Evaluation_Report

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1 Assignment 3 - SOM - Evaluation Report

1.1 Coding - Implementation f - Mnemonic SOM

1.1.1 Group f2:

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Link to GitHub repository: https://github.com/CH1525518/MnemonicSOM

1.2 Mnemonic SOM implementation

In order to compute a Mnemonic SOM, several steps have to be performed.
The first step is to load the input vectors used for the generation of the SOM. Then, the input black and white image is also load and the mnemonic template is computed. The white part corresponds to the active areas, where the grid is drawn and the active matrix is performed. Based on this active matrix, the distance matrix is computed.

Now, that the template has been computed, the SOM can be trained. To do so, we have implemented an MnemonicSOM class, which represents the overall SOM, and a SOMUnit class, which corresponds to each single unit within the SOM.
The SOM is trained based on the active and distance matrices, as well as the number of epochs for the training, the initial learning rate, the learning rate decay used to update the learning rate at each epoch, the initial neighborhood radius, and the neighborhood radius decay used to update the neighborhood radius at each epoch.
The SOM units are first initialized based on the active matrix. Then, at each epoch, the vectors of the input dataset are taken in a random order, for each of them, the best unit is found, based on the distance between the input vector and the units, and the weights of the units are updated.
Finally, the weights list can be exported in order to be used by the standard visualisations.

More information about the implementation can be found in the `code-documentation` notebook.
All the relevant code can also be found in the `src` folder.
To train a Mnemonic SOM, the script in the `main.py` file can be run, which would automatically train a Mnemonic SOM based on the `chainlink` dataset and the `stick_figure` image.

In order to train another SOM, the function `som_test` from the `main.py` file can be run by providing, the name (with extension) of a image stored in the `mnemonics` folder, the name of the input dataset and the value for all the hyperparameters.

1.3 Evaluation visualisations

In order to see the results of our Mnemonic implementation, we will visualize some SOM implementations.
This notebook can also be found and run in the `src` folder.

[1]:
```
import main
import re

import numpy as np
import matplotlib.pyplot as plt

from SOMToolBox_Parse import SOMToolBox_Parse
import os
```

[2]:
```
import warnings
warnings.filterwarnings("ignore")
```

[3]:
```
import panel as pn
import holoviews as hv
from holoviews import opts
hv.extension('bokeh')

#HitHistogram
def HitHist(_m, _n, _weights, _idata):
    hist = np.zeros(_m * _n)
    for vector in _idata:
        position = np.argmin(np.sqrt(np.sum(np.power(_weights - vector, 2),␣
↪axis=1)))
        hist[position] += 1

    return hist.reshape(_m, _n)

#U-Matrix - implementation
def UMatrix(_m, _n, _weights, _dim):
    U = _weights.reshape(_m, _n, _dim)
    U = np.insert(U, np.arange(1, _n), values=0, axis=1)
    U = np.insert(U, np.arange(1, _m), values=0, axis=0)

    #calculate interpolation
    for i in range(U.shape[0]):
        if i%2==0:
            for j in range(1,U.shape[1],2):
                U[i,j][0] = np.linalg.norm(U[i,j-1] - U[i,j+1], axis=-1)
        else:
            for j in range(U.shape[1]):
                if j%2==0:
```

```
                    U[i,j][0] = np.linalg.norm(U[i-1,j] - U[i+1,j], axis=-1)
                else:
                    U[i,j][0] = (np.linalg.norm(U[i-1,j-1] - U[i+1,j+1],␣
↪axis=-1) + np.linalg.norm(U[i+1,j-1] - U[i-1,j+1], axis=-1))/(2*np.sqrt(2))

    U = np.sum(U, axis=2) #move from Vector to Scalar

    for i in range(0, U.shape[0], 2): #count new values
        for j in range(0, U.shape[1], 2):
            region = []
            if j>0: region.append(U[i][j-1]) #check left border
            if i>0: region.append(U[i-1][j]) #check bottom
            if j<U.shape[1]-1: region.append(U[i][j+1]) #check right border
            if i<U.shape[0]-1: region.append(U[i+1][j]) #check upper border

            U[i,j] = np.median(region)

    return U

#SDH - implementation
def SDH(_m, _n, _weights, _idata, factor, approach):
    import heapq

    sdh_m = np.zeros( _m * _n)

    cs=0
    for i in range(factor): cs += factor-i

    for vector in _idata:
        dist = np.sqrt(np.sum(np.power(_weights - vector, 2), axis=1))
        c = heapq.nsmallest(factor, range(len(dist)), key=dist.__getitem__)
        if (approach==0): # normalized
            for j in range(factor):  sdh_m[c[j]] += (factor-j)/cs
        if (approach==1):# based on distance
            for j in range(factor): sdh_m[c[j]] += 1.0/dist[c[j]]
        if (approach==2):
            dmin, dmax = min(dist[c]), max(dist[c])
            for j in range(factor): sdh_m[c[j]] += 1.0 - (dist[c[j]]-dmin)/
↪(dmax-dmin)

    return sdh_m.reshape(_m, _n)
```

