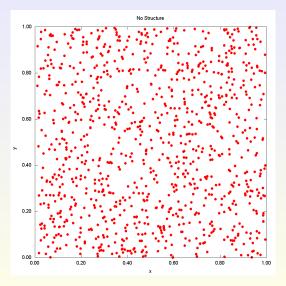
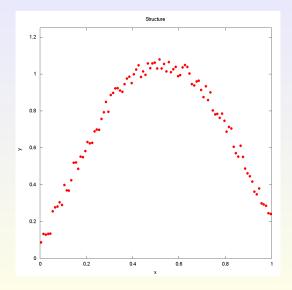
### What is Structure?

- Structure is a description of the dependencies
- Dependencies mean constraints
- Un-structured means no constraints
- Constraint means subset



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# Structure



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- Language by which the structure can be described
- Observed data is a sampled perturbed ideal
- Description is inexact
  - Closeness of the description to the observed data
  - Length of the description

## **Truth and Lies**

#### Truth

- Language is able to describe some of the underlying data structure
- Lies
  - What the language cannot describe is a lie by omission
  - Description is an estimate
  - Estimated structures have a random component
  - The difference between the true underlying structure and the estimated structure

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### Linear Regression Language

- Data: *x*<sub>1</sub>,..., *x<sub>K</sub>*
- Dimension:  $x_k = (x_k^1, \dots, x_k^N) \in \mathbb{R}^N$
- Dependency:  $x_k^N = \sum_{n=1}^{N-1} \alpha_n x_k^n$

• Error: 
$$\epsilon_k^2 = \left| x_k^N - \sum_{n=1}^{N-1} \alpha_n x_k^n \right|^2$$

Assumption: All points arise from the same process

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All observations have the same dependency



- Population
  - Healthy
  - Illnesses *A*<sub>1</sub>,..., *A*<sub>K</sub>
- It is not known how many illnesses there are
- Each person is measured with N lab tests
- The structure of the data is the inter-relationship(s) between the values of the lab tests

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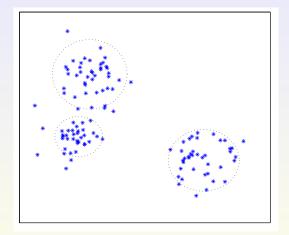
Linear Regression is the wrong Language

# **Example Test Report**

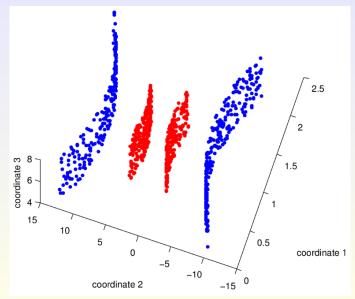
Alkaline Phosphatase	58	IU/L	25-150
Bilirubin Total	0.4	mg/dL	0.0-1.2
A/G Ratio	1.7		1.1-2.5
Globulin Total	2.5	g/dL	1.5-4.5
Albumin, Serum	4.3	g/dL	3.5-5.5
Protein, Total Serum	6.8	g/dL	6.0-8.5
Phosphorus, Serum	3.6	mg/dL	2.5-4.5
Calcium, Serum	9.3	mg/dL	8.7-10.2
Carbon Dioxide, Total	21	mmol/L	20-32
Chloride, Serum	105	mmol/L	97-108
Potassium, Serum	4.1	mmol/L	3.5-5.2
Sodium, Serum	140	mmol/L	134-144
<b>BUN/Creatinine Ratio</b>	19		9-20
eGFR If Africn Am	126	mL/min/1.73	>59
eGFR If NonAfricn Am	109	mL/min/1.73	>59
Creatinine, Serum	0.81	mg/dL	0.76-1.27
BUN	15	mg/dL	6-24

