Aligned SOMs Evaluation on Chainlink Dataset

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Github:

https://github.com/Znerual/AlignedSOM

```
import os, sys
import numpy as np

module_path = os.path.abspath(os.path.join('...'))
if module_path not in sys.path:
    sys.path.append(module_path)

from src.data import load_dataset
from src.config import config
from src.aligned_som import AlignedSom
from src.visualize import plot_aligned_som, HitHist, UMatrix, SDH

DATASET_NAME = 'chainlink'
```

```
In [ ]: def setup(som dim, num layers, aspect selection,
                  sigma=1.0,
                  learning rate=0.5,
                  layer_distance_ratio=0.1,
                  num plots=5,
                  train_steps_by_layer=1000,
                  random seed=config.SEED,
                  load existing=True):
            input_data, components, weights, classinfo = load_dataset(DATASET_NAM
            data = input_data['arr']
            aspect_selection = np.array(aspect_selection)
            asom = AlignedSom(
                som dim, data, aspect selection,
                num layers=num layers,
                sigma=sigma,
                learning_rate=learning_rate,
                layer distance ratio=layer distance ratio,
                random seed=random seed)
            os.makedirs("../results", exist ok=True)
            if load existing and os.path.exists(f"../results/{DATASET NAME} setup
                asom.set_layer_weights(np.load(f"../results/{DATASET_NAME}_setup_
            else:
                asom.train(train_steps_by_layer * num_layers)
```

```
np.save(f"../results/{DATASET_NAME}_setup_{som_dim[0]}_{som_dim[1]}
fig = plot_aligned_som(asom, data, num_plots=num_plots, upscaling_fac
fig.savefig(f"../results/{DATASET_NAME}_setup_{som_dim[0]}_{som_dim[1]}
visualization_function = UMatrix
fig_umatrix = plot_aligned_som(asom, data, num_plots=num_plots, upsca
fig_umatrix.savefig(f"../results/{DATASET_NAME}_setup_{visualization_
visualization_function = HitHist
fig_hit = plot_aligned_som(asom, data, num_plots=num_plots, upscaling
fig_hit.savefig(f"../results/{DATASET_NAME}_setup_{visualization_func}
return asom
```

Dataset

The chain link data set, sometimes also called intertwined rings, is a classic example of a data set that provokes topology preservation vialitions. The data set contains two rings, each two-dimensional, that are intertwined in a three-dimensional space. When projecting this data set to a two-dimensional output space, the rings have to "break".

http://www.ifs.tuwien.ac.at/dm/somtoolbox/datasets.html

As described in the 10 clusters notebook, the chainlink dataset is an artificial dataset, which hindered us from finding a data based aspect split. Therefore, we focused on the algorithm instead of the data.

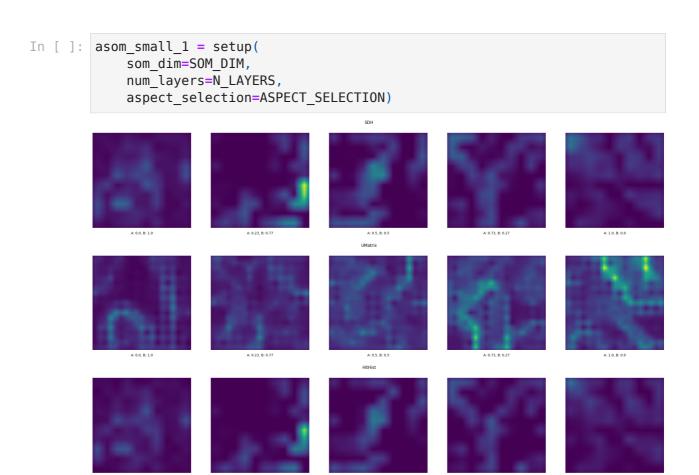
We used the same experimental design as for the 10 clusters dataset. As a result, we find similar conclusions for the plots, which led to the decision to leave out the figurewise descriptions. A detailed report of the experiment can be found in the 10 clusters dataset.

Alignd SOMs on Chainlink 10x10

```
In [ ]: SOM_DIM = (10, 10)
    N_LAYERS = 31
    ASPECT_SELECTION = [1, 1, 0]
```

Default Setup

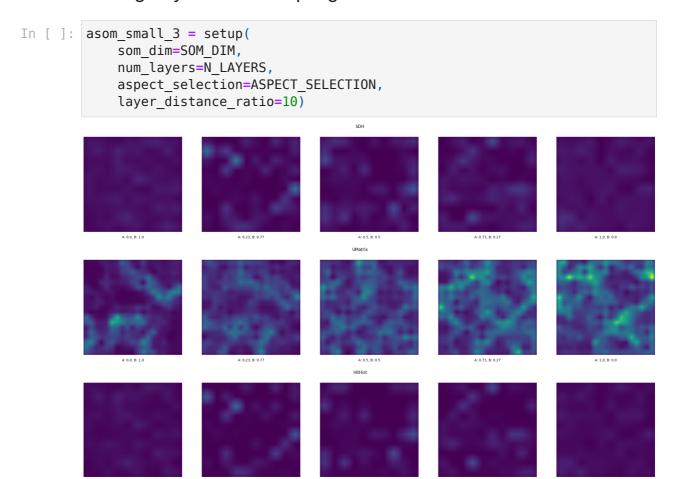
The baseline for all our experiments with the chainlink dataset consists of a 10x10 units ASOM, trained with 31 layers and a layer distance ratio of 0.1.