[4]:
```
def convert_X_to_dict(X):
    '''Convert X, dataset input vector, to a dictionary that can be used in the␣
↪visualisations'''
    ret = {}
    ret['xdim'] = len(X)
```

```
    ret['ydim'] = 1
    ret['vec_dim'] = len(X[0])
    ret['arr'] = np.array(X)
    return ret
```

[5]:
```
datasets = ['chainlink', '10clusters']
pdf = True
plot_size = {'small': (20,40), 'large': (60,100)}
```

1.3.1 Training small and large SOMs

Small (40x20) and large (100x60) SOMs have been trained using the Mnemonic SOM implementation on 3 different input images to see the effect on these images on the resulting SOMs.

The trained SOMs are stored in the folder, `trained_som`.

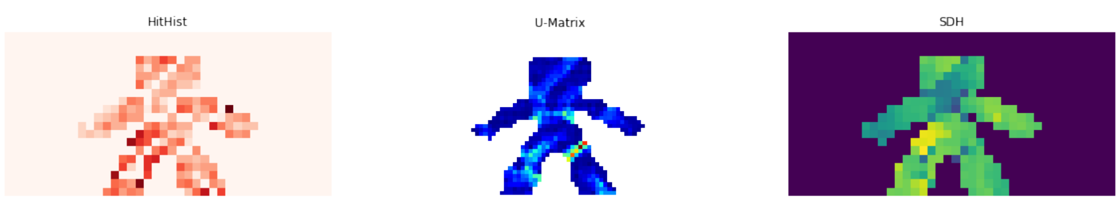
These trained SOMs are then visualized using 3 different visualisations: * HitHistogram, which visualizes the density of the SOM by counting the number of input vectors mapped onto each node of the SOM, the more active clusters are the visualised by the bright units (dark units in the pdf); * U-Matrix, which shows the distance between each unit and their neighbourhood, the dark zones delimited by brightful lines are clusters having the similar preferences when it comes to classification; * Smoothed Data Histogram, which shows the number of most likely positions for each sample, the clusters of units correspond there to the bright zones.

Chainlink dataset - 10 epochs The chainlink dataset is composed by two chains intertwined in three-dimensional space. Thus, the projection on two-dimensional space should lead to two intersections between the chains (areas with points from both chains).
The SOM implementation should show the clusters form by the input from the same chain.

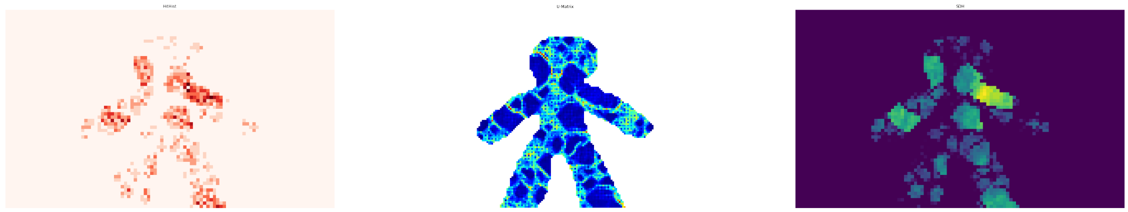
[6]:
```
dataset = datasets[0]
images = ['stick_figure.png','round.jpg','walking_icon.png']
size = ['small','large']

for image in images:
    for s in size:
        image_name = re.split('\.', image)[0]
        print(dataset, ' - ', image_name, ' - ', s, ' - PythonMnemonicSOM␣
↪implementation:')

        idata_save_path = f"../trained_som/Epochs-10/
↪idata_{dataset}_{image_name}_{s}.npy"
        weights_save_path = f"../trained_som/Epochs-10/
↪weights_{dataset}_{image_name}_{s}.npy"
        idata= np.load(idata_save_path,allow_pickle='TRUE').item()
        weights_PythonSOM = np.load(weights_save_path, allow_pickle='TRUE').
↪item()
```

```
        if pdf:
            fig, ax = plt.subplots(nrows=1, ncols = 3, figsize = plot_size[s])
            ax[0].imshow(HitHist(weights_PythonSOM['xdim'],␣
↪weights_PythonSOM['ydim'], weights_PythonSOM['arr'],
                                idata['arr']),cmap='Reds')
            ax[0].set_title('HitHist')
            ax[0].axis('off')
            ax[1].imshow(UMatrix(weights_PythonSOM['xdim'],␣
↪weights_PythonSOM['ydim'], weights_PythonSOM['arr'],
                                weights_PythonSOM['vec_dim']),cmap='jet')
            ax[1].set_title('U-Matrix')
            ax[1].axis('off')
            ax[2].imshow(SDH(weights_PythonSOM['xdim'],␣
↪weights_PythonSOM['ydim'], weights_PythonSOM['arr'],
                                idata['arr'], 25, 0),cmap='viridis')
            ax[2].set_title('SDH')
            ax[2].axis('off')
            plt.show()
        else:
            hithist = hv.Image(HitHist(weights_PythonSOM['xdim'],␣
↪weights_PythonSOM['ydim'], weights_PythonSOM['arr'], idata['arr'])).
↪opts(xaxis=None, yaxis=None)
            um = hv.Image(UMatrix(weights_PythonSOM['xdim'],␣
↪weights_PythonSOM['ydim'], weights_PythonSOM['arr'],␣
↪weights_PythonSOM['vec_dim'])).opts(xaxis=None, yaxis=None)
            sdh = hv.Image(SDH(weights_PythonSOM['xdim'],␣
↪weights_PythonSOM['ydim'], weights_PythonSOM['arr'], idata['arr'], 25, 0)).
↪opts(xaxis=None, yaxis=None)

            display(hv.Layout([hithist.relabel('HitHist').opts(cmap='kr'),
                            um.relabel('U-Matrix').opts(cmap='jet'), sdh.
↪relabel('SDH').opts(cmap='viridis')]))
```

