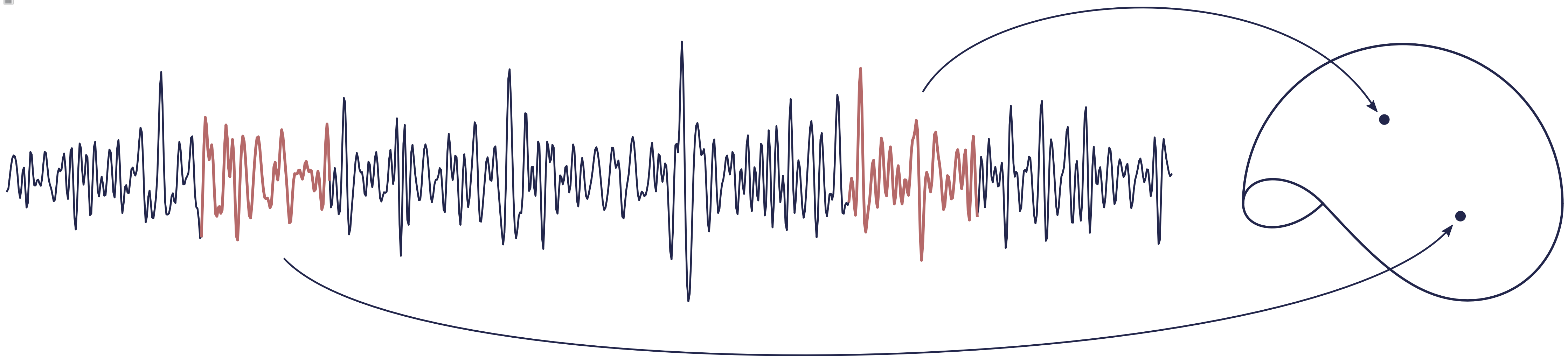
Riemannian Procrustres Analysis

Transfer Learning for Brain Computer Interfaces

Pedro L. C. Rodrigues   Marco Congedo   Christian Jutten



Presentation for the Machine Learning group at GIPSA-lab

22th May 2018, Grenoble, France

Outline

Introduction

Procrustes Analysis

Results

Concluding remarks

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Procrustes Analysis

Results

Concluding remarks

Classification of BCI signals always relies on an appropriate choice of **discriminant features**

N sensors
T samples
K trials

$$\{X_1, X_2, \ldots, X_K\}$$

$$X_i \in \mathbb{R}^{N \times T}$$

$$\{Y_1, Y_2, \ldots, Y_K\}$$

$$Y_i \in \mathbb{R}^d$$

d features

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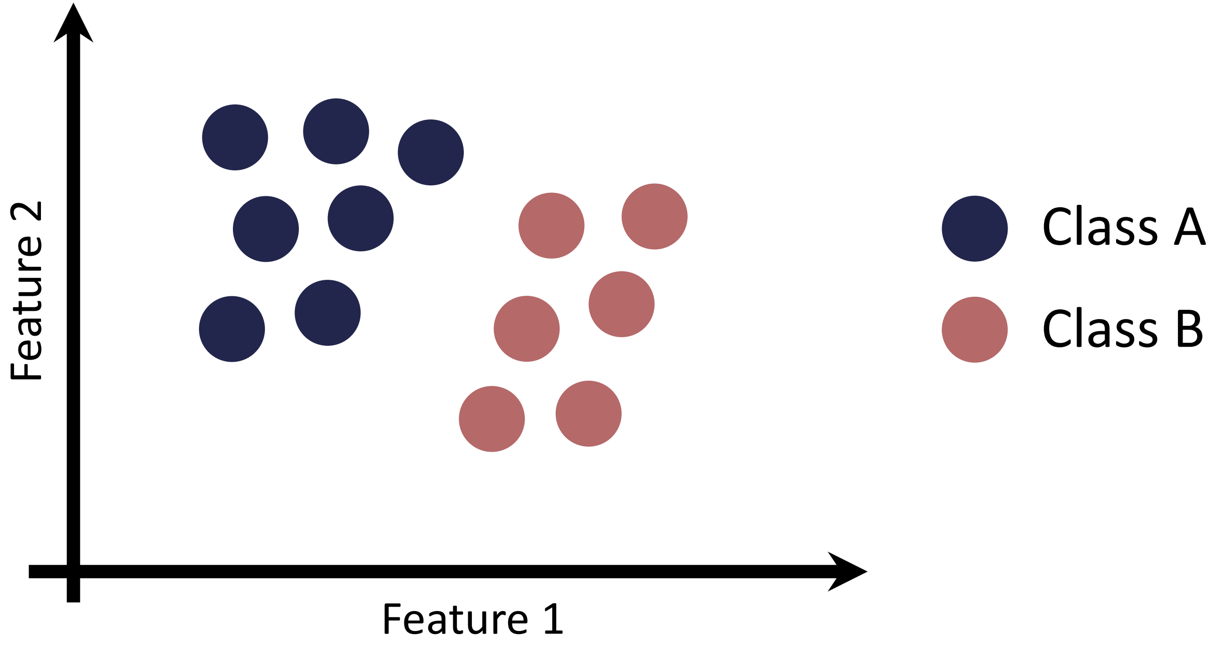

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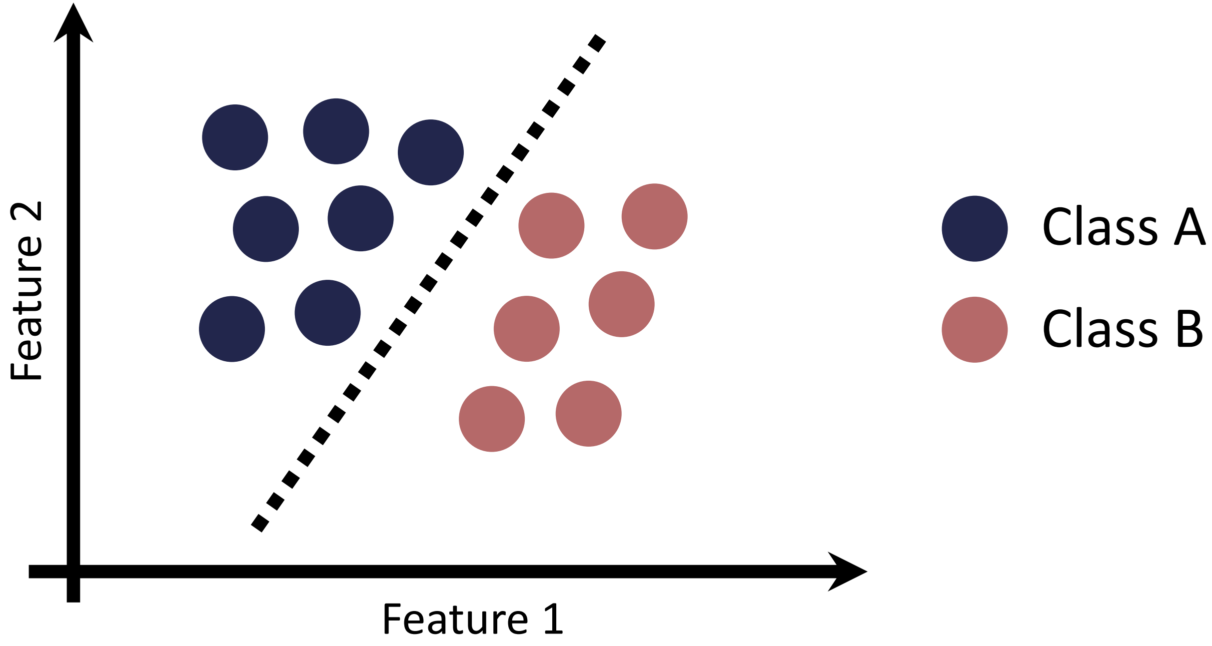

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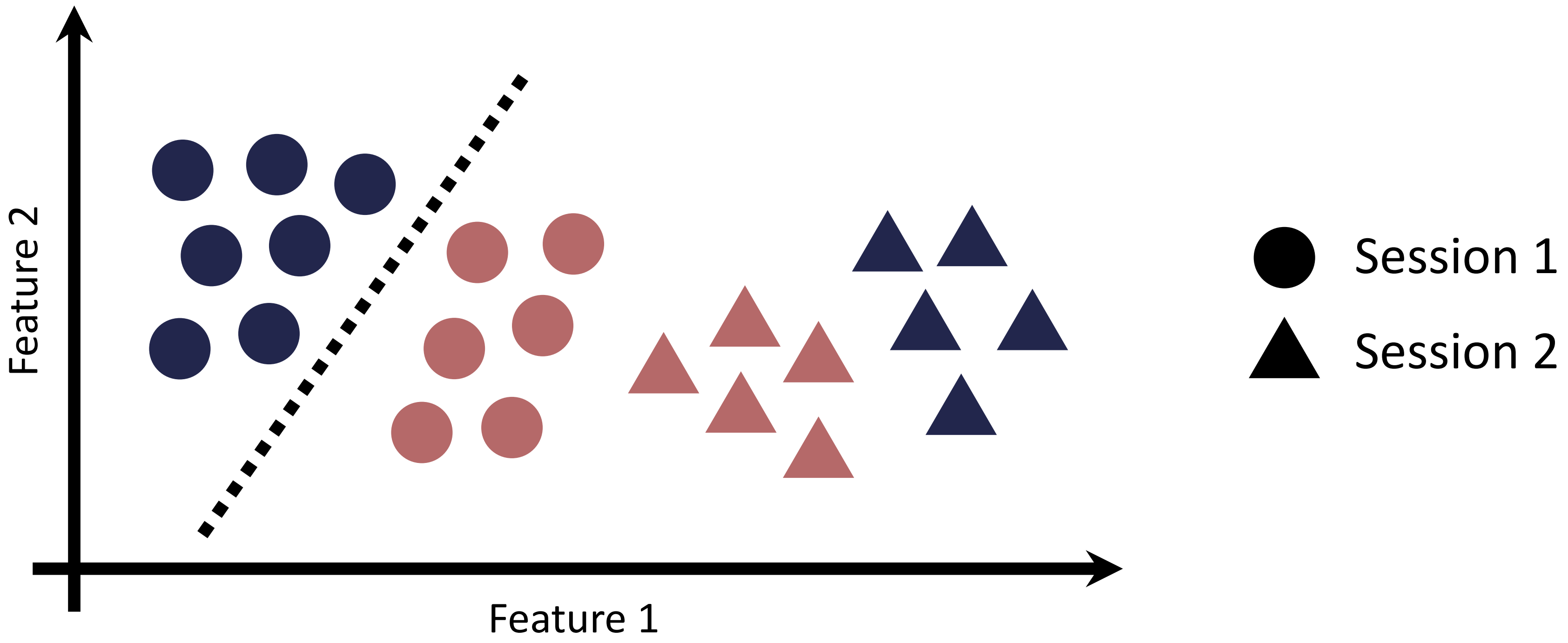
The **statistical distribution** of features may not be the same on different sessions

