Subspace Memory Clustering

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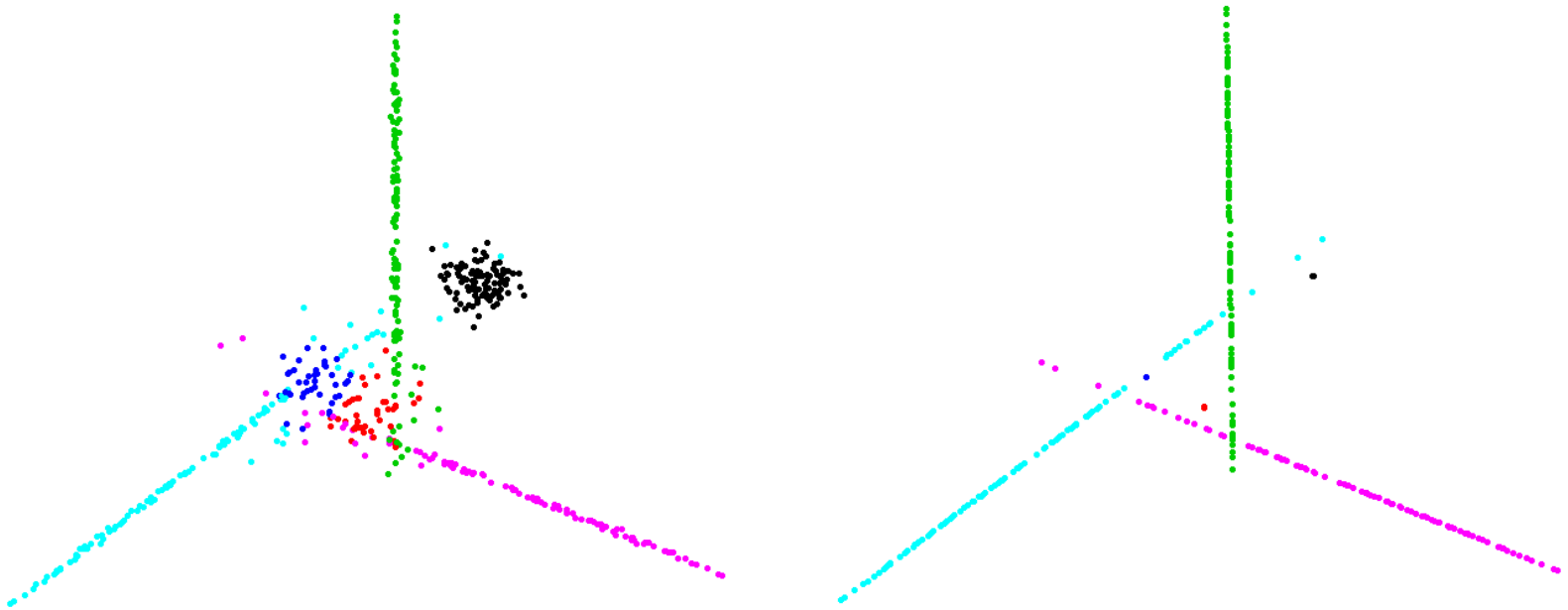
1. What is subspace clustering?
2. Our method
3. Experiments
4. Conclusions

Subspace clustering can be viewed as generalization of PCA.



(a) All points of a given dataset together with its clusters.

(b) Projections onto the subspaces.

Figure: Dividing a dataset into two zero-dimensional (points) and three one-dimensional subspaces (lines).

Why do we use subspace clustering?

We use subspace clustering in order to:

1. reduce the high number of data to several basic categories that can be used as objects for further analysis,
2. obtain a homogeneous test subjects,
3. reduce the workload and time analysis,
4. ...

