Student: Cristian Pachón García Advisor: Pedro Delicado Useros

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What is MDS?

Introduction

What is MDS?

- MDS is a family of methods that represents measurements of dissimilarity (or similarity) among pairs of objects as Euclidean distances between points of a low-dimensional space.
- Given a square matrix **D** n × n, the goal of MDS is to obtain a configuration matrix **X** n × p satisfying:
 - Columns are orthogonal.

Algorithms for MDS with Big Data

 The Euclidean distance between the rows of X is approximately equal to D.

- X can be interpreted as the matrix of p variables for the n observations.
- The columns of **X** are called *principal coordinates*.

Example



Consider the distance between some cities of Europe, as shown in the following matrix:

	Athens	Barcelona	Brussels	Calais	Cherbourg	
Athens	0	3313	2963	3175	3339	•••
Barcelona	3313	0	1318	1326	1294	
Brussels	2963	1318	0	204	583	
Calais	3175	1326	204	0	460	
Cherbourg	3339	1294	583	460	0	
:	:	:	:	:	:	٠

Table: Distances between European cities (just 5 of them are shown).

Algorithms for MDS with Big Data





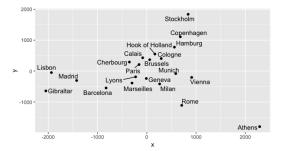


Figure: MDS configuration for European cities

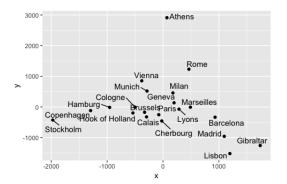


Figure: (Another) MDS configuration for European cities

Given a MDS configuration, any rotation, reflection or translation is a valid MDS configuration, since they preserve the distance. So, the solution is not unique.



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Procrustes transformation

- The Procrustes problem is concerned with fitting a configuration (testee) to another (target) as closely as possible.
- Under orthogonal transformations, the testee can be fitted to the target. In addition to such rigid motions, one may also allow for dilations and for shifts

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• Let **A** and **B** be two different MDS configurations of dimensions $n \times t$ for the same set of data. Without loss of generality, let's assume that the target is **A** and the testee is **B**. One wants to obtain $s \in \mathbb{R}$, $T \in M_{r \times r}(\mathbb{R})$ and $\mathbf{t} \in \mathbb{R}^r$ such that

$$\mathbf{A} = s\mathbf{BT} + \mathbf{1t}'$$

where \boldsymbol{T} is an orthogonal matrix.

 In Borg and Groenen (2005) are all the details needed to estimate these parameters.

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Why is it needed?



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Why is it needed?

Why is it needed?

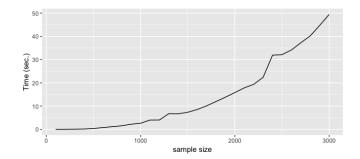


Figure: Elapsed time to compute MDS.

References

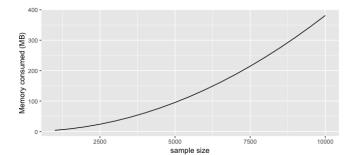


Figure: Memory consumed to compute the distance matrix.

Why is it needed?

Three algorithms for MDS with Big Data

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Three algorithms for MDS with Big Data

Three algorithms for MDS with Big Data

- Divide and Conquer MDS:
 - First approach of this thesis.
- Fast MDS:
 - It uses recursive programming.
 - Developed by (Tynia, Jinze, Leonard, and Wei 2006).
- MDS based on Gower interpolation:
 - It adds a new set of points to an existing MDS configuration.
 - See Appendix of (Gower and Hand 1995).

- Algorithms for MDS with Big Data

Algorithms for MDS with Big Data

Divide and Conquer MDS

Divide and Conquer MDS

- Let p be n/I, where I is the the size of the largest matrix that allows to run MDS efficiently, i.e, in a reasonable amount of time.
- Divide the original dataset into p partitions: X_1, \ldots, X_p .
- Calculate the MDS for the first partition: MDS(1). This solution will be used as a guide to align the MDS configuration for the remaining partitions.

- Define cum-mds equals to MDS(1) and start iterating until the last
- Given a step k, $1 < k \le p$, partitions k and k-1 are joint, i.e, $\mathbf{X}_k \cup \mathbf{X}_{k-1}$.
- MDS is calculated on this union, obtaining MDS_{k,k-1}.

partition is reached.