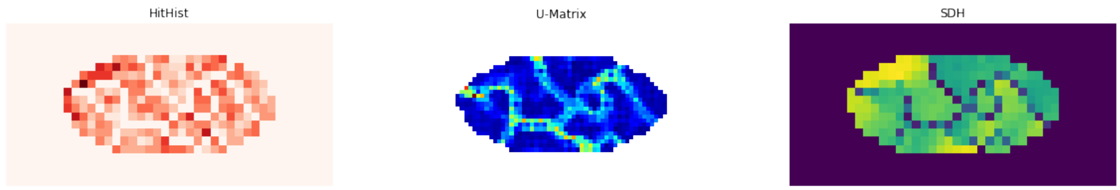
chainlink - stick_figure - small - PythonMnemonicSOM implementation:



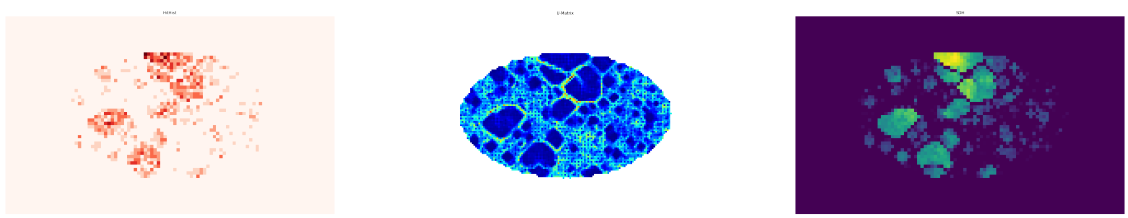
chainlink - stick_figure - large - PythonMnemonicSOM implementation:



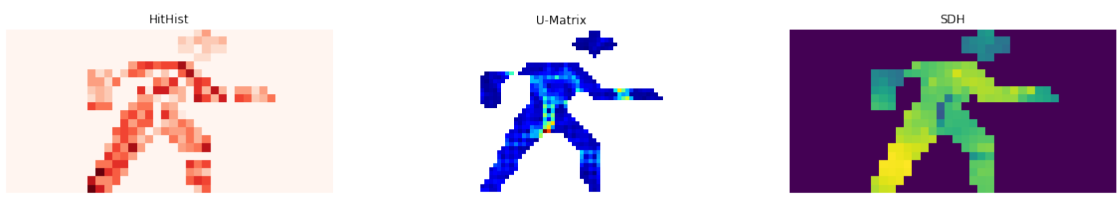
chainlink - round - small - PythonMnemonicSOM implementation:



