combination of the inputs.

What gives actual power to neurons, is that they additionally perform the nonlinear transformation of the result using activation function f

$$y = f(z)$$

The most commonly used non-linear transformations are:

In [27]:
```
def ReLU(z):
  return np.clip(z, a_min=0, a_max=np.max(z))
def LReLU(z, a=0.1):
  return np.clip(z, a_min=0, a_max=np.max(z)) + np.clip(z, a_min=np.min
(z), a_max=0) * a
def sigmoid(z):
  return 1/(1 + np.exp(-z))
def step(z):
  return np.heaviside(z, 0)
fig, ax = plt.subplots(1, 5, figsize=(16, 3))
z = np.linspace(-10, 10, 100)
ax[0].plot(z, ReLU(z))
ax[0].set_title('Rectified Linear Unit')
ax[1].plot(z, LReLU(z))
ax[1].set_title('Leaky Rectified Linear Unit')
ax[2].plot(z, sigmoid(z))
ax[2].set_title(r'$\sigma$(z)=$\frac{1}{1+e^z}$')
ax[3].plot(z, np.tanh(z))
ax[3].set_title('Hyperbolic tangent');
ax[4].plot(z, step(z)
)
ax[4].text(-6, 0.5, 'NOT USED', size=19, c='r')
ax[4].set_title('Step function');
for axi in ax:
  axi.set_xlabel('z')
```



And the reason we don't use a simple step function, is that it's not differentiable or it's derivative is zero everywhere.

The last nonlinearity to mention here is *softmax*:

$$y_i = Softmax(\bar{z})_i = \frac{e^{z_i}}{\sum_j e^{z_j}}$$

While each z_i can hav any value, the corresponding $y_i \in [0, 1]$, and $\sum_i y_i = 1$, just like probabilities!

While these y_i are only pseudo-probabilities, this nonlinearity allowes one to model probabilities, e.g. of a data-point belonging to a certain class.

3. Fully connected net

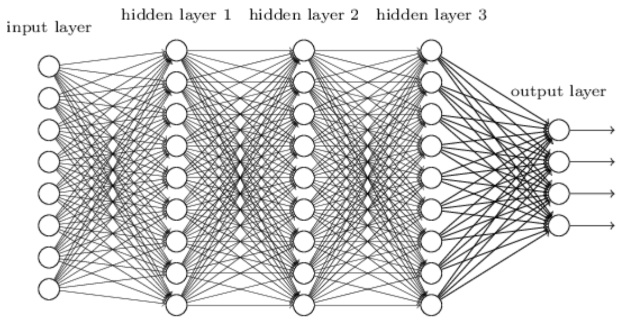
In a fully connected neural network each layer is a set of N neurons, performing different transformations of all the same layer's inputs $\bar{x} = [x_i]$ producing output vector $\bar{y} = [y_j]_{i=1..N}$:

$$y_j = f(\bar{W}_j \cdot \bar{x} + b_j)$$

Since output of each layer forms input of next layer, one can write for layer l:

$$x^l_j = f(\bar{W}^l_j \cdot \bar{x}^{l-1} + b^l_j)$$

where $\bar{x}^0$ is network's input vactor.



4. Loss function

The last part of the puzzle is the measure of network performance, which is used to optimize the network's parameters W^l_j and b^l_j. Denoting the network's output for an input x_i as $\hat{y}_i = \hat{y}_i(x_i)$ and given the label y_i:

1. In case of regression loss shows "distance" from target values:
2. L2 (MSE): $L = \sum_i (y_i - \hat{y}_i)^2$
3. L1 (MAE): $L = \sum_i |y_i - \hat{y}_i|$
4. In case of classification we can use cross-entropy, which shows "distance" from target distribution:

$$L = -\sum_i \sum_c y_{i,c} \log(\hat{y}_{i,c})$$

Here $\hat{y}_{i,c}$ - pseudo-probability of x_i belinging to class c and $y_{i,c}$ uses 1-hot encoding:

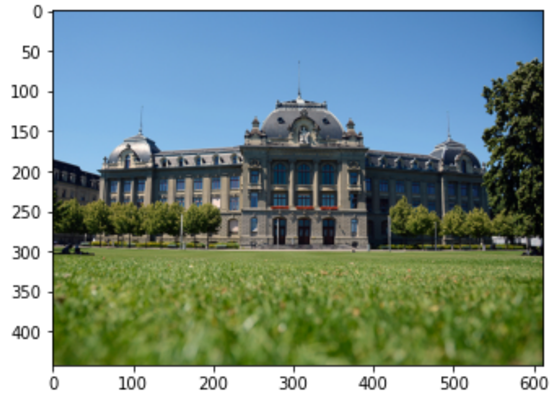
$$y_{i,c} = \begin{cases} 1, & \text{if } x_i \text{ belongs to class } c \\ 0, & \text{otherwise} \end{cases}$$

3. Regression with neural network

Here we will build a neural network to fit an image.