In order to add the rows of the k-th partition to **cum-mds**, the following steps are performed:

- Take the rows of the partition k-1 from $\mathsf{MDS_{k,k-1}}$: $\mathsf{MDS_{k,k-1}}\Big|_{k-1}$.
- Take the rows of the partition k-1 from **cum-mds**: **cum-mds** $\Big|_{k-1}$.
- Apply Procrustes to obtain the set of parameters that makes $MDS_{k,k-1}\Big|_{k-1}$ be aligned with cum-mds $\Big|_{k-1}$.
- ullet Use this set of parameters with $ullet \mathsf{MDS_{k,k-1}}ig|_k$

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• Once $MDS_{k,k-1}|_{k}$ is in the same coordinate system as **cum-mds**, add to **cum-mds**.



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Fast MDS

- It also partitions the original dataset, X into p subsets.
- The alignment is done using a set of sample points, instead of the full partition as the previous algorithm.
- For each partition, it is taken s · k points, where s is the estimated dimensionality and k is an amplification factor.
- Therefore, if I is the largest matrix that allows to run MDS efficiently, then $p = \frac{I}{ks}$ and $\frac{n}{p} < I$.

- Let $p = \frac{1}{s \cdot k}$.
- Divide X into X_1, \ldots, X_p .
- If n/p > I, call (recursively) Fast MDS.
- Otherwise, compute MDS over all the partitions.

- Get sk points from each $\boldsymbol{X_i}$ and put them into an alignment matrix $\boldsymbol{M_{align}}$.
- Run MDS over M_{align}.
- The next step is to compute Procrustes transformation to line these two sets of solutions up in a common coordinate system.

Algorithms for MDS with Big Data

MDS based on Gower interpolation



MDS based on Gower interpolation

- Gower interpolation formula (see Appendix of (Gower and Hand 1995)) allows to add a new set of points to a given MDS configuration.
- Given a matrix X n × p, a MDS configuration for this matrix of dimension n × c and a matrix X_{new} m × p, one wants to add these new m rows to the existing MDS configuration.
- So, after adding the new rows, the MDS configuration has n + m rows and c columns.

- Partition **X** into p submatrices. Again, p = n/I, being I the the size of the largest distance matrix that a computer can calculate efficiently.
- Compute MDS on the first partition.
- For the each of the remaining partitions, use *Gower interpolation* formula to compute a MDS configuration.

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MDS based on Gower interpolation

- We generate a matrix **X** with 3 independent *Normal* distributions $(\mu = 0 \text{ and } \sigma = 1)$ and 10^3 rows.
- Afterwards, we run the algorithm, obtaining MDS_{alg}, setting / equals to 500. We require the algorithm to return 3 columns.
- Procrustes is performed over X and MDS_{alg}, not allowing dilations.

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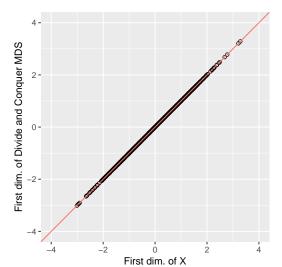


Figure: Dimension 1 **X** against dimension 1 of MDS_{Div}. In red, the line x = y.

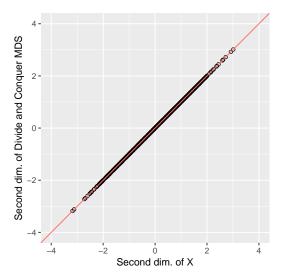


Figure: Dimension 2 **X** against dimension 2 of MDS_{Div}. In red, the line x = y.

Some results

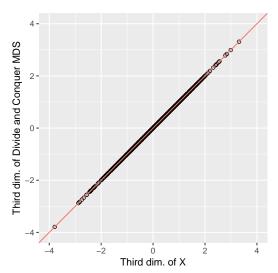


Figure: Dimension 3 of X against dimension 3 of MDS_{Div}. In red, the line x = y.

Algorithms for MDS with Big Data

	X_1	X_2	X_3
MDS_{Div1}	1	0.02	-0.04
MDS_{Div2}	0.02	1	0.02
MDS_{Div3}	-0.04	0.02	1

Table: Cross-correlation of \boldsymbol{X} and $\boldsymbol{MDS_{Div}}$.