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# **Point Clusters**

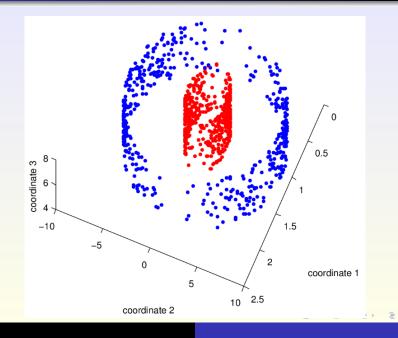


### Hyperbolic Clusters

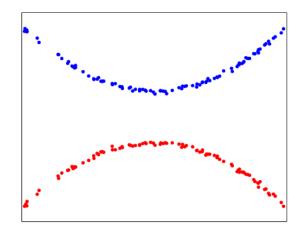


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# **Elliptic Clusters**

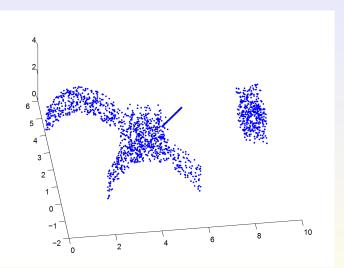


# **Manifold Clusters**



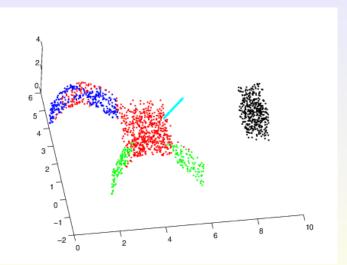
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# Manifold Clusters



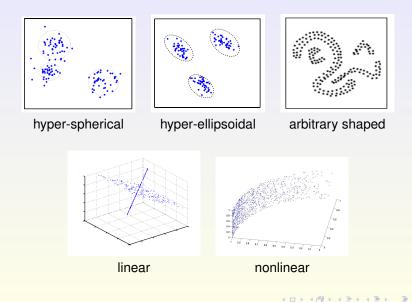
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# **Manifold Clusters**



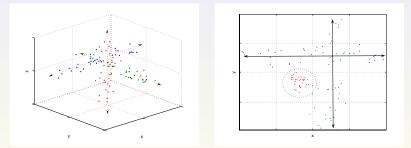
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### **Cluster Models**



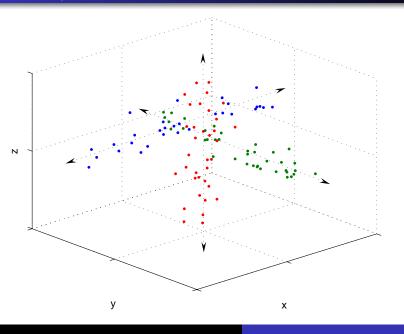
#### Subspace Clusters

 Consists of a subset of points and a corresponding subset of variables, such that these points form a dense region in a subspace defined by the set of corresponding variables.



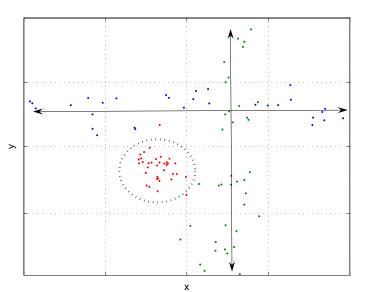
CLIQUE (Agrawal 98), MAFIA (Nagesh 99), PROCLUS (Aggarwal 99)

# Subspace Clusters



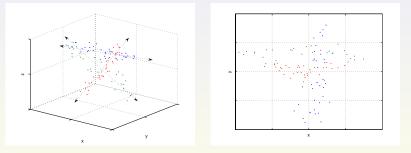
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# Subspace Clusters



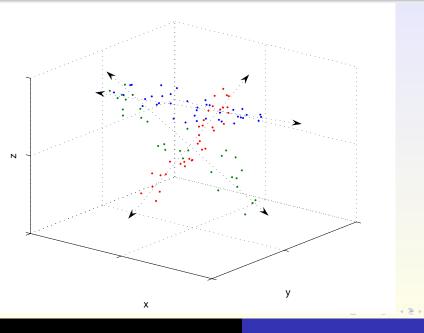
#### Arbitrary Oriented Subspace Clusters

 Consists of a subset of points and a corresponding linear combination of a subset of variables, such that these points form a dense region in a subspace defined by the set of corresponding linear combinations of variables.

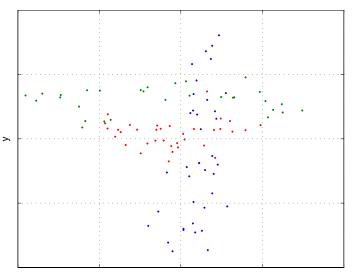


**ORCLUS** (Aggarwal 00)

# Arbitrary Oriented Subspace Clusters



### Arbitrary Oriented Subspace Clusters

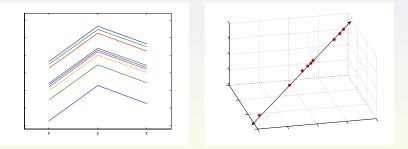


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### Pattern (Correlation) Clusters

 Consists of as a subset of objects and variables for which the participating objects show a similar trend rather than being close to each other.