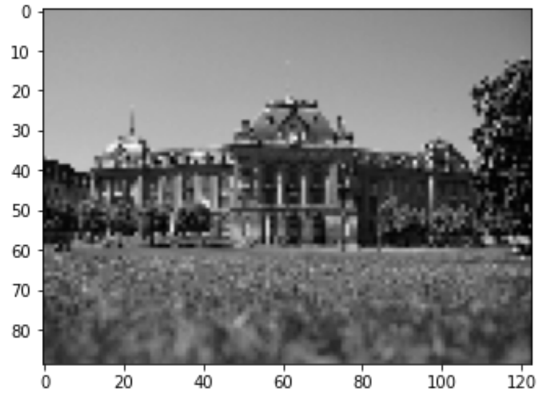
In [28]:
```
image_big = imread('https://www.unibe.ch/unibe/portal/content/carousel/s
howitem940548/UniBE_Coronavirus_612p_eng.jpg')
image_big = image_big[...,0:3]/255
plt.imshow(image_big)
```

Out[28]: <matplotlib.image.AxesImage at 0x7fa6816a3668>



In [29]:
```
image = image_big[::5, ::5]
image = image.mean(axis=2, keepdims=True)
plt.imshow(image[...,0], cmap='gray')
```

Out[29]: <matplotlib.image.AxesImage at 0x7fa68101ca90>



In [0]:
```
h, w, c = image.shape
```

In [31]:
```
X = np.meshgrid(np.linspace(0, 1, w), np.linspace(0, 1, h))
X = np.stack(X, axis=-1).reshape((-1, 2))

Y = image.reshape((-1, c))
X.shape, Y.shape
```

Out[31]: ((10947, 2), (10947, 1))

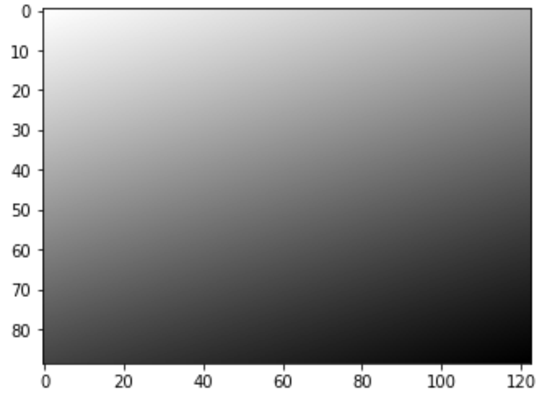
In [32]:
```
model = tf.keras.models.Sequential([
  tf.keras.layers.Flatten(input_shape=(2,)),
  tf.keras.layers.Dense(c, activation='sigmoid'),
])
model.compile(optimizer='adam',
              loss='mae',
              metrics=['mse'])
model.summary()
```

```
Model: "sequential"
_________________________________________________________________
Layer (type)                 Output Shape              Param #   
=================================================================
flatten (Flatten)            (None, 2)                 0         
_________________________________________________________________
dense (Dense)                (None, 1)                 3         
=================================================================
Total params: 3
Trainable params: 3
Non-trainable params: 0
_________________________________________________________________
```