	X_1	X_2	X_3
MDS_{Fast1}	1	0.02	0
MDS_{Fast2}	0.02	1	0.02
MDS_{Fast3}	0	0.02	1

Table: Cross-correlation of X and MDS_{Fast}.

	X_1	X_2	X_3
MDS_{Gower1}	1	0	-0.04
MDS_{Gower2}	0	1	-0.0
MDS_{Gower3}	-0.04	-0.03	1

Table: Cross-correlation of X and MDS_{Gower}



Some results

Output of the algorithms

Algorithms for MDS with Big Data

Output of the algorithms



Output of the algorithms

The three algorithms have the same type of output. It consists on a list of two parameters, which are

- A MDS configuration for the initial dataset.
- The second parameter is a list of eigenvalues.

The list of eigenvalues is built as follows:

- All the algorithms divide the initial data into a set of p partitions.
- Given a partition i, a distance matrix of dimensions $m_i \times m_i$ is calculated: $\mathbf{D_i}$.
 - Over $\mathbf{D_i}$ a singular value decomposition is performed, providing a list of length m_i that contains all the eigenvalues of the previous decomposition: list_i.
- Let norm_eigenvalues_i be $\operatorname{list}_i/m_i$, i.e, each eigenvalue is divided by the number of rows of $\mathbf{D_i}$.
- The algorithms return norm_eigenvalues₁ ∪ · · · ∪ norm_eigenvalues_p.
 We refer to this union as the normalized eigenvalues.

Comparison of the algorithms

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Introduction

Comparison of the algorithms

- Divide and Conquer MDS uses a guide (the first subset, X_1) to align the solutions as well as it uses the whole partition X_i to find Procrustes parameters. However, Fast MDS does not use a guide an it uses a set of subsamples to find Procrustes parameters.
- Fast MDS is based on recursive programming. It divides until a manageable dimensionality is found. However, Divide and Conquer MDS finds the number of partitions without applying recursive programming.

- MDS based on Gower interpolation does not need any Procrustes transformation.
- When the number of rows is not large, p=1 and the resulting algorithms are the classical one.

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Simulation study

Given the three algorithms, we would like to explore their performance:

- Performance in terms of results quality: are they able to capture the right data dimensionality?
- Performance in terms of time: are they "fast" enough? Which one is the fastest?



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Simulation study

Algorithms for MDS with Big Data

- Sample sizes: we use different sample sizes, combining small datasets and large ones. A total of six sample sizes are used, which are:
 - Small sample sizes: 10^3 , $3 \cdot 10^3$, $5 \cdot 10^3$ and 10^4 .
 - Large sample sizes: 10⁵ and 10⁶.

- Data dimensions: we generate a matrix with two different number of columns: 10 and 100.
- Main dimensions: given **X** $n \times k$, where $n \in \{10^3, 3 \cdot 10^3, 5 \cdot 10^3, 10^4, 10^5, 10^6\}$ and $k \in \{10, 100\}$, it is postmultiplied by a diagonal matrix that contains k values, $\lambda_1, \ldots, \lambda_k$.
 - All the columns with the same values of λ : $\lambda_1 = \cdots = \lambda_k = 1$ (noisy scenarios).
 - One main dimension with $\lambda_1 = 15$ and $\lambda_2 = \cdots = \lambda_k = 1$.
 - Two main dimensions of the same value λ : $\lambda_1=\lambda_2=15$ and $\lambda_3=\cdots=\lambda_k=1.$
 - Two main dimensions of different values λ : $\lambda_1=15,\ \lambda_2=10$ and $\lambda_3=\cdots=\lambda_k=1.$
 - Four main dimensions of the same value λ : $\lambda_1 = \lambda_2 = \lambda_3 = \lambda_4 = 15$ and $\lambda_5 = \cdots = \lambda_k = 1$.

Design of the simulation

Introduction

• As a probabilistic model, we use a Normal distribution with $\mu=0$ and $\sigma=1$. With this distribution, we generate a matrix of n observations and k columns, being the k columns independent.

There is a total of 60 scenarios to simulate.