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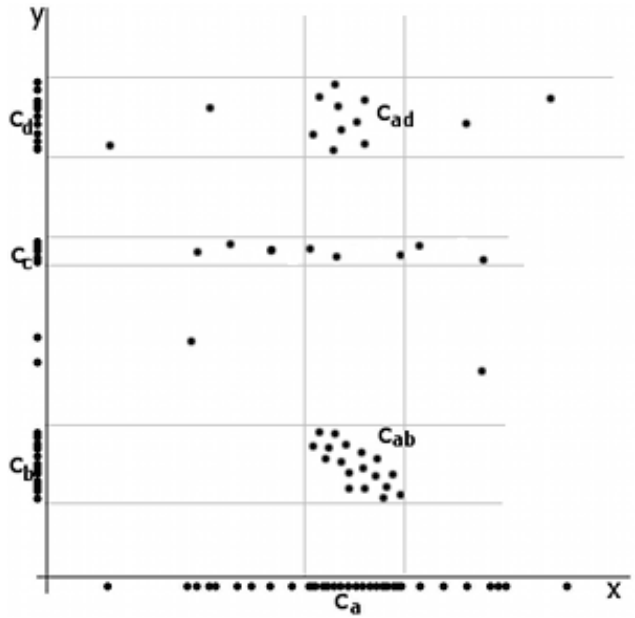
Applications:

1. image processing (e.g., image segmentation, representation and compression),
2. systems theory (e.g., hybrid system identification).

In general, subspace clustering algorithms can be divided into two main classes:

1. constructing axis parallel subspaces – this approach is used in methods: ENCLUS, MAFIA, CLTree, DOC, PROCLUS;



2. those who are able to build arbitrary subspaces – is used: ORCLUS, DBSCAN, PCA.

Our goal is to divide dataset $D \subset \mathbb{R}^N$, $N \in \mathbb{N}$ into $k \in \mathbb{N}$ pairwise disjoint clusters $D_1, \ldots, D_k$ $(D = D_1 \cup \ldots \cup D_k)$ such that each cluster is well represented by an affine subspace.

How can we do this?

For a fixed allowed memory we minimize the projection error.

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We need to answer on two questions:

1. How to calculate error?
2. What is memory?

Error:

Suppose that we have one cluster (group) $D \subset \mathbb{R}^N$ and an affine space $V \subset \mathbb{R}^N$ of dimension $n \leq N$. The total squared-error in cluster is given by

$$E[D; V] := \sum_{x \in D} \mathrm{dist}(x, V)^2,$$

where $\mathrm{dist}(x, V)$ describe distance between point and its orthogonal projection on subspace V.

We use the PCA method to construct the subspace V which minimizes the total squared-error with fixed level of allowed memory. Hence the optimal subspace is given by

$$V = \mathrm{mean}_D + \mathrm{span}(v_1, \ldots, v_n),$$

where mean_D is a mean of D and $v_1, \ldots, v_n$ are the n consecutive eigenvectors of the covariance matrix cov_D of D (ordered decreasingly with respect to eigenvalues).

This allows us to define the minimal projection error by

$$E[D, n] := E[D, \mathrm{mean}_D + \mathrm{span}(v_1, \ldots, v_n)]. \quad (1)$$

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Proposition 1 (*[I. Jolliffe. Principal component analysis. Wiley Online Library, 2005]*)

Let $D \subset \mathbb{R}^N$ be a given dataset, where $N \in \mathbb{N}$, and let $\lambda_1, \ldots, \lambda_N$ be the decreasingly ordered eigenvalues of covariance matrix of D. Then the squared error is given by

$$E[D, n] = |D| \cdot \sum_{i \in \mathbb{N},\ i > n} \lambda_i.$$

Memory:

Memory is understood as the number of scalars, which we need to describe a point after projection. We define the compression level of memory (measured by the number of used scalars) by

$$p := \frac{|D|n}{|D|N} = \frac{n}{N} \in [0, 1],$$

where $|D|$ is the cardinality of the dataset D.