Covariate Shift



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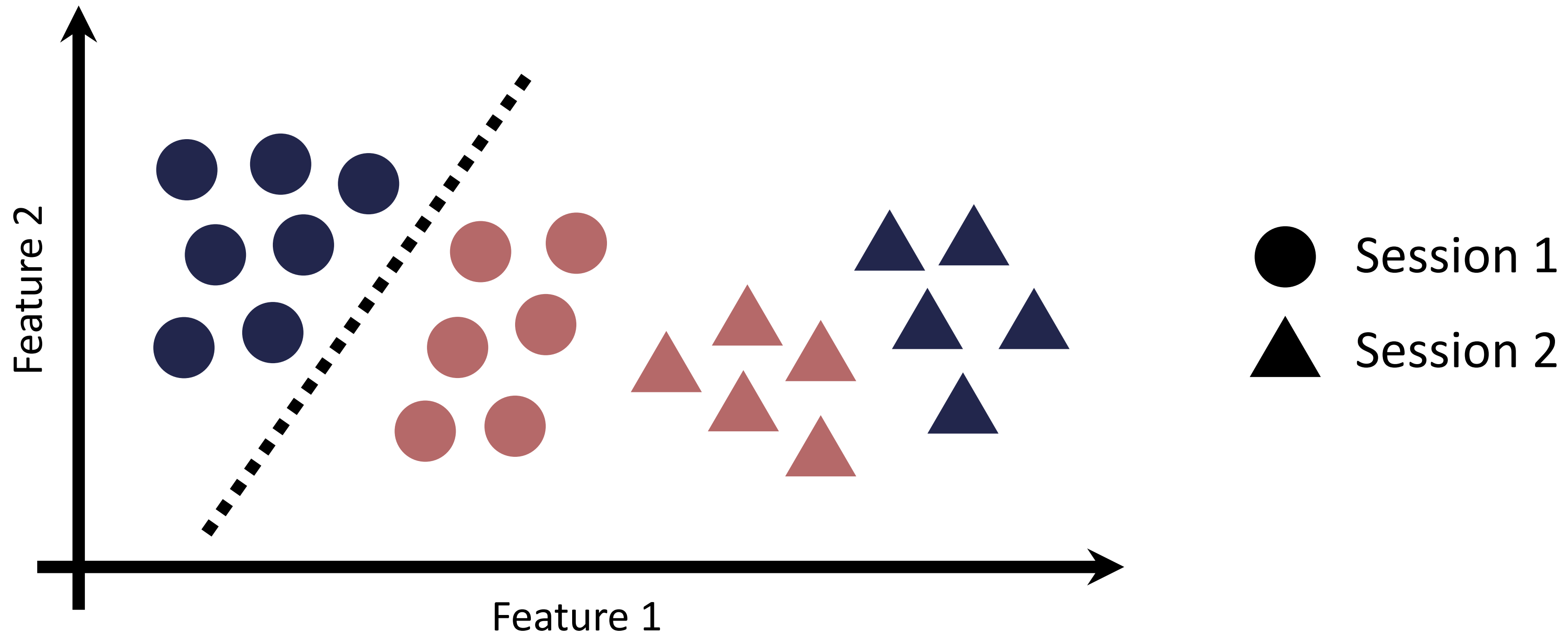

Transfer Learning aims at using the data from Session 1 to improve the classification of Session 2

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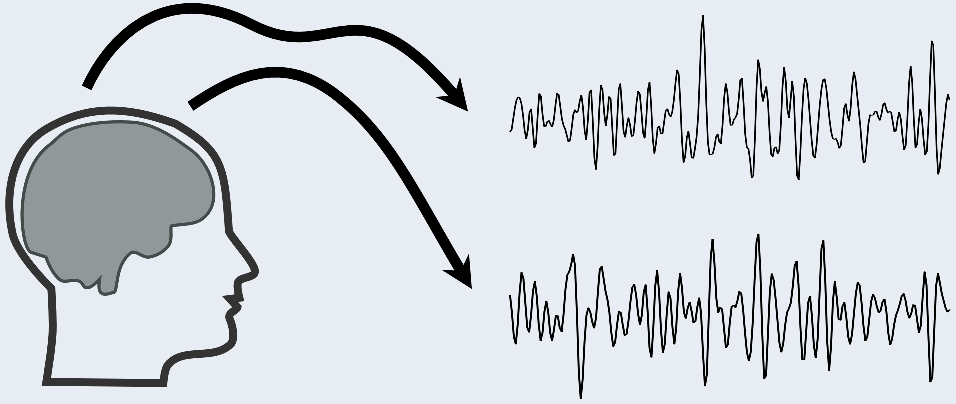
The BCI paradigm – classification of EEG epochs



Cognitive task
(*K* trials)

EEG recording

$\{X_1, \ldots, X_K\}$

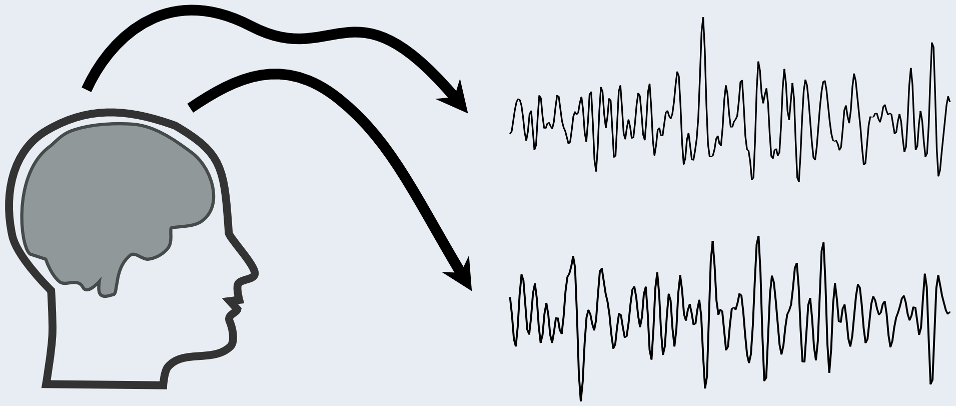
n – electrodes $X_k \in \mathbb{R}^{n \times T}$
T – samples

FEATURE ENGINEERING

Many features can be used to **describe** and **discriminate** the signals of each class

- Waveforms
- Spectra
- Neural connectivity
- Etc.

The BCI paradigm – classification of EEG epochs



Describes the instantaneous **correlations** between pairs of recorded signals

Cognitive task
(*K* trials)

EEG recording

$\{X_1, \dots, X_K\}$

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T – samples

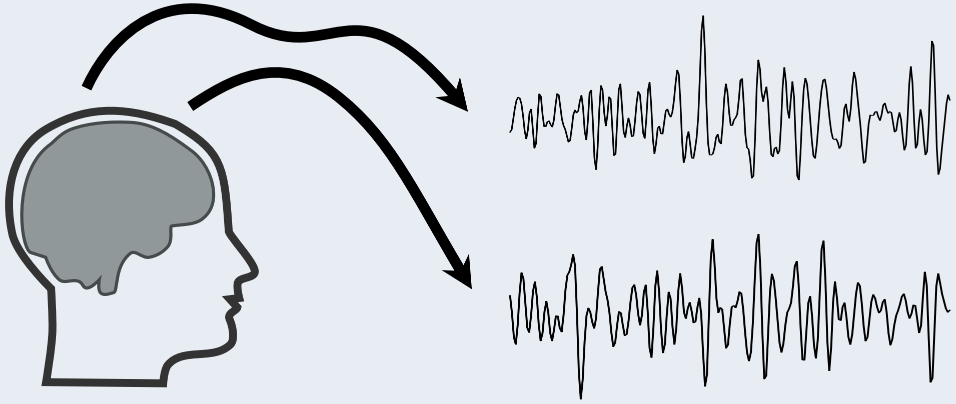
Covariance matrix

$\{C_1, \dots, C_K\}$

$C_k \in \mathbb{R}^{n \times n}$

$C_k = \frac{1}{T} X_k X_k^T$

The BCI paradigm – classification of EEG epochs



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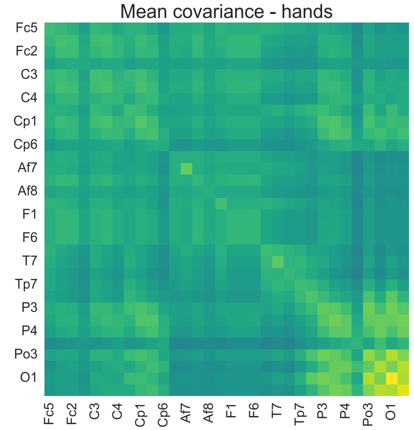
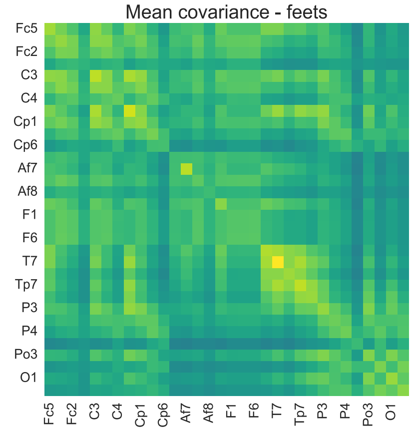
Classification





The Symmetric Positive Definite (SPD) manifold

Covariance matrix is **positive definite** → **Manifold** of positive definite matrices → Riemannian distance
Geometric mean
Tangent space

M is **positive definite** if, and only if,

$$\lambda \in \mathbb{R},\ \ \lambda_i > 0$$

(**positive** eigenvalues)

$$q_i^T q_j = \delta_{ij}$$

(**orthogonal** eigenvectors)

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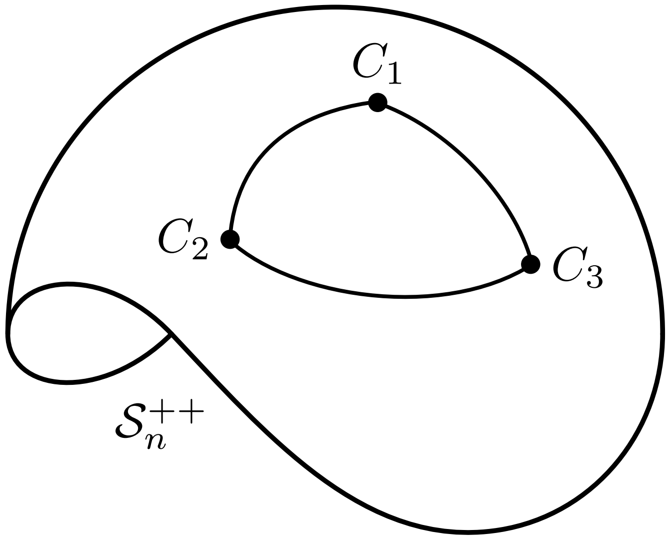

SPD manifold

The Symmetric Positive Definite (SPD) manifold

Covariance matrix
is **positive definite**

Manifold of positive
definite matrices

Riemannian distance
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Geodesic distances between
points on the globe

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The Symmetric Positive Definite (SPD) manifold

Riemannian Geometry

Covariance matrix is **positive definite** → **Manifold** of positive definite matrices → Riemannian distance, Geometric mean, Tangent space

