## CONSENSUS CLUSTERING VIA PIVOTAL METHODS

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## Summary

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## The Cluster Ensemble Framework

## K-Means Clustering Problem

K-means clustering is a simple and widely used approach for partitioning a data set into $k$ distinct, non-overlapping clusters.

Given a dataset $\mathbf{Y}=\left(y_{1}, \ldots, y_{n}\right)$, with $y_{i} \in \mathcal{Y} \subset \mathbb{R}^{d}$, K-means seeks to find a partition of the data into $K$ clusters by minimizing the sum of squared distances between every data point and its nearest cluster center, that is

$$
\underset{C_{1}, \ldots, C_{K}}{\operatorname{minimize}}\left\{\sum_{k=1}^{K} \sum_{y_{i} \in C_{k}}\left\|y_{i}-\mu_{k}\right\|^{2}\right\}
$$

where $\mu_{k}$ is the $k$-th cluster center.

## K-Means Algorithm

The $k$-means algorithm finds a local solution by iteratively assigning each data point to the cluster with the closest center, using random cluster initialization.


## K-Means Clustering: different initializations

Different initial centers may lead to different solutions:


One might have to run the algorithm multiple times with random starting centers (seeds) for each run: the final solution is the one for which the objective is minimized

## The K-Means algorithm: weaknesses

Despite its popularity, well known limitations of $k$-means algorithm are:

- convergence to a local minimum may produce 'wrong' results;
- it is sensitive to the choices of initial cluster centres
- the $k$-means algorithm works poorly in the case of unbalanced cluster sizes and non-spherical shapes.

Extensions of $k$-means and initialization strategies have been developed [Jain, 2010; Arthur \& Vassilvitskii, 2007].

## Cluster Ensembles

Cluster ensemble methods have emerged from the need to combine data partitions and generate a better clustering result [Strehl \& Ghosh (2002)]
Clustering ensembles can be generated by

- applying different clustering algorithms
- exploring different proximity measures
- using the same clustering algorithm with different parameters or initializations

Evidence accumulation clustering is based on the assumption that each clustering result as an independent evidence of data structure [Fred \& Jain (2005)]

## Pairwise-similarity based approach

Given a set of $n$ observations $\left(y_{1}, \ldots, y_{n}\right)$ and a set of $H$ partitions $\mathcal{P}=\left\{P^{1}, P^{2}, \ldots, P^{H}\right\}$ into $K$ disjoint clusters, a co-association matrix can be used to represent the ensemble information:

$$
c_{i, j}=\frac{n_{i, j}}{H}
$$

where $n_{i, j}$ is the number of times the pair $\left(y_{i}, y_{j}\right)$ is assigned to the same cluster among the $H$ partitions of the ensemble. The $n \times n$ matrix $C$

- is used to obtain the consensus partition
- fulfils the conditions of a similarity matrix
- is expected to contain a non-negligible number of zeros

Pivotal methods in K-means clustering

## Our proposal

The proposed approach can be summarized as follows:

1. cluster ensembles are created using repeated runs of a single clustering algorithm (e.g. the $K$-means technique with a random initialization of cluster centres)
2. specific units called pivots can be identified via the co-association matrix, such that they are representative of the group they belong to (because they never or very rarely co-occur with members of other groups)
3. the pivots are used to define a new initialization step in the $K$-means algorithm, in order to reduce the effect of random seeding

## Pivotal units

The starting point for the pivotal methods we propose is a partition $G_{1}, \ldots, G_{K}$ of $y_{1}, \ldots, y_{n}$ into $K$ groups (reference partition) obtained, for instance, by applying agglomerative hierarchical clustering:

- We assume that $K$ distinct pivots do exist and propose some criteria to identify them
- each pivot can be chosen so that it is as far as possible from units that might belong to other groups and/or as close as possible to units that belong to the same group

Again $C=\left(c_{i j}\right)$ denotes the co-association matrix produced by multiple clusterings of the same data set.