Algorithms for MDS with Big Data

- Given a scenario, it is replicated 100 times.
- For every simulation, it is generated a dataset (according to the scenario), and all the algorithms are run using this dataset.
- So, a total of 6000 simulations are carried out.

- 1 Generate the dataset **X** according to the scenario.
- 2 For each algorithm, we do the following steps:

Algorithms for MDS with Big Data

- Run the algorithm and get MDS configuration for the algorithm (MDS_{alg}).
- 2 Get the elapsed time to compute MDS configuration and store it.
- 3 Get normalized eigenvalues and store them.
- 4 Align MDS_{alg} and X using (Partition) Procrustes.
- Get the correlation coefficients between the main dimensions of MDS_{alg} and X and store them.

Important details:

- When running the algorithms, we ask for as many columns as the original data has.
- For Procrustes we dot not allow dilations, otherwise distance could not be preserved.
- To do the alignment, we select the main dimensions. If there is not any main dimension, (*noisy scenarios*), we just select 4 columns.
- Note that the original dataset, X, is always available and it is already the MDS configuration, since we simulate independent columns with mean value equals to 0.

- Performance of results quality:
 - Correlation between the main dimensions of the data and the main dimensions after applying the algorithms. We get the diagonal of the correlation matrix.
 - Normalized eigenvalues as an approximation of the standard deviation of the variables of X.
- Elapsed Time to get the MDS configuration.

Simulation study

Correlation coefficients

Correlation coefficients

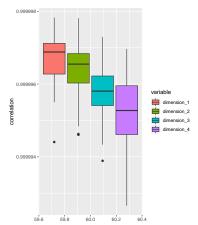


Figure: Correlation coefficients between the main dimensions of **X** and the main dimensions of **MDS**_{Div} for a scenario with the following configuration: $n = 10^6$, 100 columns and 4 main dimensions with $\lambda_i = 15$, $i \in \{1, 2, 3, 4\}$.



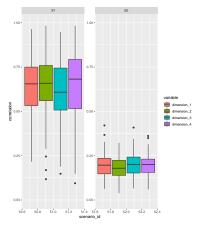


Figure: Correlation coefficients between **X** and **MDS**_{Div} for two different *noise* scenarios

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Eigenvalues

- Since the original dataset, X, is postmultiplied by a diagonal matrix $k \times k$ that contains $\lambda_1, \ldots, \lambda_k$, then $var(X_i) = \lambda_i^2$ and $sd(X_i) = \lambda_i$.
- Let ϕ_1, \ldots, ϕ_t be the normalized eigenvalues of the MDS configuration such that $\phi_1 > \phi_2 > \cdots > \phi_t$. The first highest normalized eigenvalues have to verify $\sqrt{\phi_i} \approx \lambda_i$.

$$\widehat{\mathsf{bias}} = \frac{1}{100} \sum_{i=1}^{100} \sqrt{\phi_{ij}} - \lambda_j = \overline{\sqrt{\phi_j}} - \lambda_j.$$

$$\widehat{\mathsf{MSE}} = \frac{1}{100} \sum_{i=1}^{100} (\lambda_j - \sqrt{\phi_{ij}})^2.$$

scenario_id	$\overline{\sqrt{\phi_1}}$	$\widehat{bias_1}$	$\widehat{MSE_1}$
3	14.98	-0.02	0.03
4	15.03	0.03	0.11
13	15.00	-0.00	0.00
14	14.96	-0.04	0.16
23	14.99	-0.01	0.02
24	14.99	-0.01	0.01
33	14.99	-0.01	0.01
34	14.99	-0.01	0.00
43	14.99	-0.01	0.01
44	14.99	-0.01	0.01
53	14.98	-0.02	0.03
54	14.99	-0.01	0.01

Table: Estimator, $\widehat{\text{bias}}$ and $\widehat{\text{MSE}}$ for scenarios with one main dimension $\lambda_1=15$ for *Divide and Conquer MDS*.

		_	_
scenario_id	$\sqrt{\phi_1}$	$\widehat{bias_1}$	$\widetilde{MSE_1}$
3	14.85	-0.15	2.27
4	15.01	0.01	0.01
13	14.91	-0.09	0.76
14	15.10	0.10	0.93
23	14.96	-0.04	0.14
24	15.03	0.03	0.07
33	14.33	-0.67	44.82
34	15.09	0.09	0.76
43	15.00	-0.00	0.00
44	15.00	0.00	0.00
53	14.86	-0.14	1.88
54	14.90	-0.10	1.02

Table: Estimator, $\widehat{\text{bias}}$ and $\widehat{\text{MSE}}$ for scenarios with one main dimension $\lambda_1=15$ for Fast MDS.