Bicluster (Cheng 00), Floc (Yang 02), pCluster (Wang 02)

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#### Definition

*L* is a linear manifold of vector space *V* if and only if for some subspace *S* of *V* and translation  $t \in V$ ,

$$L = \{x \in V | \textit{for some } s \in S, x = t + s\}$$

The dimension of *L* is the dimension of *S*, and if the dimension of *L* is one less than the dimension of *V* then *L* is called a hyperplane.

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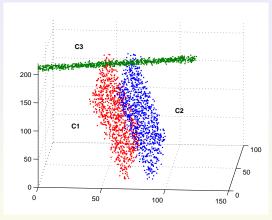
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The dimension of *L* is the dimension of *S*, and if the dimension of *L* is one less than the dimension of *V* then *L* is called a hyperplane.

A linear manifold is, in other words, a subspace that may have been shifted away from the origin.

A subspace is a linear manifold that contains the origin.

### **Dense Linear Manifold Clusters**



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The cluster model has the following properties:

• The points in each cluster lie close to a low dimensional linear manifold.

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- The manifold is arbitrarily oriented.

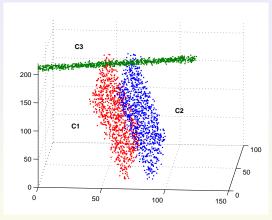
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The cluster model has the following properties:

- The points in each cluster lie close to a low dimensional linear manifold.
- The intrinsic dimensionality of the cluster is the dimensionality of the linear manifold.
- The manifold is arbitrarily oriented.
- The points in the cluster induce a correlation among two or more attributes (or linear combinations of attributes) of the data.
- In the orthogonal complement space to the manifold the points form a compact densely populated region, which can be used to cluster the data.

### **Dense Linear Manifold Clusters**



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#### Comment

Classical clustering algorithms such as K-means assume that each cluster is associated with a zero dimensional manifold (the center) and therefore omit the possibility that a cluster may have non-zero dimensional linear manifold associated with it.

#### Definition

- Let D be a set of N-dimensional points in  $\mathbb{R}^N$
- $C \subseteq D$  a subset of points that belong to a cluster
- x some point in C
- $b_1, \ldots, b_N$  an orthonormal set of vectors that span  $\mathbb{R}^N$
- (b<sub>i</sub>,...,b<sub>j</sub>) a matrix whose columns are the vectors b<sub>i</sub>,...,b<sub>j</sub>
- $\mu$  some point in  $\mathbb{R}^N$

Then each  $x \in C$  can be modeled by,

 $x = \mu + (b_1, \ldots, b_m)\lambda + (b_{m+1}, \ldots, b_N)\psi$ 

$$\begin{aligned} x &= \mu + (b_1, \dots, b_m) \lambda^{m \times 1} + (b_{m+1}, \dots, b_N) \psi^{N-m \times 1} \\ x &= \mu + B^{N \times m} \lambda^{m \times 1} + B_c^{N \times N-m} \psi^{N-m \times 1} \end{aligned}$$

- The idea is that each point in a cluster lies close to a *m*-dimensional linear manifold, defined by μ + span{b<sub>1</sub>,..., b<sub>m</sub>}.
- $\lambda^{m \times 1}$  models the spread of the points in the manifold
  - Each entry of the  $m \times 1$  random vector  $\lambda$  is i.i.d. U(-R/2, +R/2)
  - In the manifold points are uniformly distributed in each direction

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$$x = \mu + (b_1, \dots, b_m)\lambda^{m \times 1} + (b_{m+1}, \dots, b_N)\psi^{N-m \times 1}$$
  
$$x = \mu + B^{N \times m}\lambda^{m \times 1} + B_c^{N \times N-m}\psi^{N-m \times 1}$$

- $\psi^{N-m\times 1}$  a small perturbation associated with each point in the cluster. The idea is that each point may be perturbed in directions that are orthogonal to the manifold, i.e., the vectors  $b_{m+1}, \ldots, b_N$ .
- This is modeled by requiring that the (N m) × 1 random vector ψ ~ N(0, Σ), where the largest eigenvalue of Σ is much smaller than R.
- Since the variance along each of these directions is much smaller than the range *R* of the embedding, the points are likely to form a compact and densely populated region.