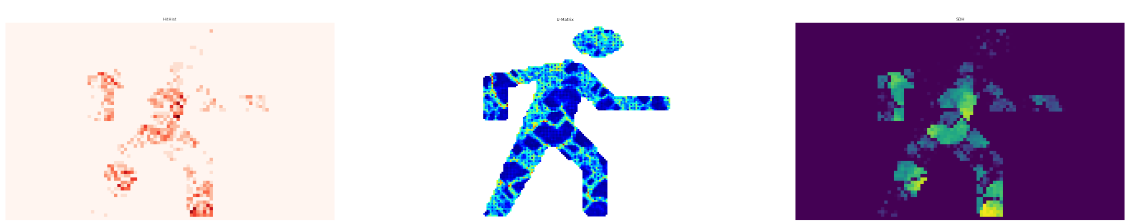
chainlink - round - large - PythonMnemonicSOM implementation:



chainlink - walking_icon - small - PythonMnemonicSOM implementation:



chainlink - walking_icon - large - PythonMnemonicSOM implementation:



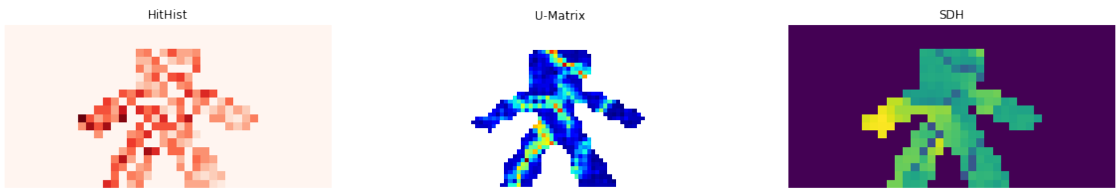
We can see within all the visualisations the apparition of clusters, the larger SOM provides better defined clusters than the smaller one, which could need more epochs for the training.
As expected, the input image as an impact on the structure of the SOM, with the positions of the clusters, but the overall structure remains the same for the different images.

Chainlink dataset - 500 epochs

[7]:
```
dataset = datasets[0]
images = ['stick_figure.png']
size = ['small']

for image in images:
    for s in size:
        image_name = re.split('\.', image)[0]
        print(dataset, ' - ', image_name, ' - ', s, ' - PythonMnemonicSOM␣
↪implementation:')

        idata_save_path = f"../trained_som/Epochs-500/
↪idata_{dataset}_{image_name}_{s}.npy"
        weights_save_path = f"../trained_som/Epochs-500/
↪weights_{dataset}_{image_name}_{s}.npy"
        idata= np.load(idata_save_path,allow_pickle='TRUE').item()
        weights_PythonSOM = np.load(weights_save_path, allow_pickle='TRUE').
↪item()

        if pdf:
            fig, ax = plt.subplots(nrows=1, ncols = 3, figsize = plot_size[s])
            ax[0].imshow(HitHist(weights_PythonSOM['xdim'],␣
↪weights_PythonSOM['ydim'], weights_PythonSOM['arr'],
                              idata['arr']),cmap='Reds')
            ax[0].set_title('HitHist')
            ax[0].axis('off')
            ax[1].imshow(UMatrix(weights_PythonSOM['xdim'],␣
↪weights_PythonSOM['ydim'], weights_PythonSOM['arr'],
                              weights_PythonSOM['vec_dim']),cmap='jet')
            ax[1].set_title('U-Matrix')
            ax[1].axis('off')
            ax[2].imshow(SDH(weights_PythonSOM['xdim'],␣
↪weights_PythonSOM['ydim'], weights_PythonSOM['arr'],
                              idata['arr'], 25, 0),cmap='viridis')
            ax[2].set_title('SDH')
            ax[2].axis('off')
            plt.show()
        else:
```

```
        hithist = hv.Image(HitHist(weights_PythonSOM['xdim'],␣
↪weights_PythonSOM['ydim'], weights_PythonSOM['arr'], idata['arr'])).
↪opts(xaxis=None, yaxis=None)
        um = hv.Image(UMatrix(weights_PythonSOM['xdim'],␣
↪weights_PythonSOM['ydim'], weights_PythonSOM['arr'],␣
↪weights_PythonSOM['vec_dim'])).opts(xaxis=None, yaxis=None)
        sdh = hv.Image(SDH(weights_PythonSOM['xdim'],␣
↪weights_PythonSOM['ydim'], weights_PythonSOM['arr'], idata['arr'], 25, 0)).
↪opts(xaxis=None, yaxis=None)

        display(hv.Layout([hithist.relabel('HitHist').opts(cmap='kr'),
                           um.relabel('U-Matrix').opts(cmap='jet'), sdh.
↪relabel('SDH').opts(cmap='viridis')]))
```

```
chainlink  -  stick_figure  -  small  - PythonMnemonicSOM implementation:
```



With more training, the small SOM provides a result a bit more closer to the big SOM.