- Natural distance between SPD matrices

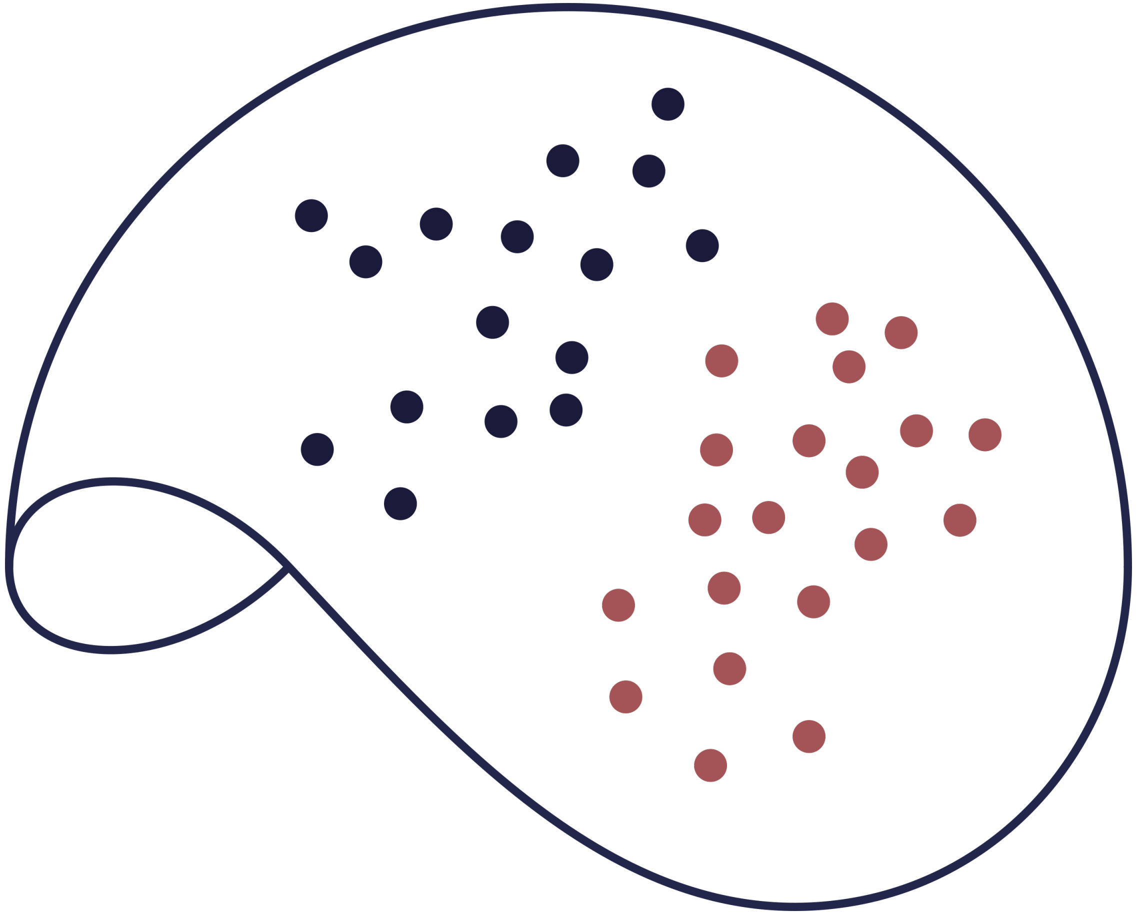
$$\delta_R^2(C_i, C_j) = \left\| \mathrm{Log}\left(C_i^{-1/2} C_j C_i^{-1/2}\right) \right\|_F^2 = \sum_{k=1}^{n} \log^2(\lambda_k)$$

- Center of mass of *K* SPD matrices

$$M = \underset{M \in \mathcal{S}_n^{++}}{\operatorname{argmin}} \sum_{k=1}^{K} \delta_R^2(M, C_k)$$

A very simple **classifier** using the geometry of the SPD manifold

$\{C_1^{(a)}, \dots, C_{K_a}^{(a)}\} \quad \{C_1^{(b)}, \dots, C_{K_b}^{(b)}\}$



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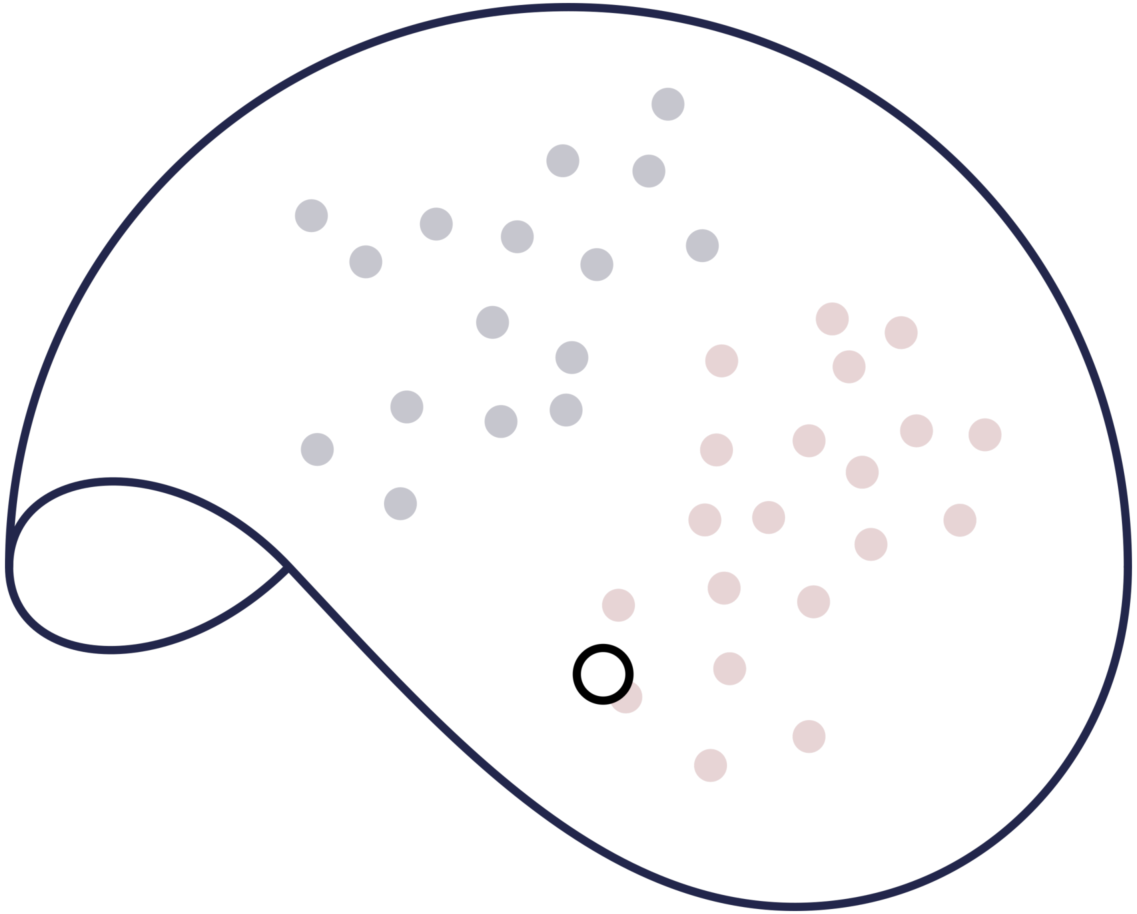

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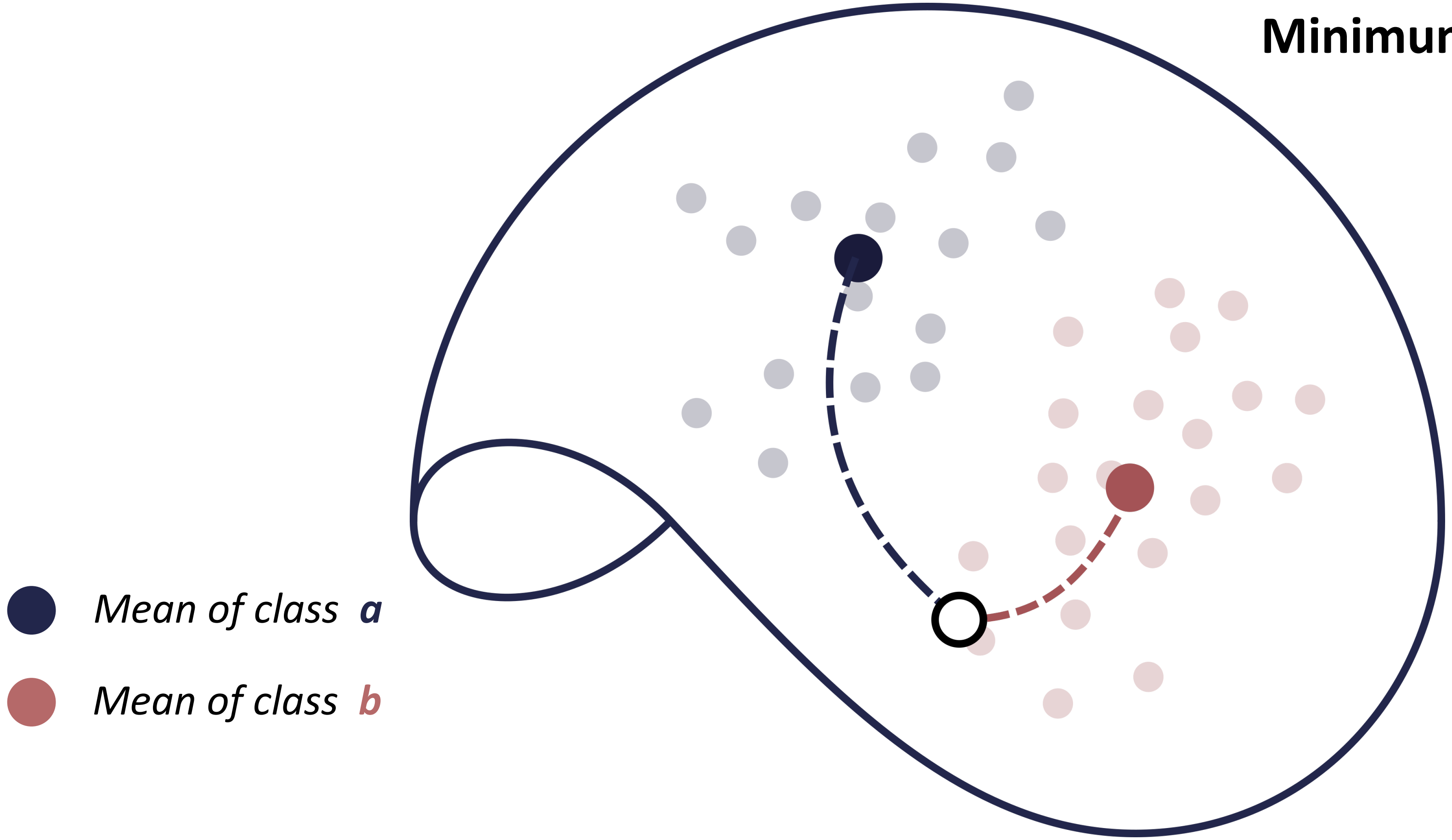
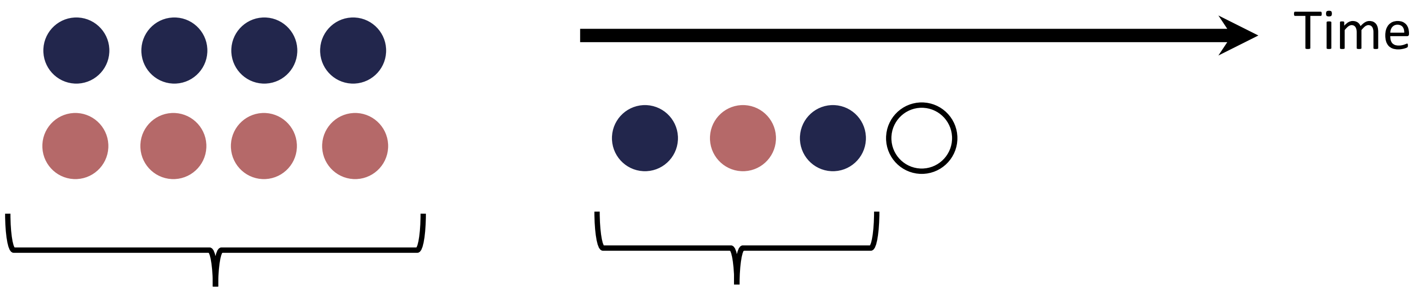
Classification based on the **Minimum Distance to Mean** (MDM)



Mean of class ***a***

Mean of class ***b***

Use data from the **source dataset** to classify the trials from the **target dataset**



Source Dataset
(all labels known)

Target Dataset
(labels available sequentially)