Optimization problem. *Let dataset $D \subset \mathbb{R}^N$, the number of cluster k and the compression level $p \in [0,1]$ be given. Our goal is to find the splitting of D into k-clusters $D_1, \ldots, D_k$ and numbers $n_1, \ldots, n_k$, which minimize the total squared error*

$$E[D_1, n_1; \ldots; D_k, n_k] := E[D_1, n_1] + \ldots + E[D_k, n_k],$$

under the condition

$$\frac{n_1|D_1| + \ldots + n_k|D_k|}{N|D|} \leq p.$$

Algorithm

Optimization procedure:

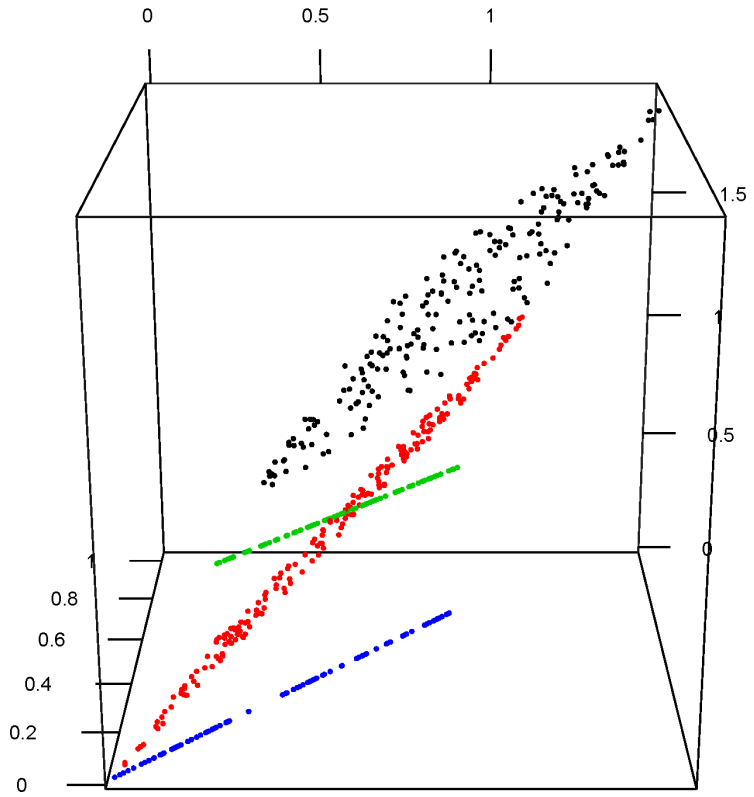
1. assign each point of D randomly to one of k clusters $D_1, \ldots, D_k$ and calculate the amount of memory $M_i = p \cdot |D_i| \cdot N$ for $i = 1, \ldots, k$,
2. proceed through all elements of the dataset D.
   a) switch position of point from the cluster where belongs $x \in D_i$ to another clusters D_j $(j \neq i)$, calculate square error of $E[\tilde{D}_i, \tilde{n}_i] + E[\tilde{D}_j, \tilde{n}_j]$ for all $j \neq i$ and we choose minimum from them (assume that it is realized by some $t \in \{1, \ldots, N\} \setminus \{i\}$),
   b) compare this minimum from $E[D_i, n_i] + E[D_t, n_t]$ and if we obtain smaller error by changing the belonging of point than we switch in 'original' cluster.
3. We repeat Step 2 until we do not switch the position of any point from our dataset.

We create two datasets $X_1, X_2 \subset \mathbb{R}^3$, which contain two 1-dimensional and two 2-dimensional clusters.