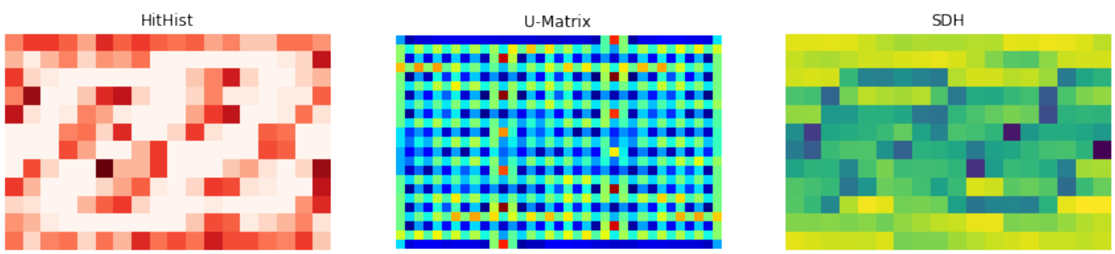
JavaSOMToolBox implementation - Chainlink dataset

[8]:
```
dataset = datasets[0]
idata_JavaSOM = SOMToolBox_Parse("../datasets/{}/{}.vec".
↪format(dataset,dataset)).read_weight_file()
weights_JavaSOM = SOMToolBox_Parse("../datasets/{}/{}.wgt".
↪format(dataset,dataset)).read_weight_file()
```

[9]:
```
print('JavaSOMToolBox implementation:')
if pdf:
    fig, ax = plt.subplots(nrows=1, ncols = 3, figsize = (15,15))
    ax[0].imshow(HitHist(weights_JavaSOM['xdim'], weights_JavaSOM['ydim'],␣
↪weights_JavaSOM['arr'],
                         idata_JavaSOM['arr']),cmap='Reds')
    ax[0].set_title('HitHist')
    ax[0].axis('off')
    ax[1].imshow(UMatrix(weights_JavaSOM['xdim'], weights_JavaSOM['ydim'],␣
↪weights_JavaSOM['arr'],
                         weights_JavaSOM['vec_dim']),cmap='jet')
    ax[1].set_title('U-Matrix')
```

```
    ax[1].axis('off')
    ax[2].imshow(SDH(weights_JavaSOM['xdim'], weights_JavaSOM['ydim'],␣
↪weights_JavaSOM['arr'],
                         idata_JavaSOM['arr'], 25, 0),cmap='viridis')
    ax[2].set_title('SDH')
    ax[2].axis('off')
    plt.show()
else:
    hithist = hv.Image(HitHist(weights_JavaSOM['xdim'], weights_JavaSOM['ydim'],␣
↪weights_JavaSOM['arr'], idata_JavaSOM['arr'])).opts(xaxis=None, yaxis=None)
    um = hv.Image(UMatrix(weights_JavaSOM['xdim'], weights_JavaSOM['ydim'],␣
↪weights_JavaSOM['arr'], weights_JavaSOM['vec_dim'])).opts(xaxis=None,␣
↪yaxis=None)
    sdh = hv.Image(SDH(weights_JavaSOM['xdim'], weights_JavaSOM['ydim'],␣
↪weights_JavaSOM['arr'], idata_JavaSOM['arr'], 25, 0)).opts(xaxis=None,␣
↪yaxis=None)

    display(hv.Layout([hithist.relabel('HitHist').opts(cmap='kr'),
                    um.relabel('U-Matrix').opts(cmap='jet'), sdh.relabel('SDH').
↪opts(cmap='viridis')]))
```

JavaSOMToolBox implementation:

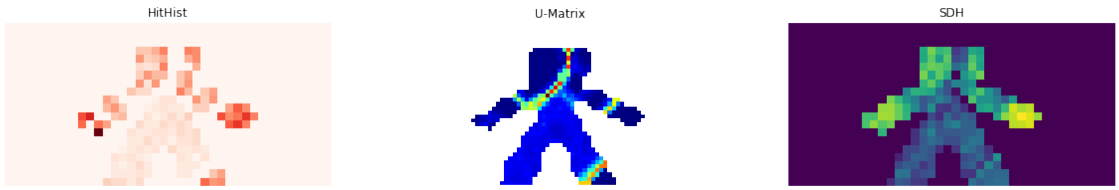


10clusters dataset - 10 epochs The 10clusters dataset is composed by points in 10-dimensional space, belonging to 10 different clusters with diffenrent densities.
The SOM implementation should show these clusters.