## Pivot identification criteria

The pivot $y_{i_{k}}$ for group $G_{k}, k=1, \ldots, K$, is chosen so that

- it maximizes the 'global' within similarity

$$
\text { (a) } \max _{i_{k}} \sum_{j \in G_{k}} c_{i_{k}, j}
$$

- it minimizes the 'global' similarity between one group and all the others

$$
\text { (b) } \quad \min _{i_{k}} \sum_{j \notin G_{k}} c_{i_{k}, j}
$$

- or maximizes the discrepancy between global within and between similarities

$$
\text { (c) } \max _{i_{k}}\left(\sum_{j \in G_{k}} c_{i_{k}, j}-\sum_{j \notin G_{k}} c_{i_{k}, j}\right)
$$

## MUS Algorithm

When the number of groups is small, an alternative strategy to detect pivotal units is the algorithm of Maxima Units Search (MUS):

- firstly introduced in the framework of label switching problem in Bayesian estimation of finite mixture models
- Given a large and sparse 0-1 matrix, the MUS algorithm seeks those elements, among a specified number of candidate pivots, whose corresponding rows contain more zeros compared to all other units
- ideally, the submatrix of $C$ with only the rows (columns) of the selected pivotal units is identical
[Egidi, Pappadà, Pauli, Torelli $(2018 a, b)$ ]


## piv_KMeans: Algorithm

1. Initialization

> [a] Generate the clustering ensemble $\mathcal{P}$ of $H$ partitions, where each clustering is the result of a $K$-means run with randomly selected cluster centers $\mu_{1}, \ldots, \mu_{K}$

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[c] Given a partition of the data set in $K$ groups, $G_{1}, \ldots, G_{K}$, apply a pivotal method to $C$, choosing among MUS, (a)-(c), to find the pivots $y_{i_{1}}, \ldots, y_{i_{k}} \rightarrow$ set $\mu_{k}=y_{i_{k}}$

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2. Obtain the consensus partition

Run the $K$-means algorithm using the pivots as initial cluster centers

## The R package 'pivmet'

The piv_KMeans algorithm is implemented in the $R$ package pivmet via the function piv_KMeans():

- x : the data, in either matrix or data frame format
- centers: the number of clusters $K$

$$
\begin{aligned}
& \text { piv_KMeans(x, centers, alg.type = "KMeans", } \\
& \text { piv.criterion }=\text { "MUS", } H=1000, \ldots \text { ) }
\end{aligned}
$$

By default piv_KMeans obtains a partition of $x$ into the number of groups specified by centers via the $K$-means algorithm.
Then, finds $K$ pivots from the co-association matrix derived from $H=1000$ runs of $K$-means with random seeds, using the selected pivotal method. If centers < 5, default is MUS.

## The piv_KMeans function

| Argument | Description |
| :---: | :---: |
| x | The data object with $N$ observations (a matrix, vector or data frame) |
| centers | The number of clusters in the solution |
| alg.type | The clustering algorithm for the initial partition: "KMeans" (default) or "hclust" |
| method | If alg.type="hclust", the agglomeration method: "single", "complete", "average", "ward.D", "ward.D2", "mcquitty", "median", "centroid" |
| piv.criterion | The pivotal criterion: "MUS", "maxsumint", "minsumnoint","maxsumdiff" |
| H | The number of distinct $k$-means runs used for building the $N \times N$ co-association matrix. Default is 1000 |
| prec_par | If piv.criterion="MUS", the user-specified value of candidate pivots for each group. |

Table 1: Overview of arguments for piv_KMeans().

## Illustration: ‘Two-sticks’ data



Figure 1: 'Two-sticks' data (two groups of 30 and 370 observations, respectively). Group centers (asterisks) and pivots (triangles) are shown on the plots.
Pivotal methods in K-means clustering $\quad$ R. Pappadà (rpappada@units.it) $15 / 27$

## Artificial Data

## Simulation settings

- We simulate 1000 bivariate datasets from a mixture of three Gaussian distributions
- The components have sample size 20,100 and 500, respectively
- The K-means algorithm with random seeds is used to generate a cluster ensemble of dimension $H=1000$
- The solution with $K=3$ from hierarchical clustering (Average-Linkage) is used as reference partition


## Comparing the clustering solutions

ARI: K-Means vs Piv_KMeans (1000 iterations)





Figure 2: ARI over 1000 runs of piv_KMeans and $K$-means on 3-component 2D Gaussian data.