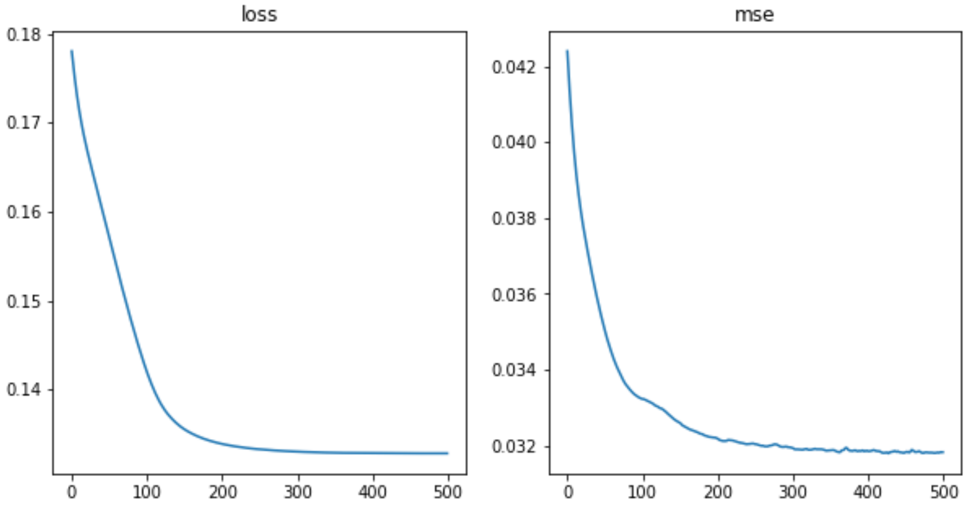
In [33]:
```
hist = model.fit(X, Y, epochs=500, batch_size=2048)
```

```
Epoch 1/500
6/6 [==============================] - 0s 4ms/step - loss: 0.1780 - mse:
0.0424
Epoch 2/500
6/6 [==============================] - 0s 3ms/step - loss: 0.1772 - mse:
0.0420
Epoch 3/500
6/6 [==============================] - 0s 3ms/step - loss: 0.1765 - mse:
0.0417
Epoch 4/500
6/6 [==============================] - 0s 3ms/step - loss: 0.1757 - mse:
0.0414
Epoch 5/500
6/6 [==============================] - 0s 4ms/step - loss: 0.1750 - mse:
0.0411
Epoch 6/500
6/6 [==============================] - 0s 3ms/step - loss: 0.1743 - mse:
0.0408
Epoch 7/500
6/6 [==============================] - 0s 3ms/step - loss: 0.1737 - mse:
0.0405
Epoch 8/500
6/6 [==============================] - 0s 3ms/step - loss: 0.1730 - mse:
0.0402
Epoch 9/500
6/6 [==============================] - 0s 3ms/step - loss: 0.1724 - mse:
0.0400
Epoch 10/500
6/6 [==============================] - 0s 4ms/step - loss: 0.1719 - mse:
0.0397
Epoch 11/500
6/6 [==============================] - 0s 3ms/step - loss: 0.1713 - mse:
0.0395
Epoch 12/500
6/6 [==============================] - 0s 3ms/step - loss: 0.1708 - mse:
0.0393
Epoch 13/500
6/6 [==============================] - 0s 3ms/step - loss: 0.1704 - mse:
0.0391
Epoch 14/500
6/6 [==============================] - 0s 3ms/step - loss: 0.1699 - mse:
0.0389
Epoch 15/500
6/6 [==============================] - 0s 3ms/step - loss: 0.1695 - mse:
0.0388
Epoch 16/500
6/6 [==============================] - 0s 3ms/step - loss: 0.1690 - mse:
0.0386
Epoch 17/500
6/6 [==============================] - 0s 3ms/step - loss: 0.1686 - mse:
0.0385
Epoch 18/500
6/6 [==============================] - 0s 3ms/step - loss: 0.1682 - mse:
0.0383
Epoch 19/500
6/6 [==============================] - 0s 4ms/step - loss: 0.1678 - mse:
0.0382
Epoch 20/500
6/6 [==============================] - 0s 3ms/step - loss: 0.1674 - mse:
0.0380
Epoch 21/500
6/6 [==============================] - 0s 3ms/step - loss: 0.1671 - mse:
0.0379
Epoch 22/500
6/6 [==============================] - 0s 3ms/step - loss: 0.1667 - mse:
0.0378
Epoch 23/500
6/6 [==============================] - 0s 3ms/step - loss: 0.1664 - mse:
```

In [34]:
```
Y_p = model.predict(X)
Y_p = Y_p.reshape((h,w,c))
im = plt.imshow(Y_p[...,0], cmap='gray')
```