#### Main Idea

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### Main Idea

 Sample minimal subsets of points to construct trial linear manifolds of various dimensions.

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# The Algorithm

### Main Idea

- Sample minimal subsets of points to construct trial linear manifolds of various dimensions.
- 2 Compute distance histograms of the data to each trial manifold.

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# The Algorithm

### Main Idea

- Sample minimal subsets of points to construct trial linear manifolds of various dimensions.
- 2 Compute distance histograms of the data to each trial manifold.
- Of all the manifolds constructed, select the one whose associated histogram shows the best separation between a mode near zero and the rest of the data.

# The Algorithm

### Main Idea

- Sample minimal subsets of points to construct trial linear manifolds of various dimensions.
- 2 Compute distance histograms of the data to each trial manifold.

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- Of all the manifolds constructed, select the one whose associated histogram shows the best separation between a mode near zero and the rest of the data.
- Partition the data based on the best separation.

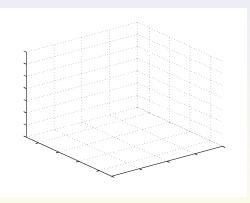
#### Main Idea

- Sample minimal subsets of points to construct trial linear manifolds of various dimensions.
- 2 Compute distance histograms of the data to each trial manifold.
- Of all the manifolds constructed, select the one whose associated histogram shows the best separation between a mode near zero and the rest of the data.
- Partition the data based on the best separation.
- Sepeat the procedure on each block of the partitioned data.

### How are trial manifolds sampled?

To construct an *m*-dimensional manifold we need to sample m + 1 points.

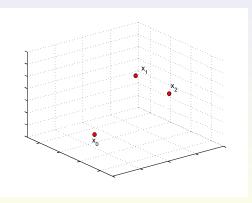
Example- constructing a 2D manifold



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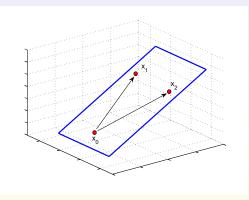
Example- constructing a 2D manifold



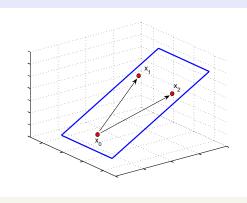
# How are trial manifolds sampled?

To construct an *m*-dimensional manifold we need to sample m + 1 points.

Example- constructing a 2D manifold



# How are the trial manifolds sampled?



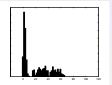
$$\mu = x_0$$
  

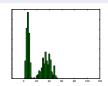
$$\hat{B} = (\hat{b}_1, \hat{b}_2) = (x_1 - x_0, x_2 - x_0)$$
  

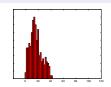
$$B = orthonormal \hat{B}$$
  

$$dist(x) = \|(I - BB')(x - \mu)\|$$

# Selecting the best trial manifold/best separation

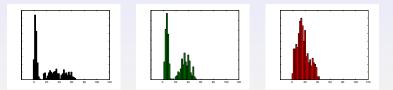








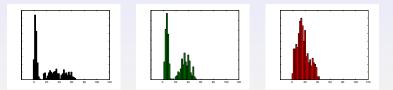
# Selecting the best trial manifold/best separation



 To compute a separation score we first need to find the two classes or distributions involved.

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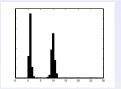
# Selecting the best trial manifold/best separation

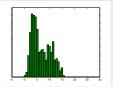


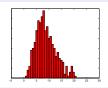
- To compute a separation score we first need to find the two classes or distributions involved.
- This problem is cast into histogram thresholding problem.