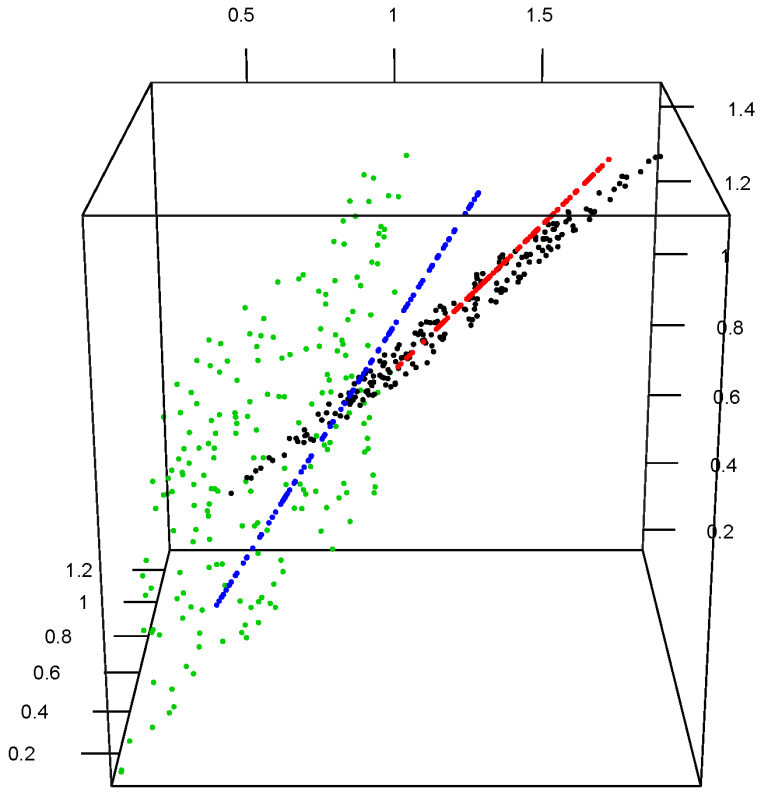
Dataset		X_1		X_2	
Dim. of clusters		1	2	1	2
Compression level for SuMC		0.33	0.66	0.33	0.66
Rand index	SuMC	0.8728381	1	0.7586923	1
	ORCLUS	1	0.7374569	0.9950417	0.8364218

Table: Comparison of SuMC and ORCLUS algorithms on synthetic datasets $X_1, X_2 \subset \mathbb{R}^3$, which have two 1-dimensional and two 2-dimensional subspaces (we divide on four clusters).

Our method allows to detect the optimal dimensions of the clusters.



(a) Clustering of dataset X_1 for $p = 0.63$.



(b) Clustering of dataset X_2 for $p = 0.56$.

In the next example we compare methods on datasets form the uci-repository `http://archive.ics.uci.edu/ml`. We consider three datasets from this repository: *glass*, *wine* and *yeast*.

Dim.	Rand index								
	Glass			Wine			Yeast		
	p	SuMC	ORCLUS	p	SuMC	ORCLUS	p	SuMC	ORCLUS
1	0.11	0.6715809	0.4869027	0.07	0.5330413	0.5588142	0.12	0.7325302	0.6405561
2	0.22	0.6973367	0.590935	0.15	0.629277	0.5567828	0.25	0.7277601	0.4985987
3	0.33	0.6814971	0.5919881	0.23	0.643433	0.5339935	0.37	0.7062958	0.6327916
4	0.44	0.6872888	0.6412619	0.31	0.6604456	0.5365962	0.5	0.6856921	0.6980632
5	0.55	0.6803563	0.6620157	0.38	0.5821748	0.5584333	0.62	0.6272326	0.7041102
6	0.66	0.6391558	0.6520995	0.46	0.5590681	0.5677649	0.75	0.6363158	0.6994391
7	0.77	0.6410425	0.669036	0.54	0.556275	0.5484035	0.87	0.7035431	0.7031342
8	0.88	0.5298144	0.6895704	0.61	0.5622421	0.6423538	1	0.7215641	0.7008795
9	1	0.6546444	0.6442017	0.69	0.5571002	0.5890307	—	—	—
10	—	—	—	0.77	0.5509427	0.6494001	—	—	—
11	—	—	—	0.85	0.568971	0.6478131	—	—	—
12	—	—	—	0.92	0.5589412	0.6065511	—	—	—
13	—	—	—	1	0.5534819	0.6621596	—	—	—

The main advantage of our methods:

1. automatically finds the optimal dimensions of the clusters,
2. we do not need to explicitly specify dimensions of groups.