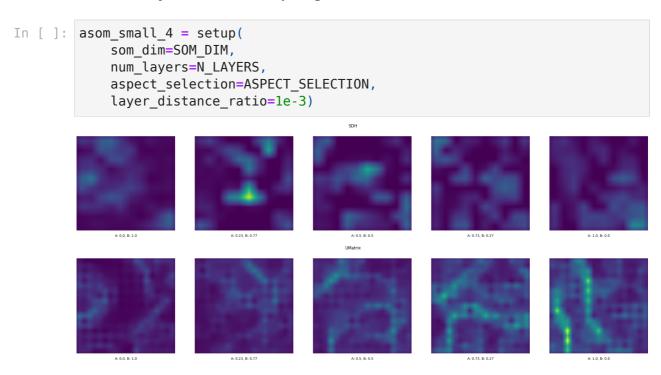
Many In-Between Layers



Strong Layer-Wise Coupling

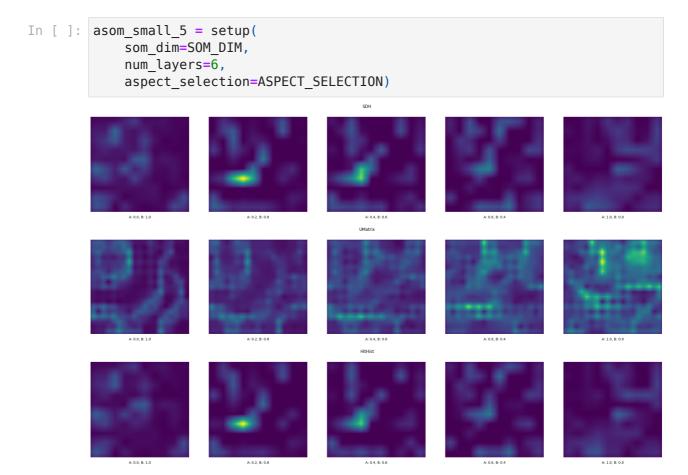


Weak Layer-Wise Coupling



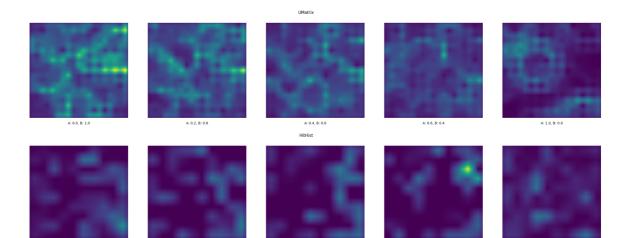


Few In-Between Layers



Switch Aspect Indices

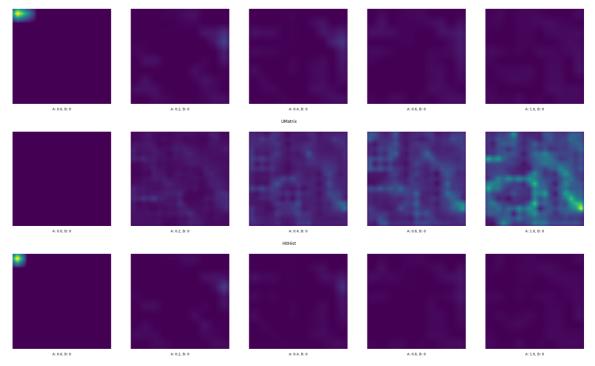




Only Aspect A



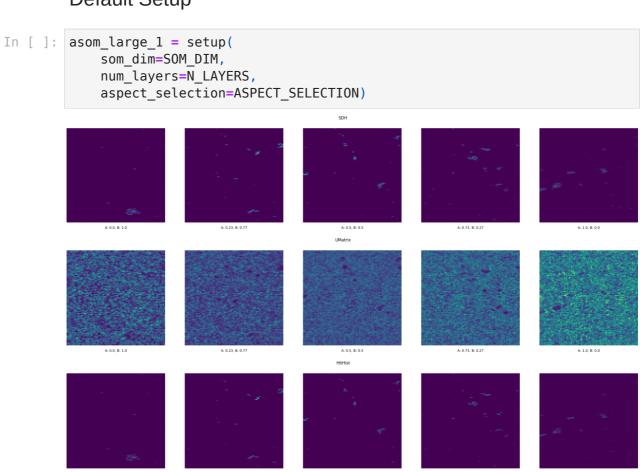
Only Aspect B



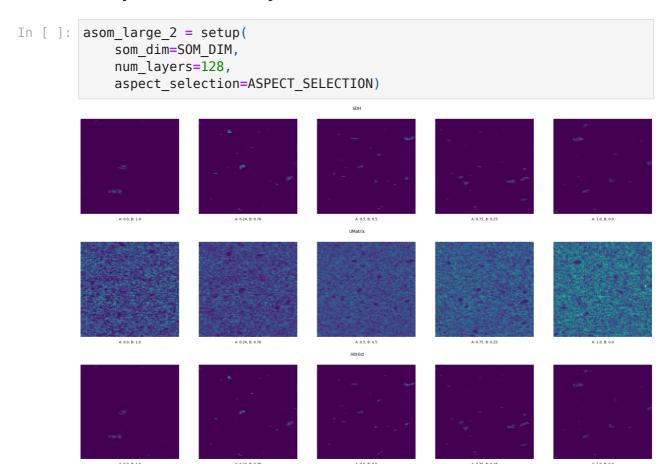
Alignd SOMs on Chainlink 100x60