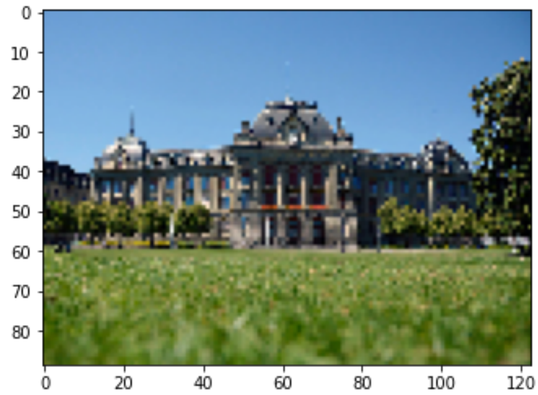
In [35]:
```
fig, axs = plt.subplots(1, 2, figsize=(10,5))
axs[0].plot(hist.epoch, hist.history['loss'])
axs[0].set_title('loss')
axs[1].plot(hist.epoch, hist.history['mse'])
axs[1].set_title('mse')
plt.show()
```



Let's try the same with an RGB image:

In [36]:
```
image = image_big[::5, ::5]
plt.imshow(image)
```

Out[36]: <matplotlib.image.AxesImage at 0x7fa67be874a8>



In [37]:
```
h, w, c = image.shape
X = np.meshgrid(np.linspace(0, 1, w), np.linspace(0, 1, h))
X = np.stack(X, axis=-1).reshape((-1, 2))

Y = image.reshape((-1, c))
X.shape, Y.shape
```

Out[37]: ((10947, 2), (10947, 3))

In [38]:
```
model = tf.keras.models.Sequential([
  tf.keras.layers.Flatten(input_shape=(2,)),
  tf.keras.layers.Dense(c, activation='sigmoid'),
])
model.compile(optimizer='adam',
              loss='mae',
              metrics=['mse'])
model.summary()
```

```
Model: "sequential_1"
_________________________________________________________________
Layer (type)                 Output Shape              Param #
=================================================================
flatten_1 (Flatten)          (None, 2)                 0
_________________________________________________________________
dense_1 (Dense)              (None, 3)                 9
=================================================================
Total params: 9
Trainable params: 9
Non-trainable params: 0
_________________________________________________________________
```

But now we will save images during the course of training, at first every 2 epochs, then every 20, every 200 and finally every 1000. (**Remember**: call to `model.fit` does NOT reinitialize trainable variables. Every time it continues from the previous state):

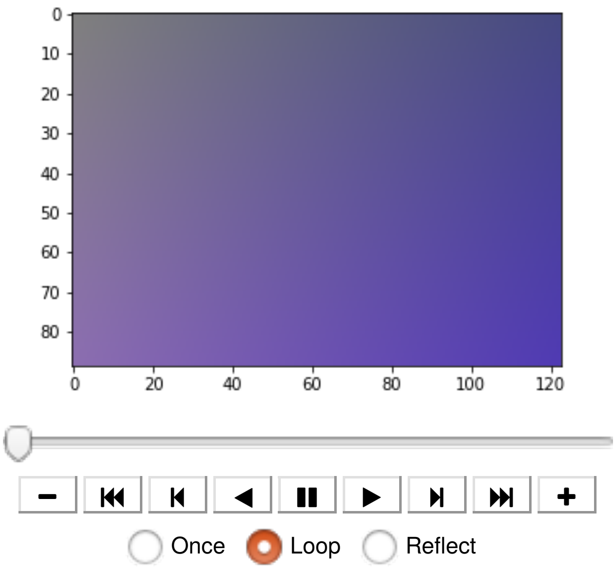
In [39]:
```
ims = []
n_ep_tot = 0
for i in range(170):
  if i % 10 == 0:
    print(f'epoch {i}', end='\n')
  ne = (2 if (i<50) else (20 if (i<100) else (200 if (i<150) else 100
0)))
  model.fit(X, Y, epochs=ne, batch_size=1*2048, verbose=0)

  Y_p = model.predict(X)
  Y_p = Y_p.reshape((h, w, c))
  ims.append(Y_p)
  n_ep_tot += ne

print(f'total numer of epochs trained:{n_ep_tot}')
```

```
epoch 0
epoch 10
epoch 20
epoch 30
epoch 40
epoch 50
epoch 60
epoch 70
epoch 80
epoch 90
epoch 100
epoch 110
epoch 120
epoch 130
epoch 140
epoch 150
epoch 160
total numer of epochs trained:31100
```

In [0]:
```
%%capture
plt.rcParams["animation.html"] = "jshtml"  # for matplotlib 2.1 and abov
e, uses JavaScript

fig = plt.figure()
im = plt.imshow(ims[0])


def animate(i):
    img = ims[i]
    im.set_data(img)
    return im

ani = animation.FuncAnimation(fig, animate, frames=len(ims))
```

```
In [41]: ani
```

Out[41]:



While the colors properly represent the target image, out model still poses very limited capacity, allowing it to effectively represent only 3 boundaries.