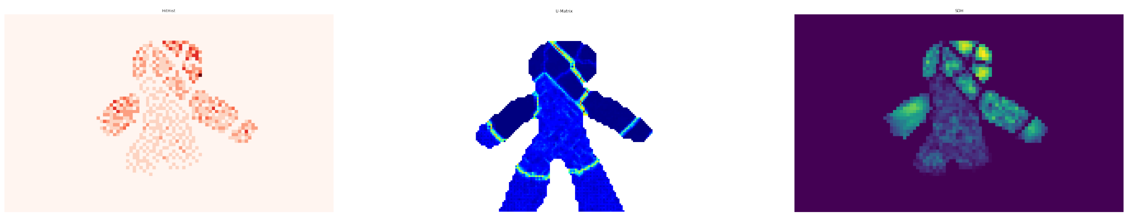
[10]:
```
dataset = datasets[1]
images = ['stick_figure.png','round.jpg','walking_icon.png']
size = ['small','large']

for image in images:
    for s in size:
        image_name = re.split('\.', image)[0]
        print(dataset, ' - ', image_name, ' - ', s, ' - PythonMnemonicSOM␣
↪implementation:')
```

```
        idata_save_path = f"../trained_som/Epochs-10/
↪idata_{dataset}_{image_name}_{s}.npy"
        weights_save_path = f"../trained_som/Epochs-10/
↪weights_{dataset}_{image_name}_{s}.npy"
        idata= np.load(idata_save_path,allow_pickle='TRUE').item()
        weights_PythonSOM = np.load(weights_save_path, allow_pickle='TRUE').
↪item()

        if pdf:
            fig, ax = plt.subplots(nrows=1, ncols = 3, figsize = plot_size[s])
            ax[0].imshow(HitHist(weights_PythonSOM['xdim'],␣
↪weights_PythonSOM['ydim'], weights_PythonSOM['arr'],
                                idata['arr']),cmap='Reds')
            ax[0].set_title('HitHist')
            ax[0].axis('off')
            ax[1].imshow(UMatrix(weights_PythonSOM['xdim'],␣
↪weights_PythonSOM['ydim'], weights_PythonSOM['arr'],
                                weights_PythonSOM['vec_dim']),cmap='jet')
            ax[1].set_title('U-Matrix')
            ax[1].axis('off')
            ax[2].imshow(SDH(weights_PythonSOM['xdim'],␣
↪weights_PythonSOM['ydim'], weights_PythonSOM['arr'],
                                idata['arr'], 25, 0),cmap='viridis')
            ax[2].set_title('SDH')
            ax[2].axis('off')
            plt.show()
        else:
            hithist = hv.Image(HitHist(weights_PythonSOM['xdim'],␣
↪weights_PythonSOM['ydim'], weights_PythonSOM['arr'], idata['arr'])).
↪opts(xaxis=None, yaxis=None)
            um = hv.Image(UMatrix(weights_PythonSOM['xdim'],␣
↪weights_PythonSOM['ydim'], weights_PythonSOM['arr'],␣
↪weights_PythonSOM['vec_dim'])).opts(xaxis=None, yaxis=None)
            sdh = hv.Image(SDH(weights_PythonSOM['xdim'],␣
↪weights_PythonSOM['ydim'], weights_PythonSOM['arr'], idata['arr'], 25, 0)).
↪opts(xaxis=None, yaxis=None)

            display(hv.Layout([hithist.relabel('HitHist').opts(cmap='kr'),
                            um.relabel('U-Matrix').opts(cmap='jet'), sdh.
↪relabel('SDH').opts(cmap='viridis')]))
```

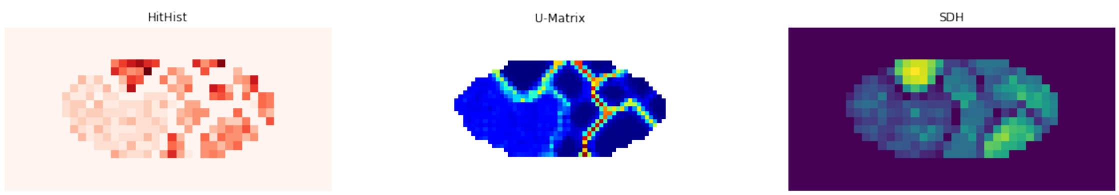
```
10clusters  -  stick_figure  -  small  - PythonMnemonicSOM implementation:
```



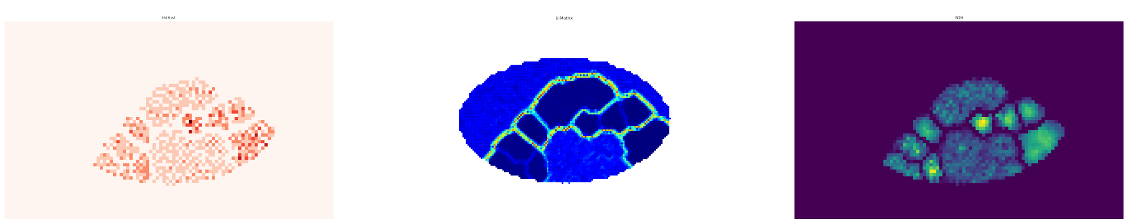
10clusters - stick_figure - large - PythonMnemonicSOM implementation:



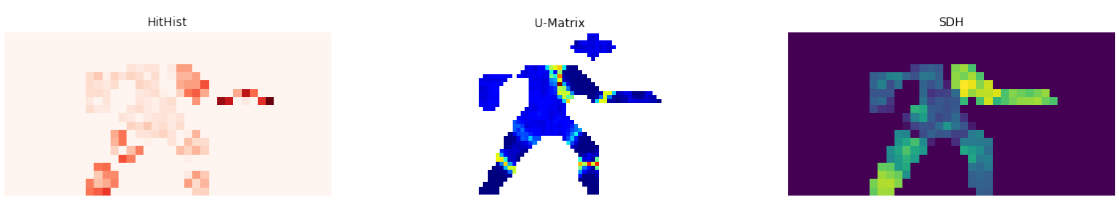
10clusters - round - small - PythonMnemonicSOM implementation:



10clusters - round - large - PythonMnemonicSOM implementation:



10clusters - walking_icon - small - PythonMnemonicSOM implementation:



10clusters - walking_icon - large - PythonMnemonicSOM implementation:

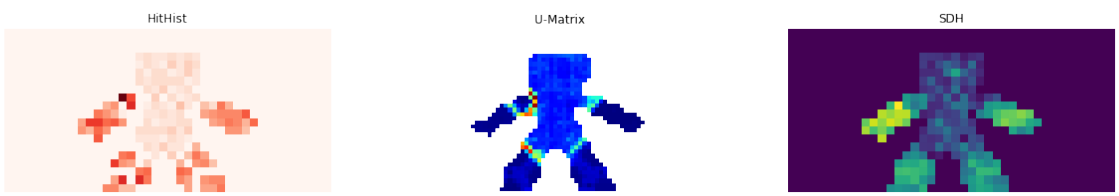
Similar observations as with the **chainlink** dataset can be found here.
Big SOMS have a better cluster definition. The difference of density between the clusters is also more easily noticeable.

10clusters dataset - 500 epochs

[11]:
```
dataset = datasets[1]
images = ['stick_figure.png']
size = ['small']

for image in images:
    for s in size:
        image_name = re.split('\.', image)[0]
        print(dataset, ' - ', image_name, ' - ', s, ' - PythonMnemonicSOM␣
↪implementation:')

        idata_save_path = f"../trained_som/Epochs-500/
↪idata_{dataset}_{image_name}_{s}.npy"
        weights_save_path = f"../trained_som/Epochs-500/
↪weights_{dataset}_{image_name}_{s}.npy"
        idata= np.load(idata_save_path,allow_pickle='TRUE').item()
        weights_PythonSOM = np.load(weights_save_path, allow_pickle='TRUE').
↪item()

        if pdf:
            fig, ax = plt.subplots(nrows=1, ncols = 3, figsize = plot_size[s])
            ax[0].imshow(HitHist(weights_PythonSOM['xdim'],␣
↪weights_PythonSOM['ydim'], weights_PythonSOM['arr'],
                                 idata['arr']),cmap='Reds')
            ax[0].set_title('HitHist')
            ax[0].axis('off')
            ax[1].imshow(UMatrix(weights_PythonSOM['xdim'],␣
↪weights_PythonSOM['ydim'], weights_PythonSOM['arr'],
                                 weights_PythonSOM['vec_dim']),cmap='jet')
```

```
            ax[1].set_title('U-Matrix')
            ax[1].axis('off')
            ax[2].imshow(SDH(weights_PythonSOM['xdim'],␣
↪weights_PythonSOM['ydim'], weights_PythonSOM['arr'],
                                idata['arr'], 25, 0),cmap='viridis')
            ax[2].set_title('SDH')
            ax[2].axis('off')
            plt.show()
        else:
            hithist = hv.Image(HitHist(weights_PythonSOM['xdim'],␣
↪weights_PythonSOM['ydim'], weights_PythonSOM['arr'], idata['arr'])).
↪opts(xaxis=None, yaxis=None)
            um = hv.Image(UMatrix(weights_PythonSOM['xdim'],␣
↪weights_PythonSOM['ydim'], weights_PythonSOM['arr'],␣
↪weights_PythonSOM['vec_dim'])).opts(xaxis=None, yaxis=None)
            sdh = hv.Image(SDH(weights_PythonSOM['xdim'],␣
↪weights_PythonSOM['ydim'], weights_PythonSOM['arr'], idata['arr'], 25, 0)).
↪opts(xaxis=None, yaxis=None)

            display(hv.Layout([hithist.relabel('HitHist').opts(cmap='kr'),
                               um.relabel('U-Matrix').opts(cmap='jet'), sdh.
↪relabel('SDH').opts(cmap='viridis')]))
```

```
10clusters  - stick_figure  - small  - PythonMnemonicSOM implementation:
```