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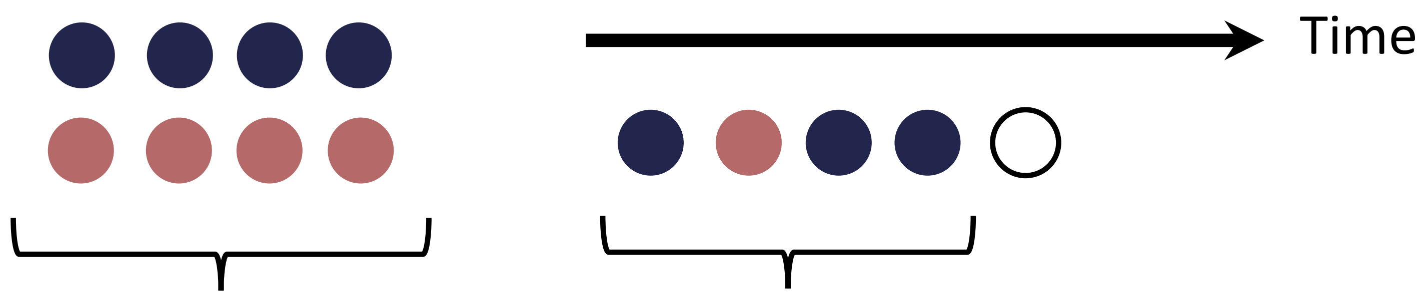

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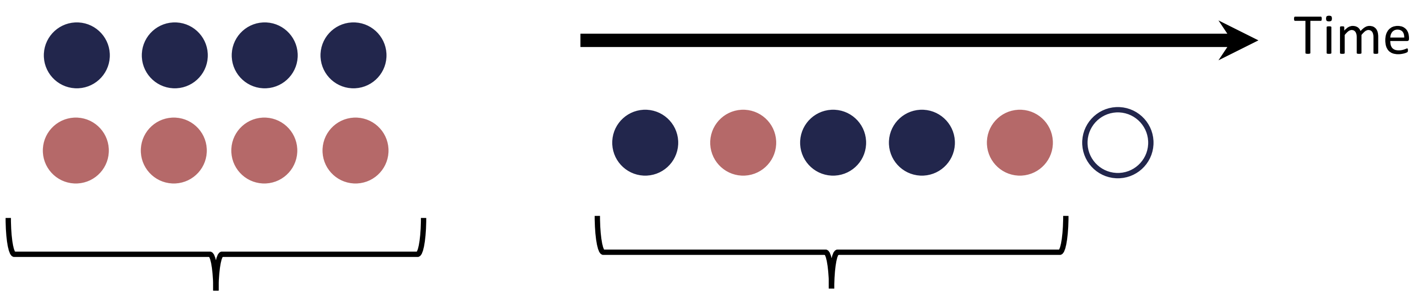

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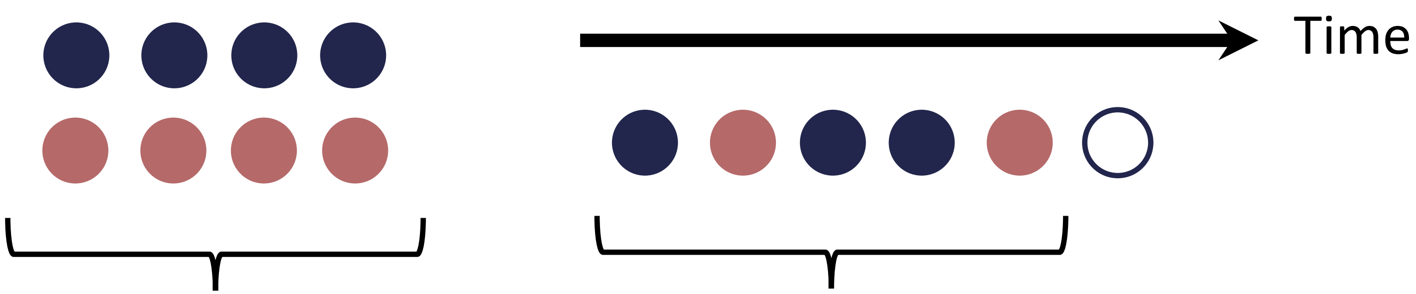

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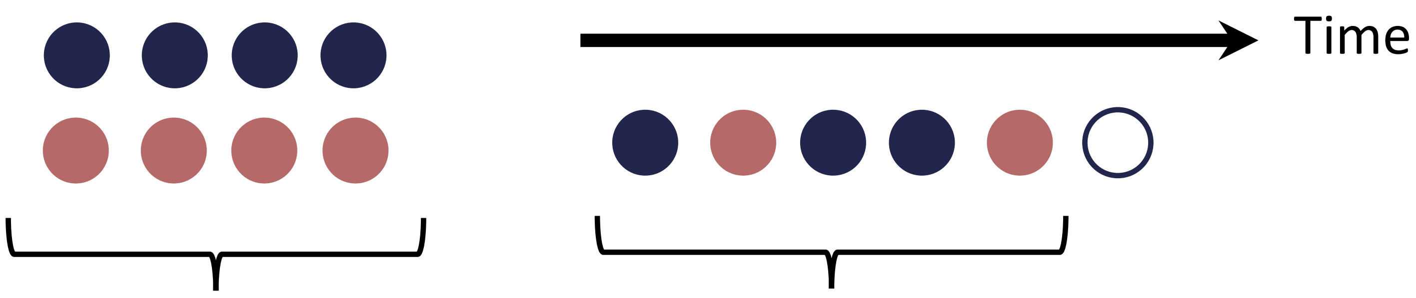
We do Transfer Learning via **distribution matching**

1) Fit classifier *C* to source dataset
2) Match target and source distributions
3) Classify unknown trial using *C*

Use data from the **source dataset** to classify the trials from the **target dataset**



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Match statistical distributions by applying geometrical **transformations** to the data points !

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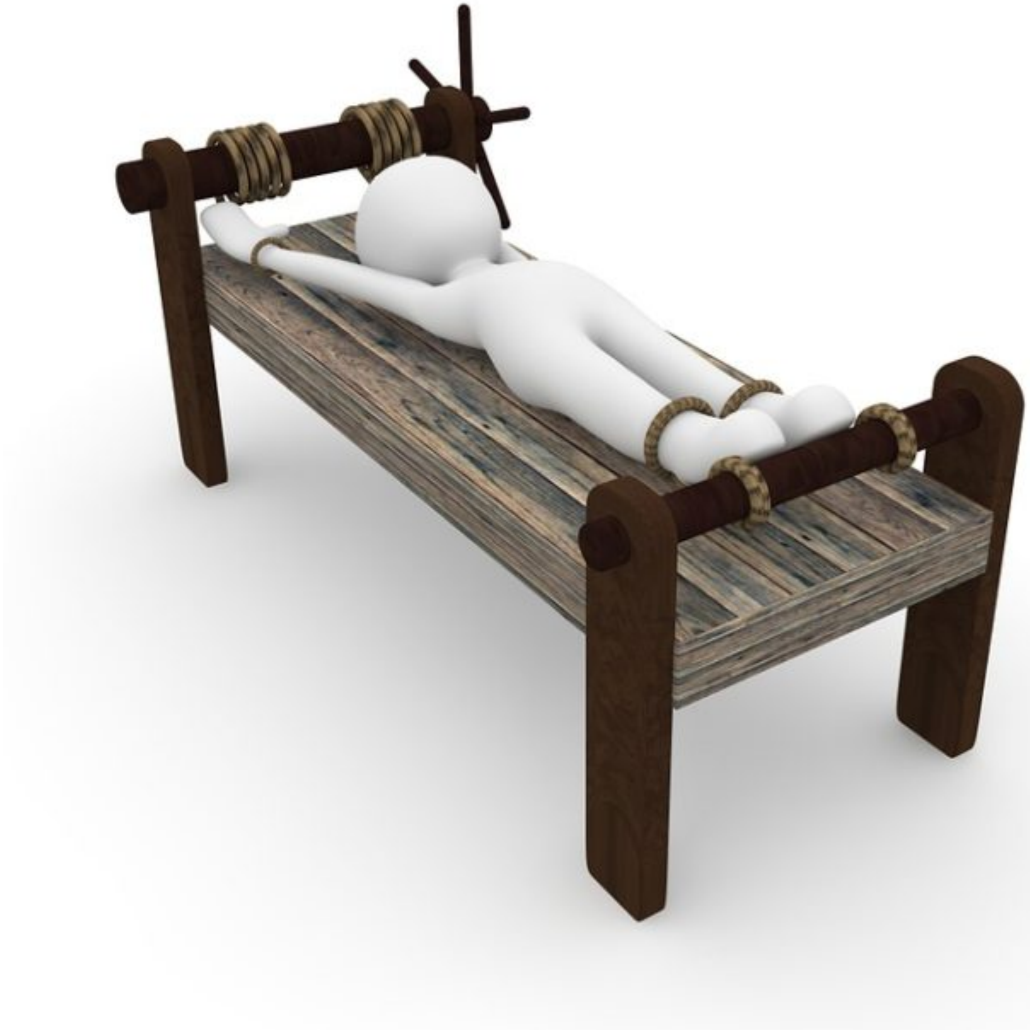
Outline

The **Procrustes bed** appears in Greek mythology

(The word *Procrustean* is used to describe situations where different lengths or sizes or properties are **fitted** to a **standard**)



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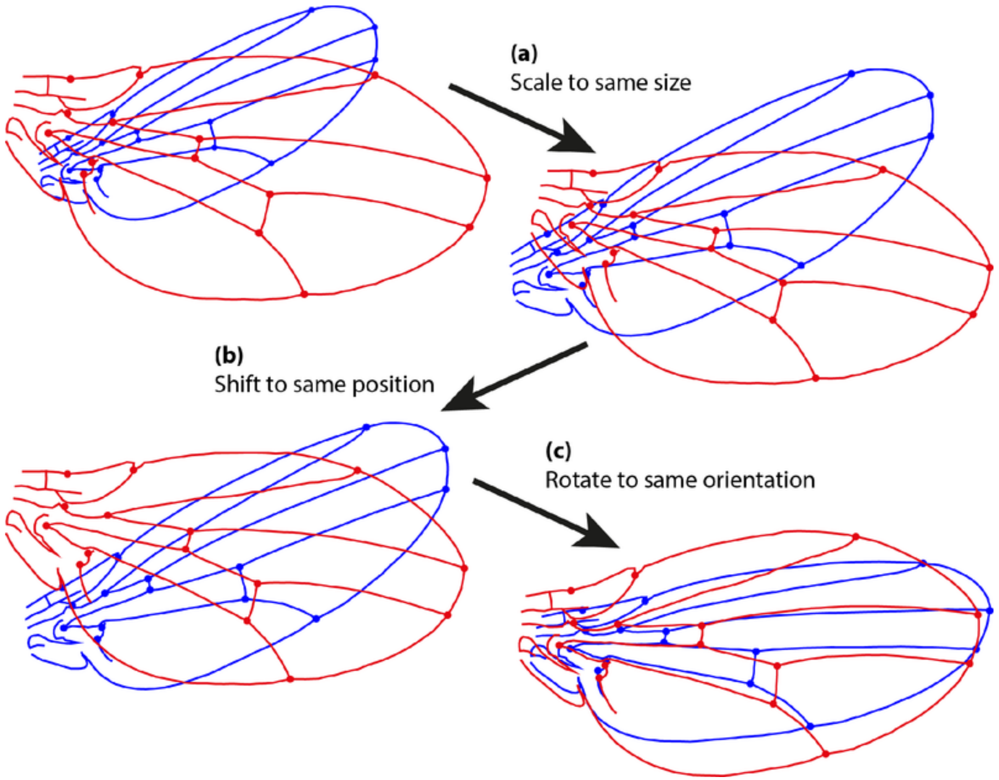
Procrustes **analysis** is commonly used in statistical shape analysis to and consists of matching shapes via