Eigenvalues

scenario_id	$\overline{\sqrt{\phi_1}}$	$\widehat{bias_1}$	$\widehat{MSE_1}$
3	15.05	0.05	0.22
4	15.02	0.02	0.04
13	14.94	-0.06	0.36
14	15.04	0.04	0.20
23	14.98	-0.02	0.04
24	15.02	0.02	0.05
33	14.99	-0.01	0.01
34	15.06	0.06	0.31
43	15.04	0.04	0.19
44	14.97	-0.03	0.07
53	14.98	-0.02	0.06
54	14.90	-0.10	1.07

Table: Estimator, $\widehat{\text{bias}}$ and $\widehat{\text{MSE}}$ for scenarios with one main dimension $\lambda_1=15$ for MDS based on Gower interpolation.



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sample_size	n_dim	mean_divide_conquer	mean_fast	mean_gower
10 ³	10	0.27	0.14	0.10
10^{3}	100	0.78	0.69	0.28
$3 \cdot 10^{3}$	10	0.78	0.32	0.16
$3 \cdot 10^{3}$	100	2.50	3.14	0.52
$5\cdot 10^3$	10	1.37	0.54	0.20
$5 \cdot 10^3$	100	4.25	5.69	0.84
10^{4}	10	2.60	1.81	0.31
10^{4}	100	8.85	11.79	1.37
10^{5}	10	28.10	11.46	2.44
10^{5}	100	106.30	116.46	18.02
10^{6}	10	420.29	106.59	53.15
106	100	2365.46	1070.19	813.15

Table: Mean of elapsed time (in seconds) to compute each algorithm.



We do an ANOVA test using three factors:

Algorithms for MDS with Big Data

- The sample size, which has 6 levels.
- The number of dimensions, which has 2 levels.
- The algorithm, which has 3 levels.
- Instead of using the elapsed time variable, we use its logarithm.

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
algorithm	2	9283.73	4641.86	32143.99	< 2e - 16
sample_size	5	108572.93	21714.59	150369.26	< 2e - 16
n_dimensions	1	12868.36	12868.36	89110.86	< 2e - 16
Residuals	17991	2598.05	0.14		

Table: Results for ANOVA test for differences in log(elapsed_time) using algorithm, sample size and num. dimensions as factors.

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-1.4058	0.0085	-165.44	< 2e - 16
algorithmfast	-0.4313	0.0069	-62.17	< 2e - 16
algorithmgower	-1.6926	0.0069	-243.96	< 2e - 16
sample_size3000	0.9473	0.0098	96.54	< 2e - 16
sample_size5000	1.4434	0.0098	147.10	< 2e - 16
sample_size10000	2.1505	0.0098	219.17	< 2e - 16
sample_size1e+05	4.4286	0.0098	451.35	< 2e - 16
sample_size1e+06	7.2782	0.0098	741.78	< 2e - 16
n_dimensions100	1.6910	0.0057	298.51	< 2e - 16

Table: Linear model for response log(elapsed_time).

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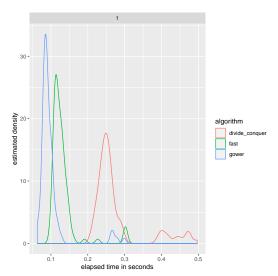


Figure: Estimated density of elapsed time (in sec.) for each algorithm and scenario with $n=10^3$, 10 columns and $\lambda_i=1$ $i\in\{1,\dots,10\}$

Time to compute MDS

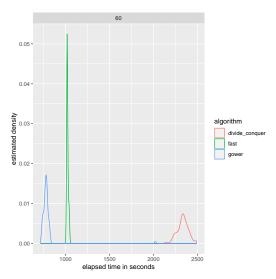


Figure: Estimated density of elapsed time (in sec.) for each algorithm and scenario with $n = 10^6$, 100 columns and $\lambda_i = 15$ $i \in \{1, 2, 3, 4\}$.

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Thank You

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