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# Selecting the best trial manifold

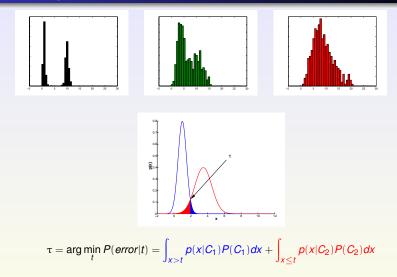




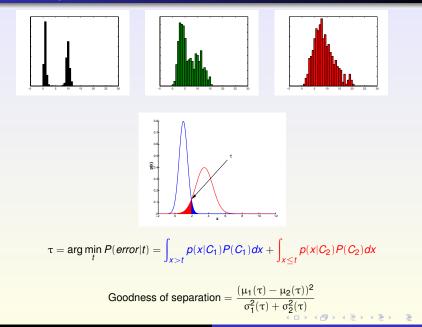




# Selecting the best trial manifold

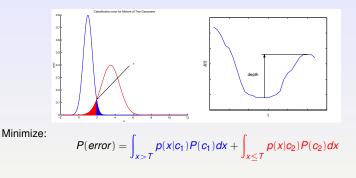


# Selecting the best trial manifold

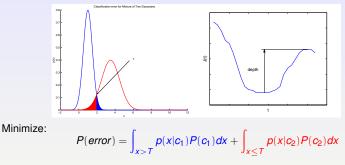






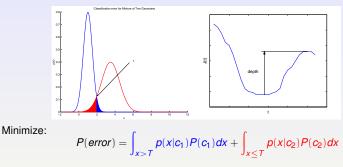






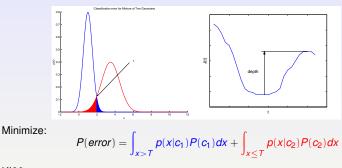
KI86:

 $J(T) = 1 + 2(P_1(T)\log\sigma_1(T) + P_2(T)\log\sigma_2(T)) - 2(P_1(T)\log P_1(T) + P_2(T)\log P_2(T))$ 



KI86:

 $J(T) = 1 + 2(P_1(T)\log \sigma_1(T) + P_2(T)\log \sigma_2(T)) - 2(P_1(T)\log P_1(T) + P_2(T)\log P_2(T))$ Depth = J(T') - J(T)



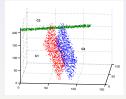
KI86:

 $\begin{aligned} J(T) &= 1 + 2 \left( P_1(T) \log \sigma_1(T) + P_2(T) \log \sigma_2(T) \right) - 2 \left( P_1(T) \log P_1(T) + P_2(T) \log P_2(T) \right) \\ Depth &= J(T') - J(T) \end{aligned}$ 

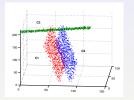
Goodness of separation:

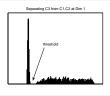
$$\label{eq:Discriminability} \textit{Discriminability} = \frac{(\mu_1(T) - \mu_2(T))^2}{\sigma_1^2(T) + \sigma_2^2(T)} \quad \times \quad \textit{Depth}$$

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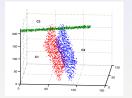


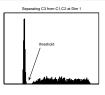
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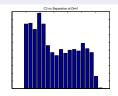




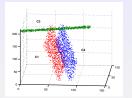
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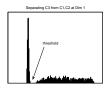


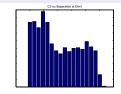


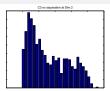


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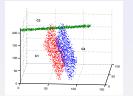


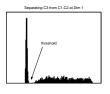


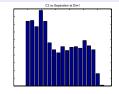




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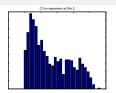


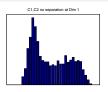


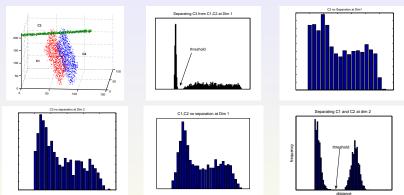


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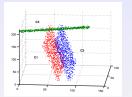


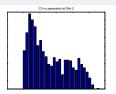


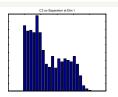


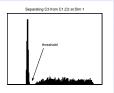
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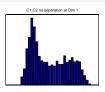
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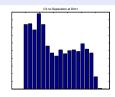