Let's upscale out model:

```
In [42]: model = tf.keras.models.Sequential([
           tf.keras.layers.Flatten(input_shape=(2,)),
           tf.keras.layers.Dense(128, activation='relu'),
           tf.keras.layers.Dense(8, activation='relu'),
           tf.keras.layers.Dense(c, activation='sigmoid'),
         ])
         model.compile(optimizer='adam',
                       loss='mae',
                       metrics=['mse'])
         model.summary()
```

```
Model: "sequential_2"
_________________________________________________________________
Layer (type)                 Output Shape              Param #   
=================================================================
flatten_2 (Flatten)          (None, 2)                 0         
_________________________________________________________________
dense_2 (Dense)              (None, 128)               384       
_________________________________________________________________
dense_3 (Dense)              (None, 8)                 1032      
_________________________________________________________________
dense_4 (Dense)              (None, 3)                 27        
=================================================================
Total params: 1,443
Trainable params: 1,443
Non-trainable params: 0
_________________________________________________________________
```

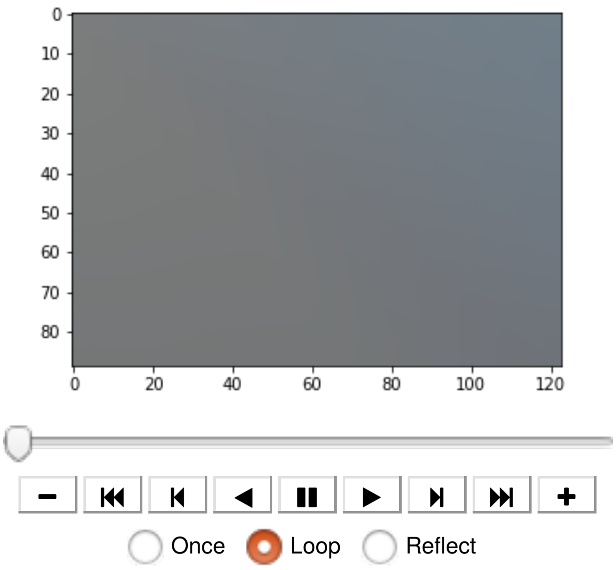
In [43]:
```
ims = []
n_ep_tot = 0
for i in range(180):
  if i % 10 == 0:
    print(f'epoch {i}', end='\n')
  ne = (2 if (i<50) else (20 if (i<100) else (200 if (i<150) else 100
0)))
  model.fit(X, Y, epochs=ne, batch_size=1*2048, verbose=0)

  Y_p = model.predict(X)
  Y_p = Y_p.reshape((h, w, c))
  ims.append(Y_p)
  n_ep_tot += ne

print(f'total numer of epochs trained:{n_ep_tot}')
```

```
epoch 0
epoch 10
epoch 20
epoch 30
epoch 40
epoch 50
epoch 60
epoch 70
epoch 80
epoch 90
epoch 100
epoch 110
epoch 120
epoch 130
epoch 140
epoch 150
epoch 160
epoch 170
total numer of epochs trained:41100
```

In [0]:
```
%%capture
fig = plt.figure()
im = plt.imshow(ims[0])

def animate(i):
    img = ims[i]
    im.set_data(img)
    return im

ani = animation.FuncAnimation(fig, animate, frames=len(ims))
```

In [45]:
```
ani
```

Out[45]:



In [0]:
```
%%capture
fig = plt.figure()
im = plt.imshow(imsa[0])

def animate(i):
    img = imsa[i]
    im.set_data(img)
    return im

ani = animation.FuncAnimation(fig, animate, frames=len(imsa))
```

EXERCISE 4.

Load some image, downscale to a similar resolution, and train a deeper model, for example 5 layers, more parameters in widest layers.

In [0]:
```
# 1. Load your image

# 2. build a deeper model

# 3. inspect the evolution
```