## Comparison with other consensus methods

Ensemble methods based on the pairwise similarity amongst data points uses the co-association matrix $C=\left(c_{i, j}\right)$ that summarizes the entire ensemble in order to define the dissimilarities

$$
d_{i, j}=1-c_{i, j}
$$

The final clustering result is generated by applying any similaritybased clustering algorithm (as a consensus function) to this matrix (e.g. agglomerative hierarchical clustering (agnes), PAM for partitioning 'around medoids')

## Comparison with other consensus methods



Figure 3: Mixture of three Gaussian distributions (sample size $n=620$ ) with mean vectors $\mu_{1}=(1,5), \mu_{2}=(4,0), \mu_{3}=(6,6)$, and covariance matrix the $2 \times 2$ identity matrix.

Pivotal methods in $K$-means clustering

## Preliminary results

The table shows the mean Adjusted Rand Index (1000 simulations) between the consensus partition and the true data partition for the 2D Gaussian data.

| Pivotal | MUS | $(a)$ | $(b)$ | $(c)$ |
| :--- | :--- | :--- | :--- | :--- |
| methods | 0.857 | 0.865 | 0.883 | 0.779 |
| Other consensus | agnes $(A L)$ | agnes $(S L)$ | agnes $(C L)$ | PAM |
| methods | 0.512 | 0.535 | 0.514 | 0.506 |

## Concluding remarks

## To sum up

We propose a modified version of the standard $K$-means algorithm, by considering a pivot-based initialization step:

- The co-association derived from a cluster ensemble is used to identify pivotal units, different criteria can be used
- Simulation results reveal that a careful seeding based on pivotal units may improve the final clustering results
- Pivotal methods for relabelling and data clustering are implemented in the R package pivmet, available from the Comprehensive R Archive Network
- Ongoing work explores the advantage of using pivotal methods for selecting the appropriate number of groups


## References

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## Thank you for your attention!

## Appendix

## MUS Algorithm

Consider a large and sparse $n \times n$ symmetric matrix where each row (column) is a statistical unit and the units belongs to $\mathcal{K}$ groups Here $\mathcal{K}=3$ and groups are $C_{1}=\{1,2,3\}, C_{2}=\{4,5,6\}$, $C_{3}=\{7,8,9\}$.

$$
\begin{aligned}
& \begin{array}{lllllllll}
1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 & 9
\end{array} \\
& X=\begin{array}{l}
1 \\
2 \\
3 \\
3 \\
4 \\
5 \\
6 \\
7 \\
7 \\
8 \\
9
\end{array}\left(\begin{array}{lllllllll}
1 & 1 & 1 & 1 & 1 & 0 & 1 & 0 & 0 \\
1 & 1 & 0 & 0 & 1 & 0 & 1 & 0 & 0 \\
1 & 0 & 1 & 0 & 1 & 0 & 1 & 0 & 0 \\
1 & 0 & 0 & 1 & 1 & 0 & 1 & 1 & 0 \\
1 & 1 & 1 & 1 & 1 & 1 & 1 & 0 & 1 \\
0 & 0 & 0 & 0 & 1 & 1 & 1 & 0 & 0 \\
1 & 1 & 1 & 1 & 1 & 1 & 1 & 0 & 1 \\
0 & 0 & 0 & 1 & 0 & 0 & 0 & 1 & 0 \\
0 & 0 & 0 & 0 & 1 & 0 & 1 & 0 & 1
\end{array}\right)
\end{aligned}
$$