- Translation
- Stretching
- Rotation



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Each dot represents a **trial** in the dataset

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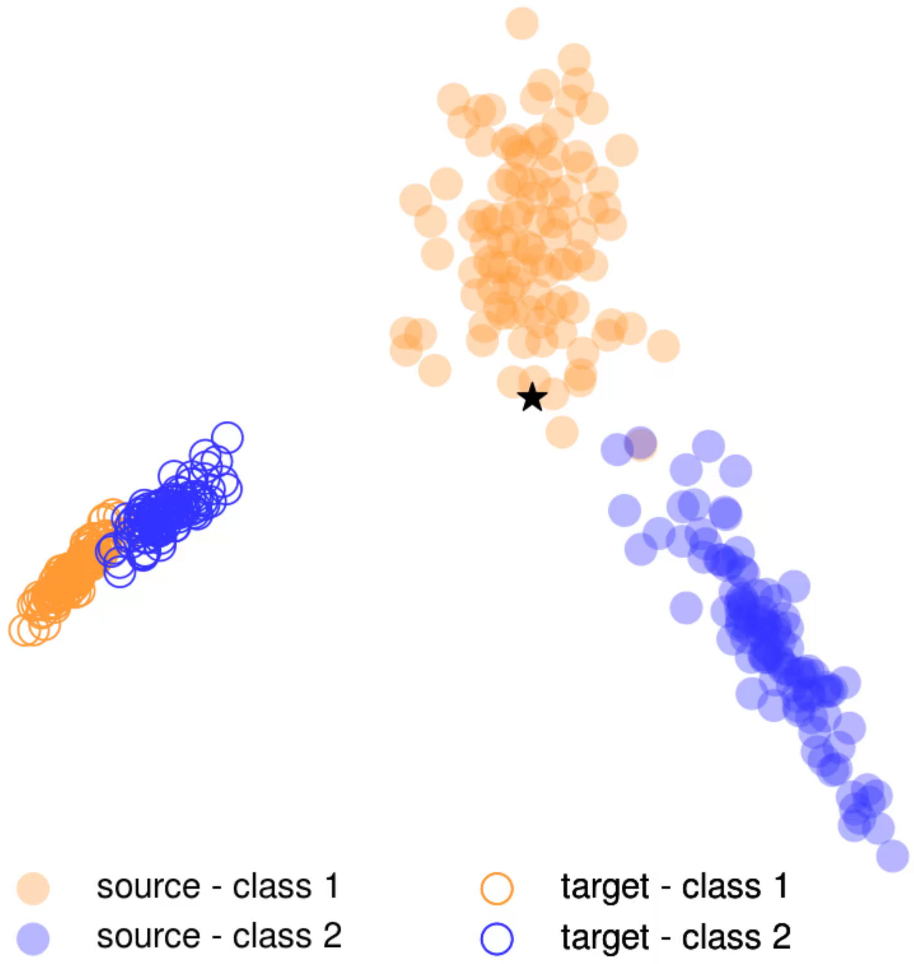
We propose a PA in the SPD manifold to **match** the **shape** of the statistical **distributions** of sessions



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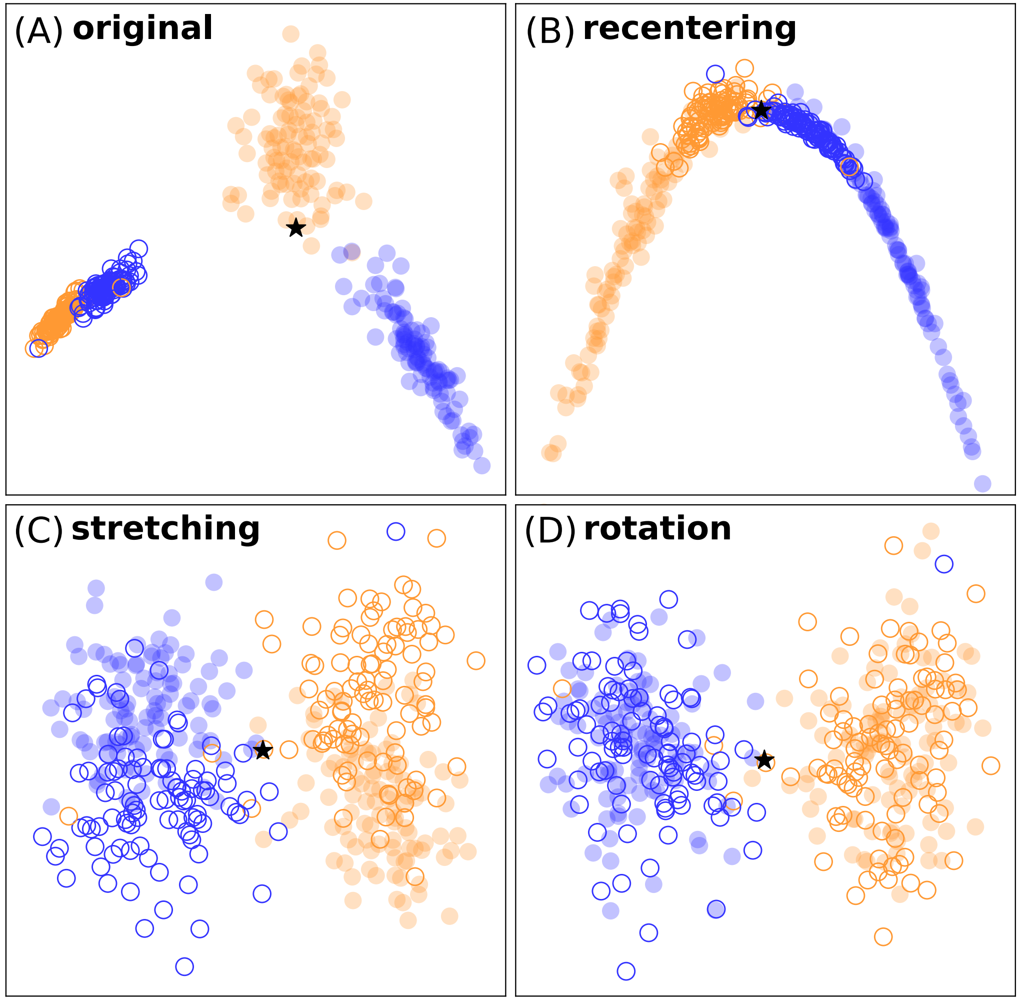

The transformations have to respect the **intrinsic geometry** of the SPD manifold

Suppose we have a set of *K* matrices $\{C_1, \ldots, C_K\}$ and their geometric mean is M

RECENTERING

$$C_i^{(\mathrm{rct})} = M^{-1/2} C_i M^{-1/2}$$

STRETCHING

$$C_i^{(\mathrm{str})} = \left(C_i^{(\mathrm{rct})}\right)^p$$

ROTATION

$$C_i^{(\mathrm{rot})} = U C_i^{(\mathrm{str})} U^T$$ with $UU^T = \mathbf{I}$

Outline

Introduction

Procrustes Analysis

Results

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Four datasets on three BCI paradigms

Publicly Available

Physionet EEG MI database	(109 subjects, 40 trials, 2 classes)
GigaDB EEG MI database	(37 subjects, 200 trials, 2 classes)
SSVEP Chevallier database	(12 subjects, 24 trials, 3 classes, 2 sessions)
P300 Brain Invaders database	(24 subjects, 576 trials, 2 classes)

For each dataset, Transfer Learning was always done in the **cross-subject** case

Cross-subject accuracy

Get the accuracies in classification when :

(Consider an **increasing** number of available points in the target dataset)

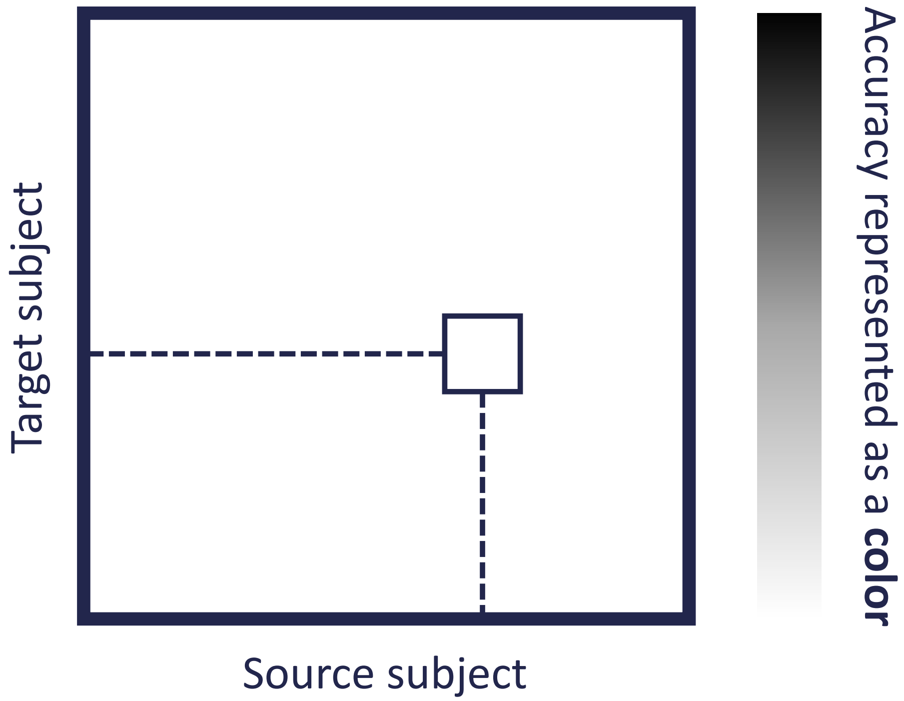
Compare the results for **three** methods :

ORIGINAL

RECENTERING

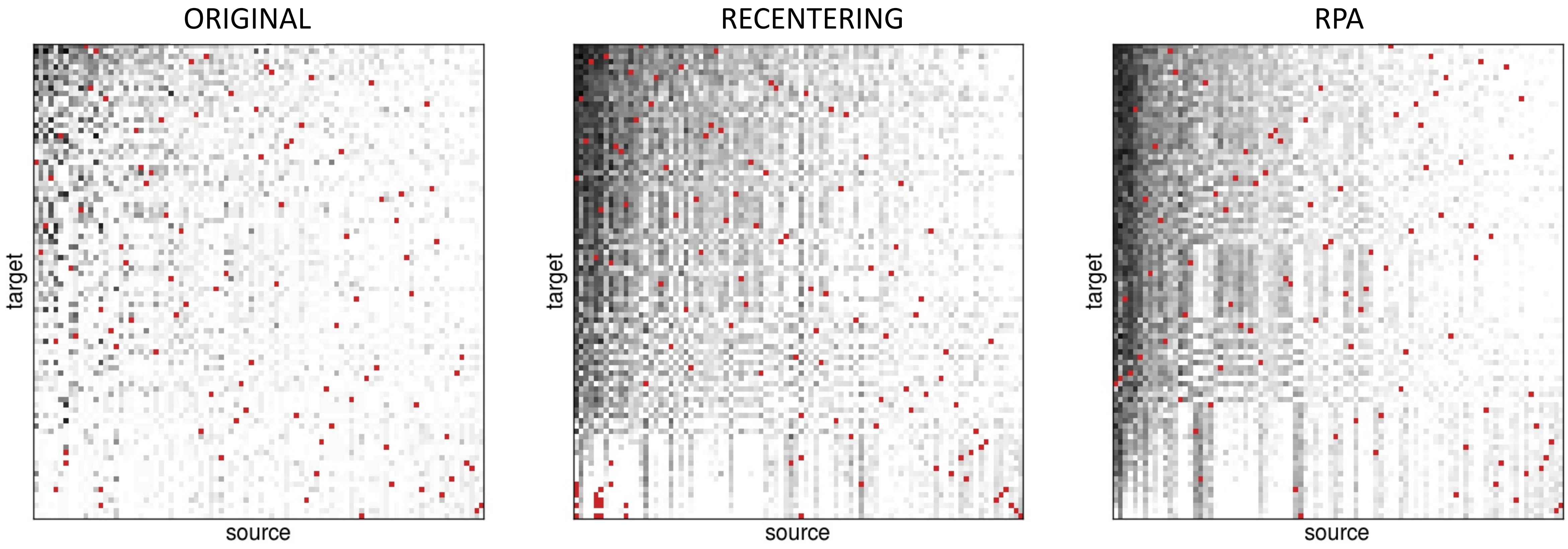
RPA

1) Classifier *C* is fitted to **source** subject dataset
2) Match target and source statistical distributions
3) Classify unknown trials from **target** dataset