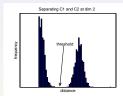


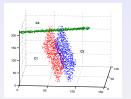


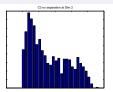


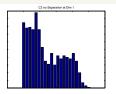


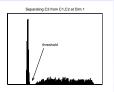


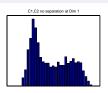


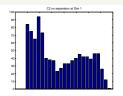


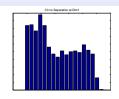


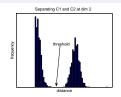


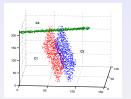


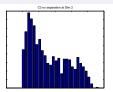


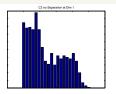


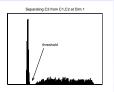


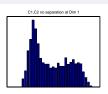


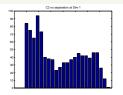


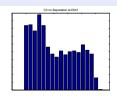


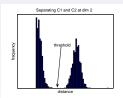


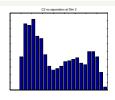












# **Empirical Evaluation**

- Evaluation Criteria:
  - Accuracy
  - Efficiency and Scalability
  - Stability
- Data Sets:
  - Synthetic
  - Real
- Algorithms Compared Against:
  - DBSCAN  $O(N^2d)$  (Ester at el. 96)
  - ORCLUS  $O(K^3 + kNd + K^2d^3)$  (Aggarwal 00)

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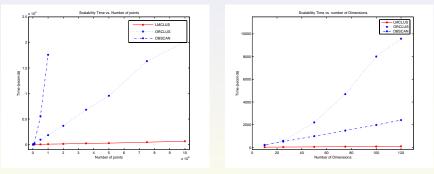
• HPCluster (Haralick at el. 04)

# **Empirical Evaluation- Accuracy**

	size	clusters	dim	LM dim	LMCLUS	ORCLUS	DBSCAN	HPCluster
$D_1$	3000	3	4	2-3	95% / 0:0:08	80% / 0:0:22	34.6% / 0:0:9	72% / 0:0:51
$D_2$	3000	3	20	13-17	98.4% / 0:0:33	58.8% / 0:2:18	65.5% / 0:0:36	97.4% / 0:1:39
$D_3$	30000	4	30	1-4	100% / 0:15:38	64.9% / 1:5:30	100% / 1:31:52	99.3% / 0:1:32
$D_4$	6000	3	30	4-12	99.9% / 0:9:22	98.3% / 0:8:20	66.5% / 0:3:49	97.1% / 0:0:12
$D_5$	4000	3	100	2-3	100% / 0:0:20	87.9% / 0:54:30	65.3% / 0:5:24	99% / 0:3:54
$D_6$	90000	3	10	1-2	99.99% / 0:0:29	100% / 0:29:02	66.7% / 4:58:49	100% / 0:1:23
$D_7$	5000	4	10	2-6	99.24% / 0:2:05	99.3% / 0:2:41	74.1% / 0:0:54	96% / 0:0:35
$D_8$	10000	5	50	1-4	99.9% / 0:1:42	63.64% / 1:33:52	100% / 0:17:00	99.2% / 0:3:43
$D_9$	80000	8	30	2-7	99.9% / 3:12:46	96.9% / 13:30:30	100% / 10:51:15	99.9% / 0:4:57
$D_{10}$	5000	5	3	1-2	86.5% / 0:0:48	68.2% / 0:0:45	59.6% / 0:0:5	78% / 0:0:33
$*D_{11}$	1500	3	3	1	98.5% / 0:0:01	99.6% / 0:0:10	42.6% / 0:0:02	33.3% / 0:0:52
$*D_{12}$	1500	3	3	2	97% / 0:0:02	99% / 0:0:11	33.8% / 0:0:02	33.3% / 0:0:26
$*D_{13}$	1500	3	7	3	97.7% / 0:0:05	99.1% / 0:0:17	33.9% / 0:0:04	33.3% / 0:0:34
$*D_{14}$	5000	5	20	4	99.9% / 0:5:46	100% / 0:10:42	21.1% / 0:1:39	20% / 0:1:30
$*D_{15}$	4000	4	50	3	99% / 0:9:14	100% / 0:25:52	25% / 0:2:34	25% / 0:3:20

# **Empirical Evaluation- Efficiency and Scalability**

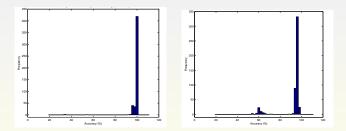
### $O(N^2K^2L^3d)$



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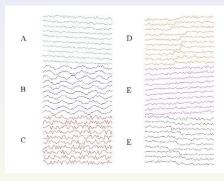
# **Empirical Evaluation- Stability**