## MUS Algorithm: Step (i)

For $k \in\{1,2,3\}$ first select $\bar{m}$ units in the $k$-th group with a higher number of zeros with respect to the other groups

$$
\mathrm{X}=\left(\begin{array}{lllllllll}
\mathbf{1} & \mathbf{1} & \mathbf{1} & 1 & 1 & 0 & 1 & 0 & 0 \\
\mathbf{1} & \mathbf{1} & \mathbf{0} & 0 & 1 & 0 & 1 & 0 & 0 \\
\mathbf{1} & \mathbf{0} & \mathbf{1} & 0 & 1 & 0 & 1 & 0 & 0 \\
1 & 0 & 0 & \mathbf{1} & \mathbf{1} & \mathbf{0} & 1 & 1 & 0 \\
1 & 1 & 1 & \mathbf{1} & \mathbf{1} & \mathbf{1} & 1 & 0 & 1 \\
0 & 0 & 0 & \mathbf{0} & \mathbf{1} & \mathbf{1} & 1 & 0 & 0 \\
1 & 1 & 1 & 1 & 1 & 1 & \mathbf{1} & \mathbf{0} & \mathbf{1} \\
0 & 0 & 0 & 1 & 0 & 0 & \mathbf{0} & \mathbf{1} & \mathbf{0} \\
0 & 0 & 0 & 0 & 1 & 0 & \mathbf{1} & \mathbf{0} & \mathbf{1}
\end{array}\right)
$$

$\mathcal{K}=3$
$\overline{\mathbf{m}}=\mathbf{2}:$ Candidates $=\{2,3,4,6,8,9\}$

## MUS Algorithm - Step (ii)

a. For each group $k$ and each candidate $i^{*}$, consider the set of units in a different group with a zero in the corresponding cell (denote it by $\mathcal{P}^{k}$ )
b. count the identity matrices of rank $\mathcal{K}$ that can be constructed with $i^{*}$ and units in $\mathcal{P}^{k}$.

Example: Group $C_{1}$ (red), unit $i_{1}^{*}=2$

$$
X=\left(\begin{array}{l|llllllll}
1 & 1 & 1 & 1 & 1 & 0 & 1 & 0 & 0 \\
1 & 1 & 0 & 0 & 1 & 0 & 1 & 0 & 0 \\
1 & 0 & 1 & 0 & 1 & 0 & 1 & 0 & 0 \\
1 & 0 & 0 & 1 & 1 & 0 & 1 & 1 & 0 \\
1 & 1 & 1 & 1 & 1 & 1 & 1 & 0 & 1 \\
0 & 0 & 0 & 0 & 1 & 1 & 1 & 0 & 0 \\
1 & 1 & 1 & 1 & 1 & 1 & 1 & 0 & 1 \\
0 & 0 & 0 & 1 & 0 & 0 & 0 & 1 & 0 \\
0 & 0 & 0 & 0 & 1 & 0 & 1 & 0 & 1
\end{array}\right)
$$

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Example: Group $C_{1}$ (red), unit $i_{1}^{*}=2$


## MUS Algorithm

Group $C_{1}$ (red), unit $i_{1}^{*}=3$

$$
X=\left(\begin{array}{ll|l|llllll}
1 & 1 & 1 & 1 & 1 & 0 & 1 & 0 & 0 \\
1 & 1 & 0 & 0 & 1 & 0 & 1 & 0 & 0 \\
1 & 0 & 1 & 0 & 1 & 0 & 1 & 0 & 0 \\
1 & 0 & 0 & 1 & 1 & 0 & 1 & 1 & 0 \\
1 & 1 & 1 & 1 & 1 & 1 & 1 & 0 & 1 \\
0 & 0 & 0 & 0 & 1 & 1 & 1 & 0 & 0 \\
1 & 1 & 1 & 1 & 1 & 1 & 1 & 0 & 1 \\
0 & 0 & 0 & 1 & 0 & 0 & 0 & 1 & 0 \\
0 & 0 & 0 & 0 & 1 & 0 & 1 & 0 & 1
\end{array}\right)
$$

## MUS Algorithm

Group $C_{1}$ (red), unit $i_{1}^{*}=3$

## MUS Algorithm

Group $C_{1}$ (red), unit $i_{1}^{*}=3$

Step (iii) For group $C_{1}=\{1,2,3\}$, the pivot is $i_{1}^{*}=2$ if $M_{2}>M_{3}, i_{1}^{*}=3$, otherwise.