Cross-subject accuracy – Physionet MI

\# of data points in the target dataset : **1**

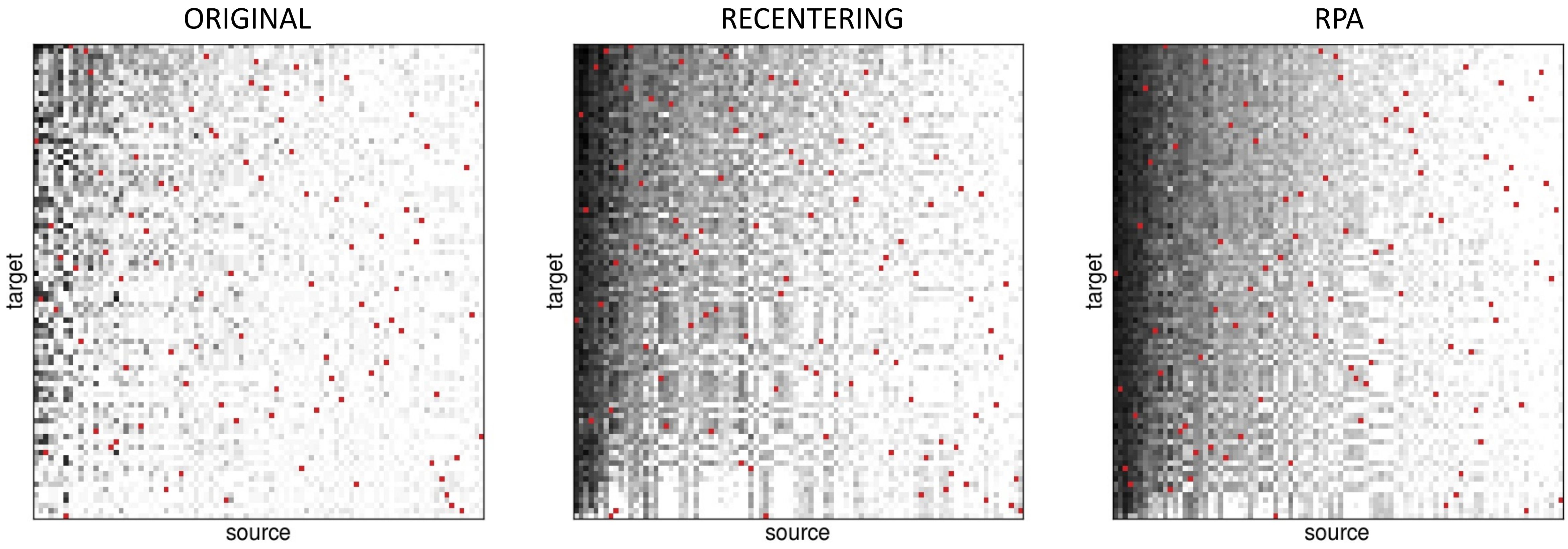


(Colormap : **white** indicates 0.5 accuracy and **black** is 1.0)

Source subject = Target subjet

Cross-subject accuracy – Physionet MI

of data points in the target dataset : **5**



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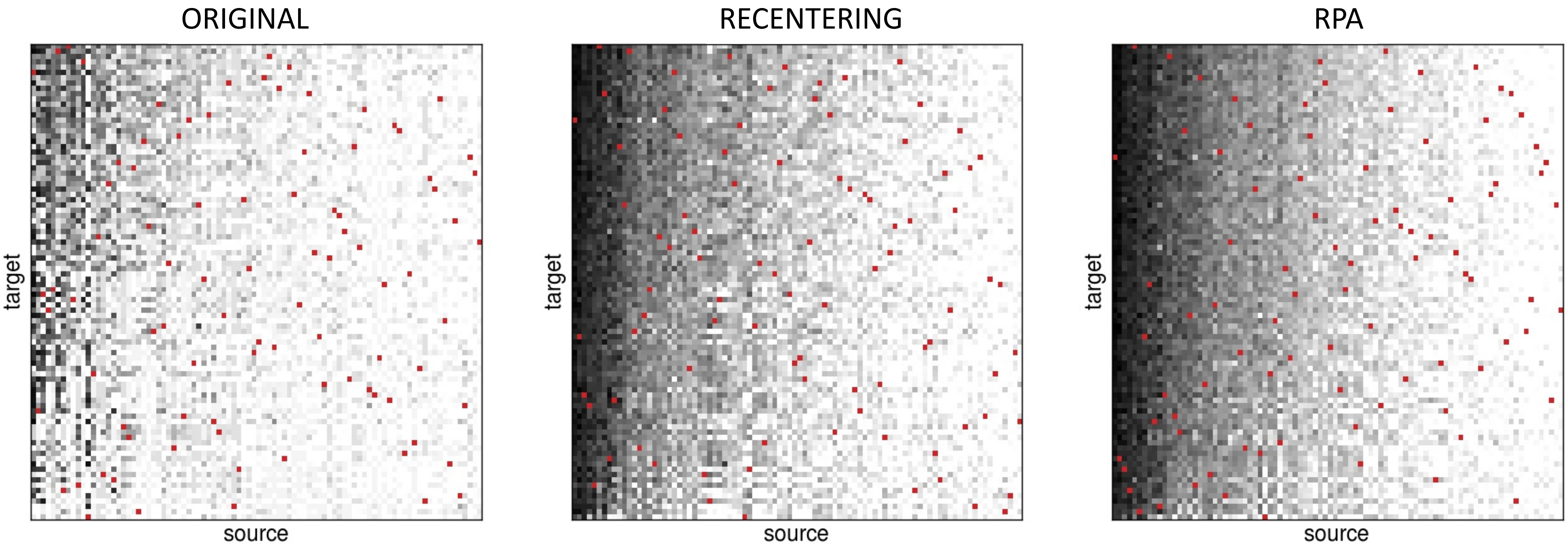
Cross-subject accuracy – Physionet MI

\# of data points in the target dataset : **10**



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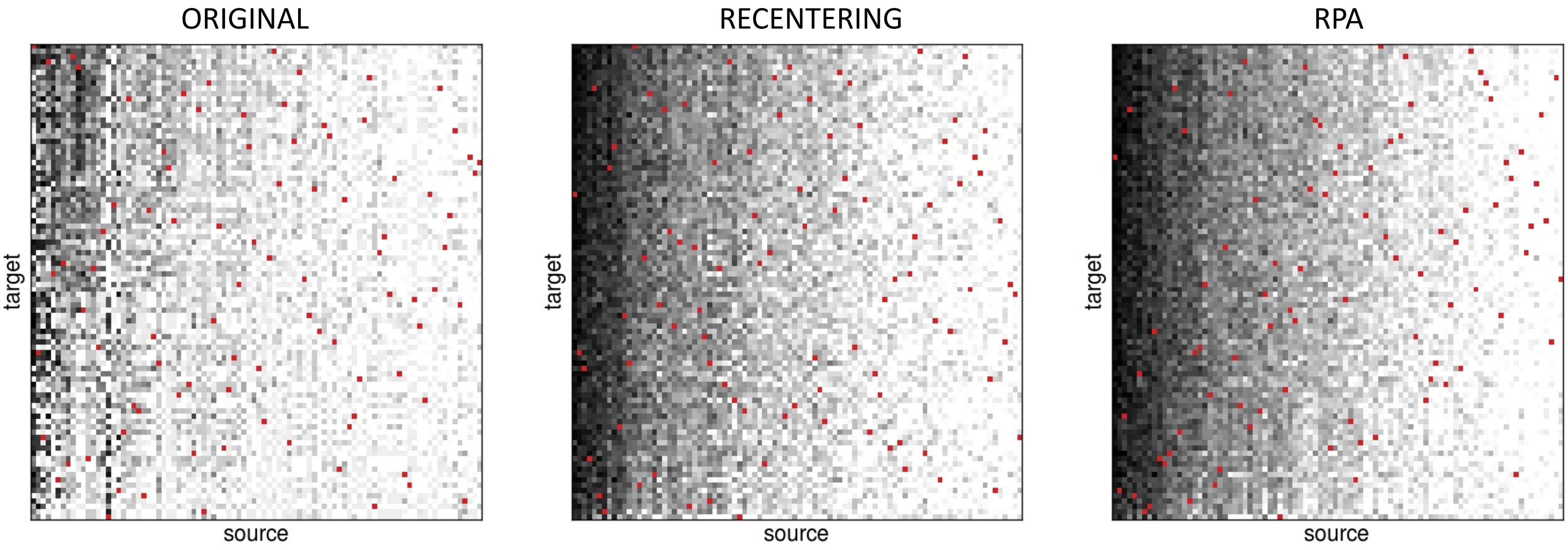
Source subject = Target subjet

Cross-subject accuracy – Physionet MI

of data points in the target dataset : **15**



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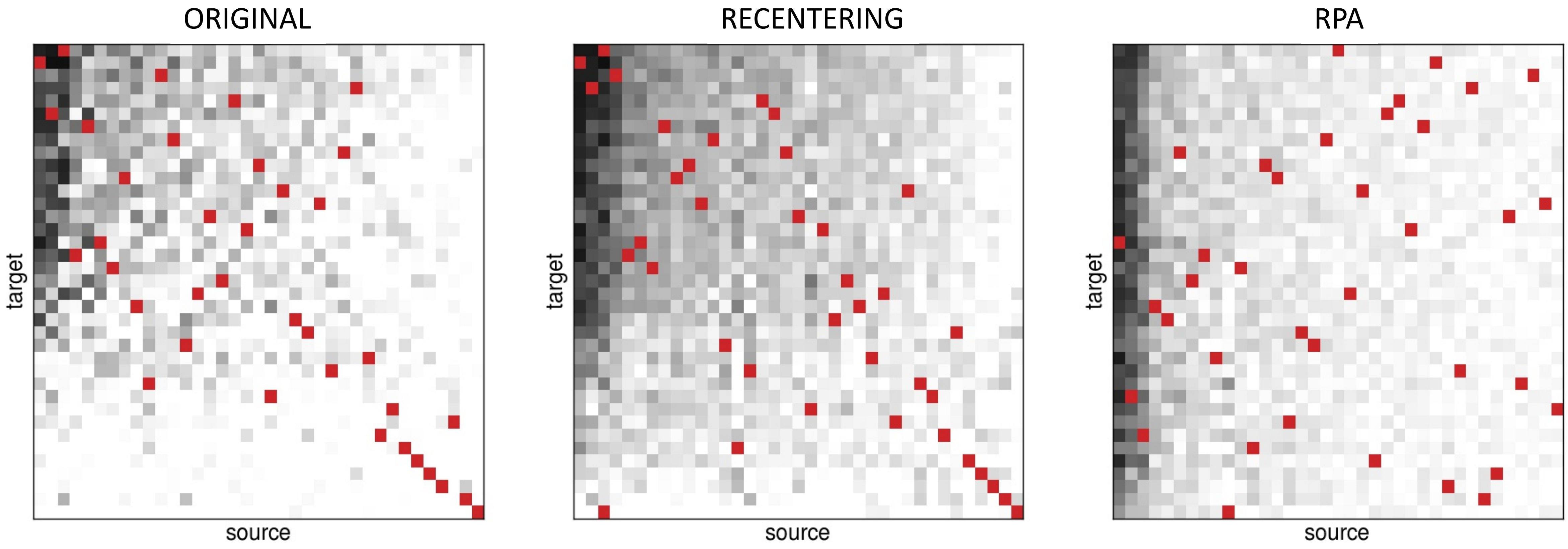
Cross-subject accuracy – GigaDB MI

of data points in the target dataset : **1**



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Cross-subject accuracy – GigaDB MI