```
In [ ]: SOM_DIM = (100, 60)
N_LAYERS = 31
ASPECT_SELECTION = [1, 1, 0]
```

Default Setup



Many In-Between Layers

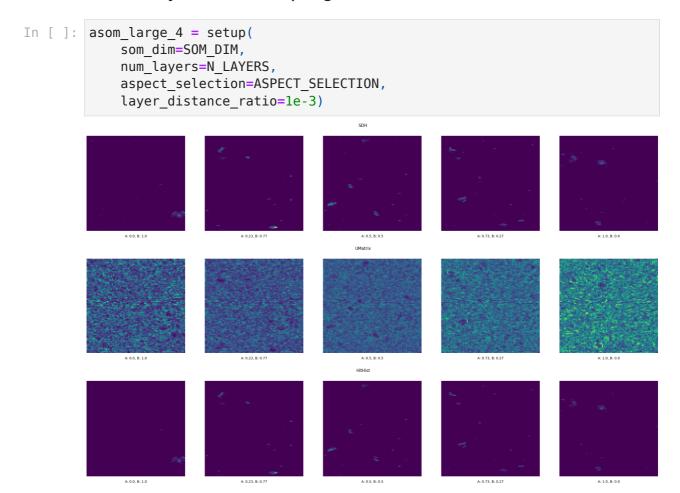


Strong Layer-Wise Coupling



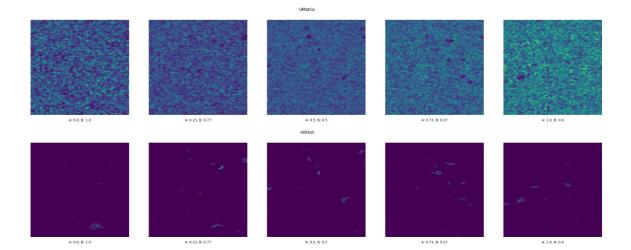


Weak Layer-Wise Coupling

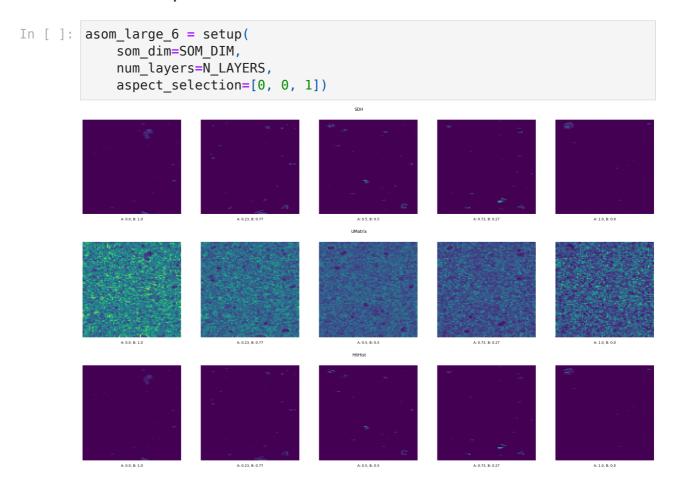


Few In-Between Layers



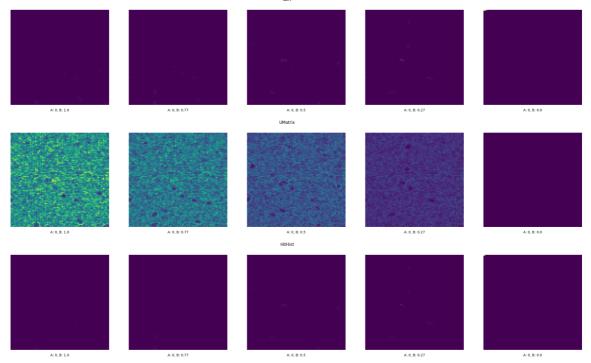


Switch Aspect Indices



Only Aspect B

SDH



Only Aspect A