		LMCLUS	ORCLUS	
1st data set	mean	99.1	92.1	
	median	99.9	95.5	
	std	4.7	10.56	
2nd data set	mean	97.36	99.26	
	median	97.4	99.47	
	std	0.0053	0.0049	



# Time Series Clustering (UCI KDD Archive)

# $600 \times 60$ , A-decreasing trend, B-cyclic, C-normal, D-upward shift, E-increasing trend, F-downward shift.



	in1	in2	in3	in4	in5	in6	total
out1	0	0	0	57	0	0	57
out2	0	0	80	0	1	0	81
out3	0	0	0	43	0	99	142
out4	0	0	20	0	98	0	118
out5	99	0	0	0	0	0	99
out6	0	41	0	0	0	0	41
out7	0	23	0	0	0	0	23
out8	1	36	0	0	1	1	39
total	100	100	100	100	100	100	600

Total Correct=533 Accuracy=88.8333

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#### model: $x = \mu + \mathbf{1}\phi + \psi$

# Time Series Clustering (UCI KDD Archive)

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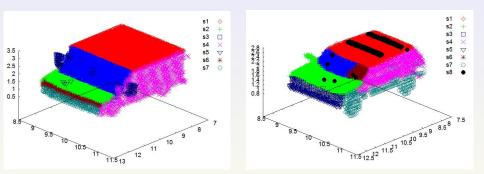
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# E3D Point Cloud Segmentation (ALPHATECH Inc.)



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### Clustering Techniques Have A Variety of Ways

- Specify Number of Clusters
- Specify Minimum Cluster Size
- Specify a Minimum Quality Score for a Cluster

# Minimum Description Length

- Clustering details the Structure of the data
- The Structure of the data should be more compact that a list of coordinates of each data point
- Good Clustering
  - The Description Length needed for describing the structure of the data is less

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# Manifold Cluster Description Length

- Description Length for Manifold
- Description Length for points projected to the manifold
- Error Toleration Parameter
- Description Length for point perturbation off the manifold

• To within Error Tolerance

# Manifold Description Length

- 1: Dimension K of Cluster
- N: Offset vector from origin
- Orthonormal Manifold basis set
  - Basis Vectors KN
  - Norm 1: K constraints
  - Orthogonality:  $\frac{K(K-1)}{2}$  constraints

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- $KN \frac{K(K+1)}{2}$  numbers
- Each number B bits

• Total: 
$$B[1 + N + K(N - \frac{K+1}{2})]$$

# Manifold Cluster Description Length

- M Data points on a manifold are described by their manifold coordinates
- A Data Point in a *K*-dimensional manifold has *K* coordinates
- The *K* coordinates are the coefficients of its basis vector representation  $x^{N \times 1} = \mu^{N \times 1} + B^{N \times K} \lambda^{K \times 1}$
- An observed data point is near but not on the manifold
  - Determine the number of bits that it would take to encode the perturbation that brings a point from its coordinates on the manifold to its associated observation off the manifold to within the Error Tolerance
  - Entropy E of the N K perturbation distribution
  - Total: *MK* + *E*

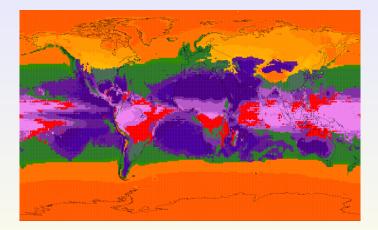
- X = BMN: Number of bits to represent the *M* data points of a cluster in its original representation
- $Y = B[1 + N + K(N \frac{(K+1)}{2}) + BKM + E$ : Number of bits to represent the *M* data points in the manifold cluster
- If Y << X keep the cluster

- $\frac{1}{2}^{\circ}$ , 1°, 2°
- A few decades
- By Month
  - Average Temperature
  - Average Precipitation

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24-Dimensional

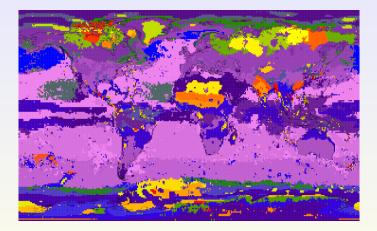
# **Climate Zones Ground Truth**



Done manually

Ground Truth Data is known to be faulty

# Linear Manifold Clusters



- Done automatically
- Temperature and Precipitation