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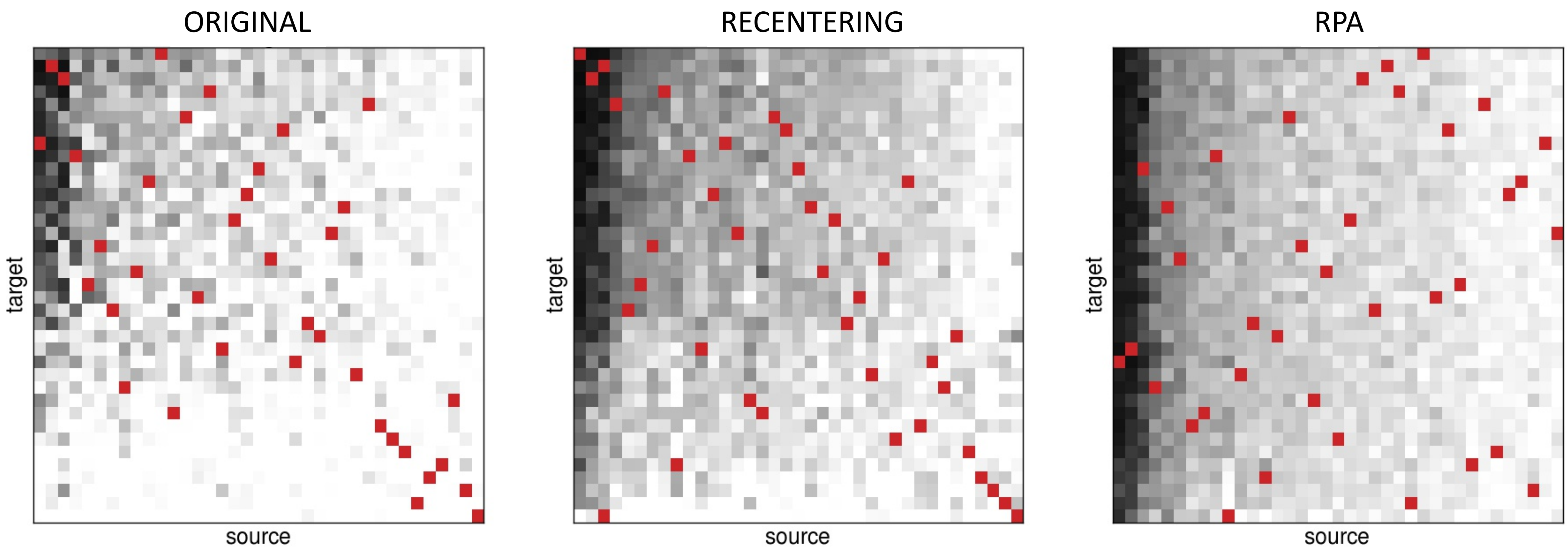

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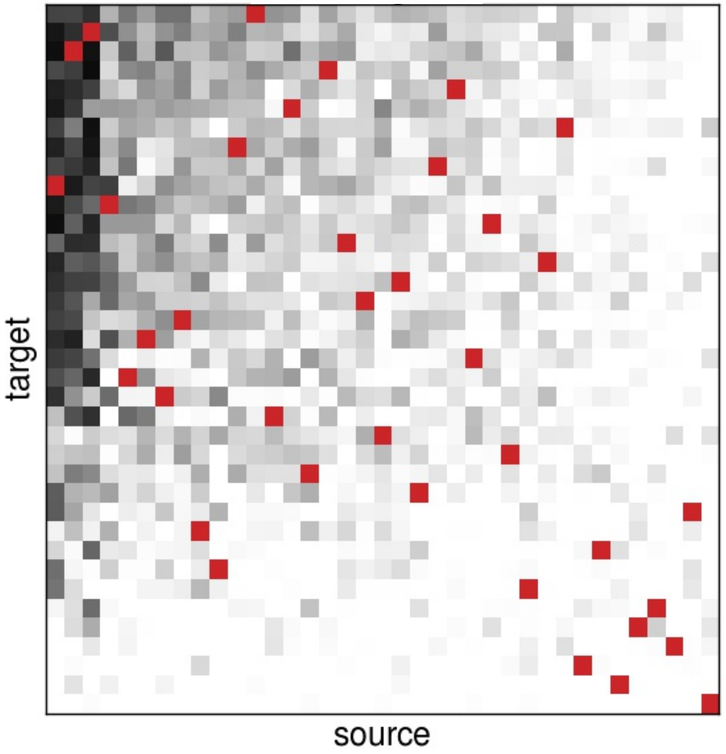
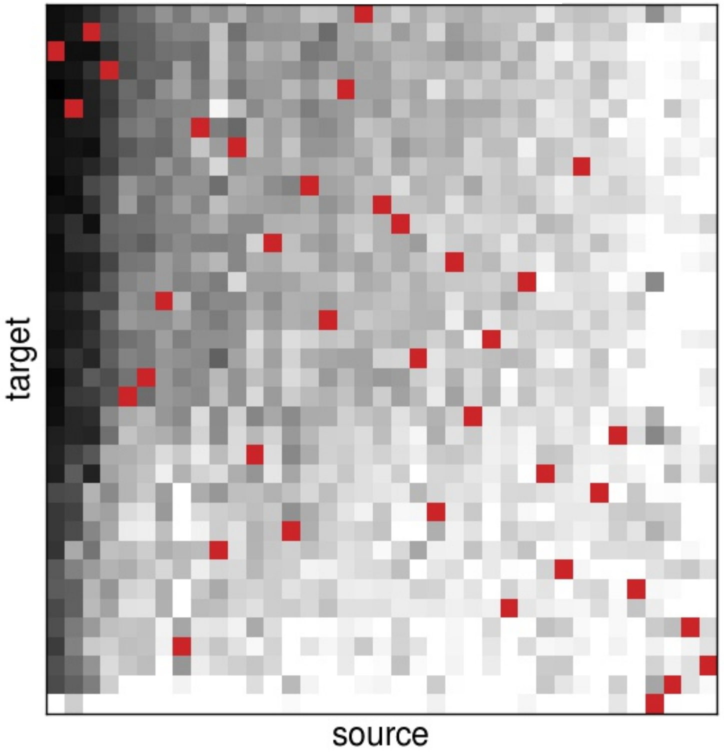
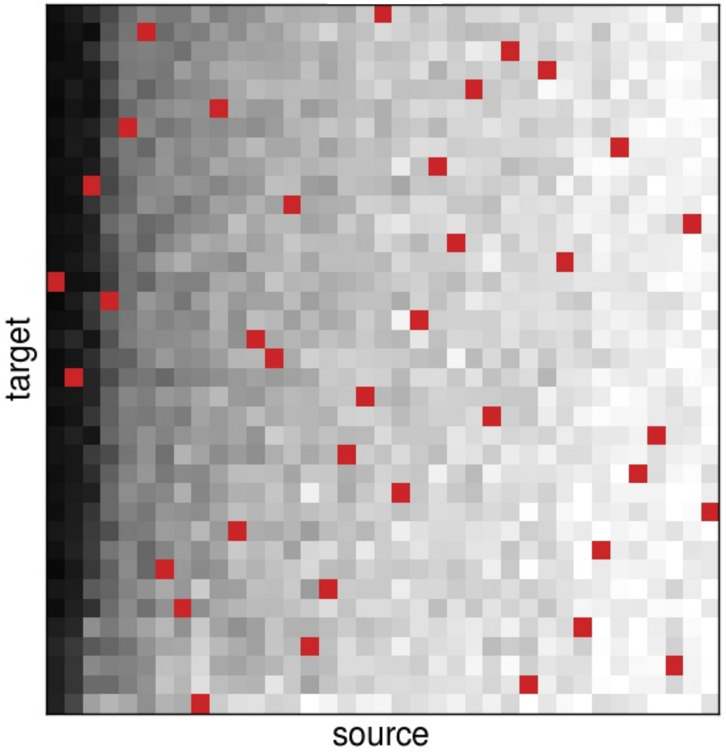


RECENTERING



RPA



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Source subject = Target subjet

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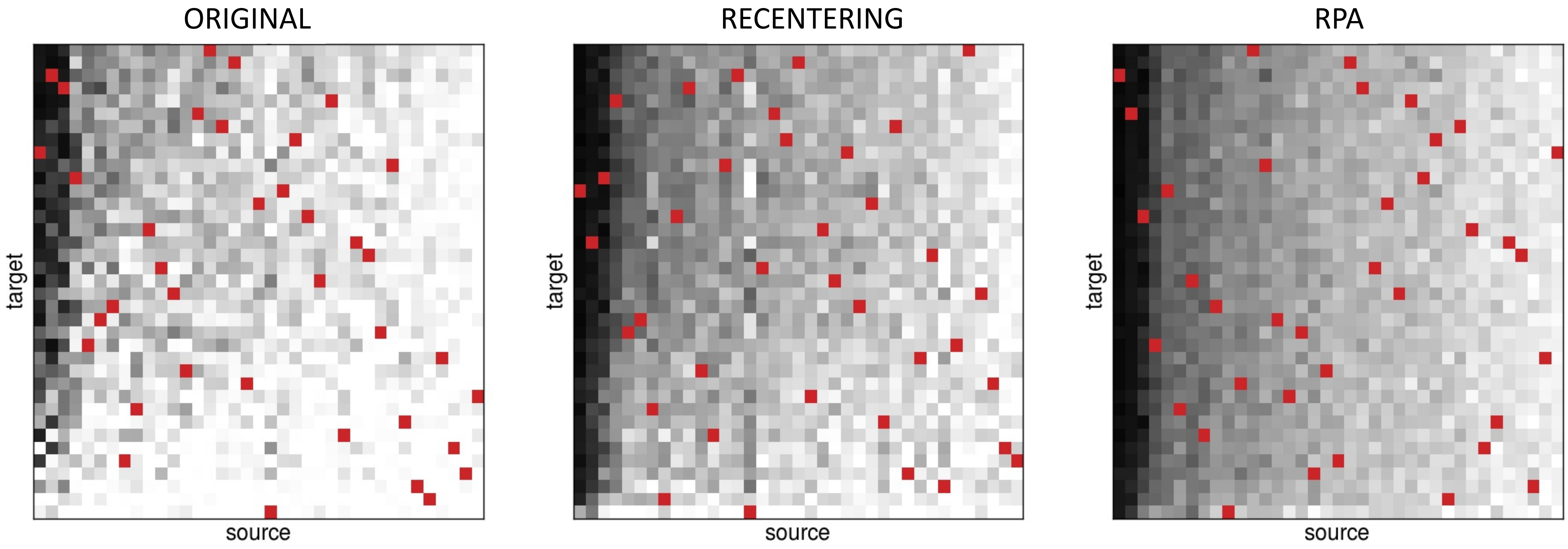
Cross-subject accuracy – GigaDB MI

of data points in the target dataset : **25**



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Source subject = Target subjet

Cross-subject accuracy

MI-Physionet	MEAN ACCURACY		
N	direct	recent.	RPA
1	0.52	0.55	0.55
5	0.53	0.59	0.61
10	0.54	0.61	0.63
15	0.55	0.63	0.64

MI-GigaDB	MEAN ACCURACY		
N	direct	recent.	RPA
1	0.55	0.58	0.55
5	0.55	0.60	0.61
10	0.56	0.62	0.64
25	0.58	0.65	0.67

SSVEP	MEAN ACCURACY		
N	direct	recent.	RPA
1	0.59	0.59	0.61
2	0.64	0.65	0.68
4	0.71	0.72	0.76
6	0.75	0.77	0.80

P300	MEAN AUC		
N	direct	recent.	RPA
6	0.49	0.59	0.55
12	0.50	0.57	0.57
32	0.52	0.54	0.57
48	0.53	0.54	0.56

Outline

Our method works for **any** BCI paradigm : it depends only on the choice of SPD matrices

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In every dataset there are **good** and **bad** source subjects. How to deal with this ?