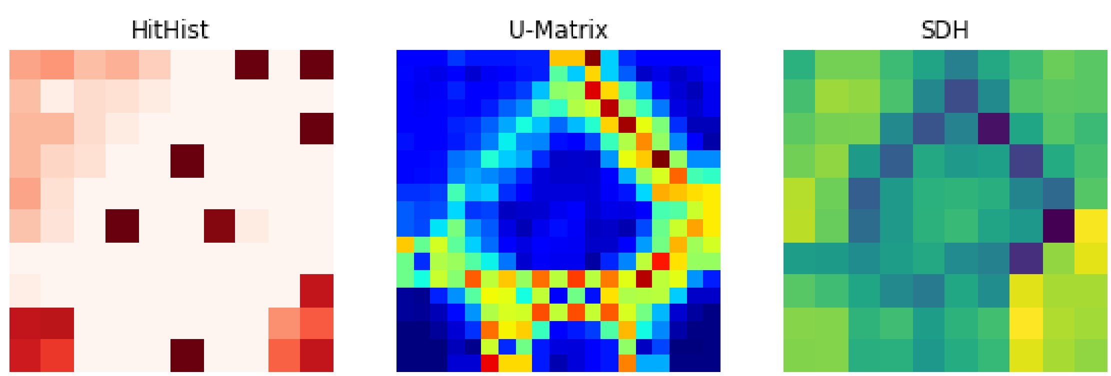
JavaSOMToolBox implementation - 10clusters dataset

[12]:
```
dataset = datasets[1]
idata_JavaSOM = SOMToolBox_Parse("../datasets/{}/{}.vec".
↪format(dataset,dataset)).read_weight_file()
weights_JavaSOM = SOMToolBox_Parse("../datasets/{}/{}.wgt".
↪format(dataset,dataset)).read_weight_file()
```

[13]:
```
if pdf:
    fig, ax = plt.subplots(nrows=1, ncols = 3, figsize = (10,10))
    ax[0].imshow(HitHist(weights_JavaSOM['xdim'], weights_JavaSOM['ydim'],␣
↪weights_JavaSOM['arr'],
```

```
                        idata_JavaSOM['arr']),cmap='Reds')
    ax[0].set_title('HitHist')
    ax[0].axis('off')
    ax[1].imshow(UMatrix(weights_JavaSOM['xdim'], weights_JavaSOM['ydim'],␣
↪weights_JavaSOM['arr'],
                        weights_JavaSOM['vec_dim']),cmap='jet')
    ax[1].set_title('U-Matrix')
    ax[1].axis('off')
    ax[2].imshow(SDH(weights_JavaSOM['xdim'], weights_JavaSOM['ydim'],␣
↪weights_JavaSOM['arr'],
                        idata_JavaSOM['arr'], 25, 0),cmap='viridis')
    ax[2].set_title('SDH')
    ax[2].axis('off')
    plt.show()
else:
    hithist = hv.Image(HitHist(weights_JavaSOM['xdim'], weights_JavaSOM['ydim'],␣
↪weights_JavaSOM['arr'], idata_JavaSOM['arr'])).opts(xaxis=None, yaxis=None)
    um = hv.Image(UMatrix(weights_JavaSOM['xdim'], weights_JavaSOM['ydim'],␣
↪weights_JavaSOM['arr'], weights_JavaSOM['vec_dim'])).opts(xaxis=None,␣
↪yaxis=None)
    sdh = hv.Image(SDH(weights_JavaSOM['xdim'], weights_JavaSOM['ydim'],␣
↪weights_JavaSOM['arr'], idata_JavaSOM['arr'], 25, 0)).opts(xaxis=None,␣
↪yaxis=None)

    display(hv.Layout([hithist.relabel('HitHist').opts(cmap='kr'),
                um.relabel('U-Matrix').opts(cmap='jet'), sdh.relabel('SDH').
↪opts(cmap='viridis')]))
```

```
JavaSOMToolBox implementation:
```



We can also see on the JavaSOM implementation the different clusters.
Nevertheless the position of these clusters differ from our Mnemonic implementation due to our input images which modify the computation of the distances.

Conslusion Our Mnemonic SOM implementation allows to train SOMs on using an input shape diffenrent than a simple square.
The visualisation of diffenrent trained SOMs shows that our implementation generates clusters as expected and provides more readable results on the bigger SOMs.
The hyperparameters also have to be tuned depending on the dataset to provide the best results.