## Adaptive batch SOM for multiple dissimilarity data tables

# Anderson Dantas Francisco de Carvalho {absd, fatc}@cin.ufpe.br







#### Introduction

- Clustering methods organize a set of items into clusters
- Items within a given cluster have a high degree of similarity
- Feature data (vector)
- Relational data (relationship)



### **Objective**

Hard clustering algorithm that is able to **partition** objects taking into account **simultaneously** their relational descriptions given by **multiple** dissimilarity matrices



### **Objective**

#### The algorithm is designed to give:

- Partition
- Prototype for each cluster
- Relevance weight



#### **Cost function**

$$J = \sum_{e_i \in E} \sum_{l=1}^{c} K^{T}(\delta(\chi(e_i), l)) D_{\lambda_l}(e_i, G_l)$$

- $D_{\lambda_l}$  is the dissimilarity between  $e_i$  and  $G_l$  parameterized by relevance weight vector  $\lambda_l = (\lambda_{l1}, \dots, \lambda_{lp})$
- Neighbourhood through kernel functions K, parameterized by T defines the influence region around each neuron



## **Matching function**

$$D_{\boldsymbol{\lambda}_{l}}(\boldsymbol{e}_{l},\boldsymbol{G}_{l}) = \sum_{j=1}^{p} \lambda_{lj} D_{j}(\boldsymbol{e}_{i},\boldsymbol{G}_{l}) = \sum_{j=1}^{p} \lambda_{lj} d_{j}(\boldsymbol{e}_{i},\boldsymbol{G}_{l})$$

- To compare clusters and theirs prototypes using a different matching measure
- d<sub>j</sub>(e<sub>i</sub>, G<sub>l</sub>) is the local dissimilarity between an example and the cluster prototype

## Adaptive B-SOM for data based on multiple dissimilarity matrices

Iterative three-step algorithm
Representation, weighting and affectation



## Representation step: computation of the best prototypes

Compute the prototype  $G_I^{(t)}=G^*\in E^{(q)}$  of cluster  $P_I^{(t-1)}$  (  $I=1,\ldots,c$ ) according to:

$$G^* = argmin_{e \in E^{(q)}} \sum_{e_i \in E} K^T(\delta(\chi^{(t-1)}(e_i), I)) \sum_{j=1}^p \lambda_{Ij}^{(t-1)} d_j(e_i, G_I)$$



## Weighting step: definition of the best vectors of weights

The vectors of weights  $\lambda_{l}^{(t)}=(\lambda_{l1}^{(t)},\ldots,\lambda_{lp}^{(t)})$   $(l=1,\ldots,c)$ , under  $\lambda_{lj}^{(t)}>0$  and  $\prod_{j=1}^{p}\lambda_{lj}^{(t)}=1$ , have their weights  $\lambda_{lj}^{(t)}$   $(j=1,\ldots,p)$  calculated according to:

$$\lambda_{lj}^{(t)} = \frac{\left\{ \prod_{h=1}^{p} \left[ \sum_{e_i \in E} K^T(\delta(\chi^{(t-1)}(e_i), I)) d_h(e_i, G_l) \right] \right\}^{\frac{1}{p}}}{\left[ \sum_{e_i \in E} K^T(\delta(\chi^{(t-1)}(e_i), I)) d_j(e_i, G_l) \right]}$$



## Affectation step: definition of the best partition

$$m = (\chi^{(t)}(e_i))^{(t)} = argmin_{1 \le r \le c} \sum_{l=1}^{c} K^T(\delta(r, l)) \sum_{i=1}^{p} \lambda_{lj}^{(t)} d_j(e_i, G_l)$$



### **Experiments**

- Databases from the UCI Machine Learning Repository
- Measures: corrected Rand index (CR), F-measure, overall error rate of classification (OERC)
- Confusion matrix
- Data sets described by a matrix of objects x real-valued attributes
- Original batch SOM for single dissimilarity matrix
- Adaptive batch SOM for multiple dissimilarity matrices

#### Wine dataset

#### **Parameters**

• Topology: 2x5;

• *T<sub>min</sub>*: 0.3;

• *T<sub>max</sub>*: 3.0;

• N<sub>iter</sub>: 500

Indexes	B-SOM	AB-SOM for multiple dissimilarity matrices
CR	0.31	0.42
F – measure	0.45	0.52
OERC	27.00%	9.00%

#### **Confusion matrix**

Cluster/Class	1	2	3	Majority Class
0,0	0	5	16	3
0,1	0	1	4	3
0,2	0	21	0	2
0,3	2	22	0	2
0,4	6	10	0	2
1,0	0	0	15	3
1,1	0	0	13	3
1,2	0	9	0	2
1,3	24	2	0	1
1,4	27	1	0	1



## Final relevance weight matrix

Cluster/Matrix	1	2	3	4	5	6
0,0	1.03	0.27	1.31	1.07	0.48	0.90
0,1	0.99	1.05	0.55	1.09	0.27	0.69
0,2	1.28	0.52	0.41	0.43	1.47	0.60
0,3	0.69	0.33	0.93	2.64	1.32	0.48
0,4	0.77	4.19	0.27	0.99	0.16	1.92
1,0	1.02	0.37	0.63	0.89	0.47	1.68
1,1	0.46	0.21	0.79	0.90	1.85	0.49
1,2	0.42	0.61	0.51	1.35	0.16	2.93
1,3	0.77	0.55	0.69	0.16	0.29	1.38
1,4	0.48	6.01	0.37	0.33	0.61	1.64



#### **Conclusions**

- The algorithm is able to partition objects taking into account their relational description given by multiple dissimilarity matrices.
- Learn relevance weights that change at each iteration and are different from one cluster to another.
- Performed better than batch SOM for single dissimilarity matrix on most data bases.



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