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Our method could be used with **boosting** and other strategies for **combining** classifiers

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Some **interesting** works related to ours

Zanini et al. – *"Transfer Learning: a Riemannian geometry framework with applications to Brain-Computer Interfaces"* (2018)

Gayraud et al. – *"Optimal Transport Applied to Transfer Learning"* (2017)

Arvaneh et al. – *"EEG data space to reduce intersession nonstationarity in brain-computer interface"* (2013)

Thank you for your attention :-)

Questions ?

Riemannian Procrustres Analysis

Transfer Learning for Brain Computer Interfaces

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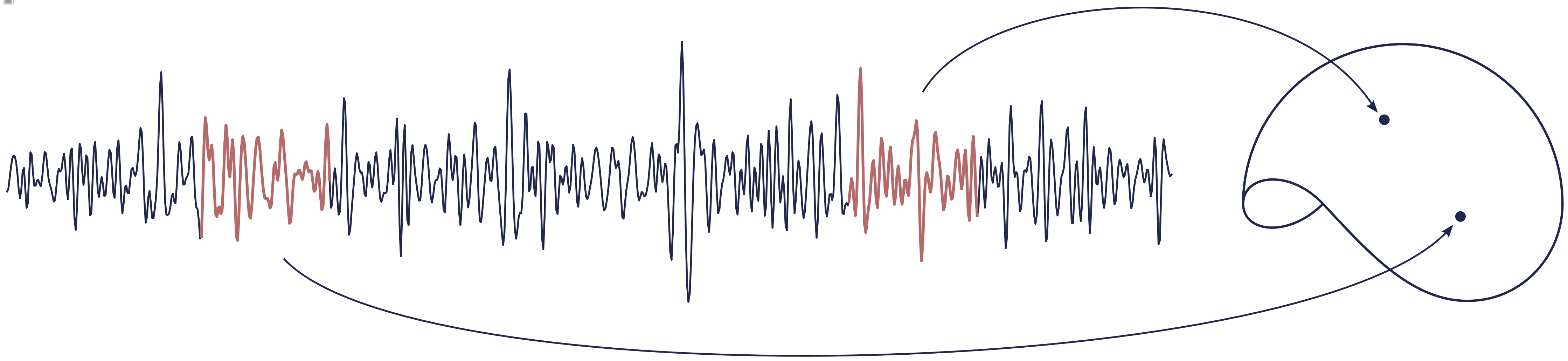


Presentation for the Machine Learning group at GIPSA-lab

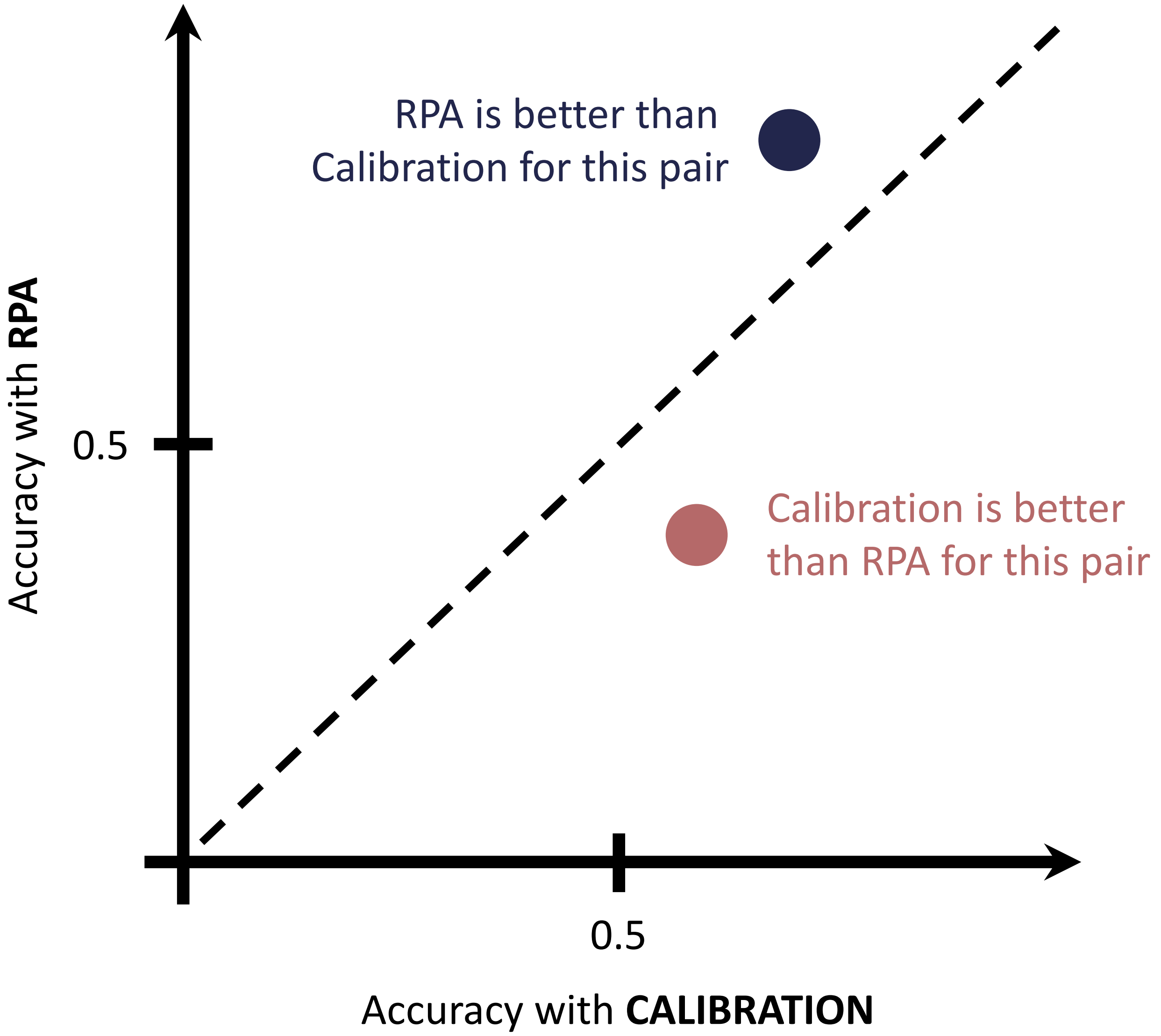
22th May 2018, Grenoble, France

Better than calibration ?

Compare RPA to **Calibration**

(Consider an **increasing** number of available points in the target dataset)

Use the Wilcoxon Paired statistical test to check if one method is **superior** to the other in **average** (for all pairs of subjects)



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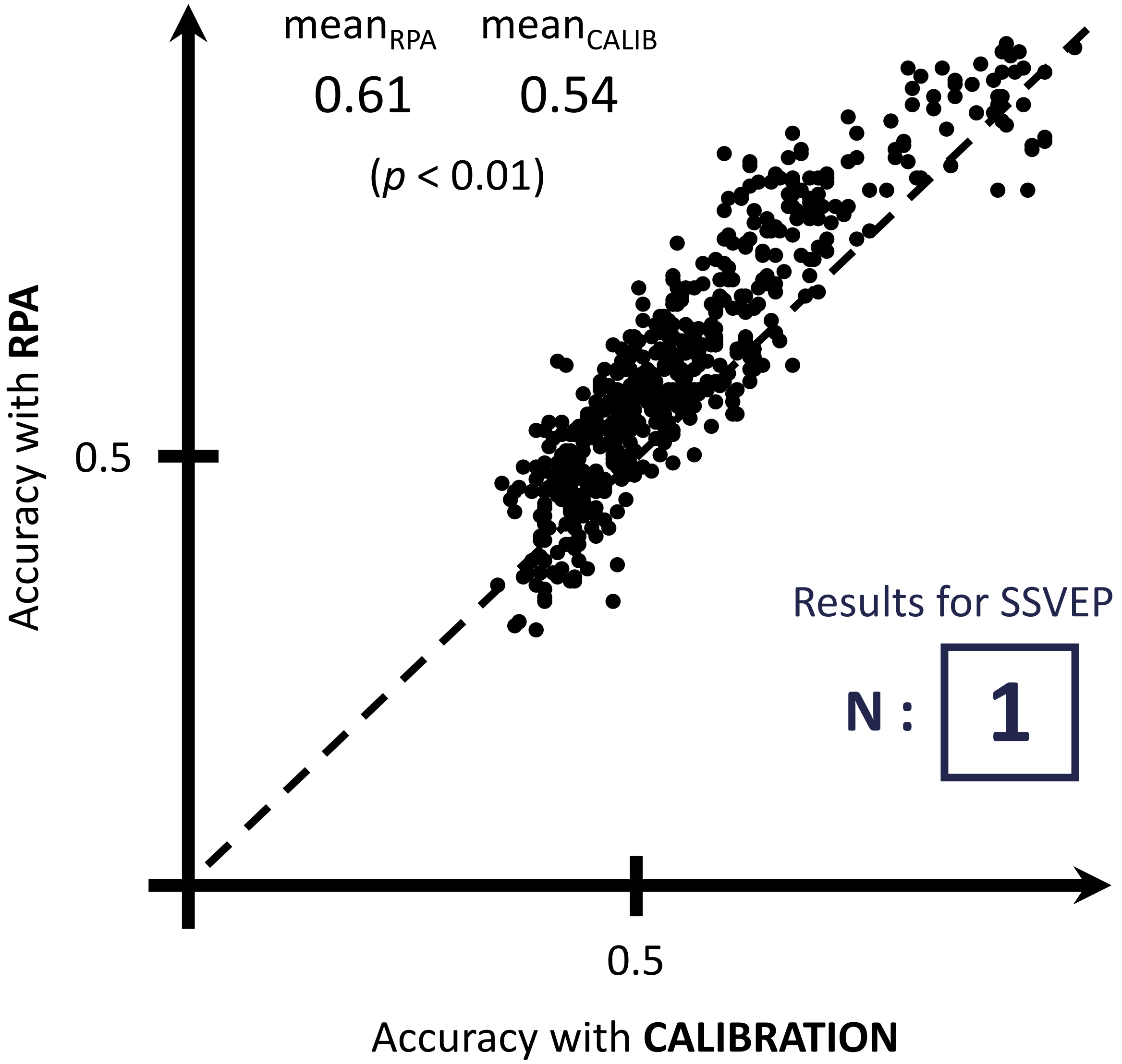

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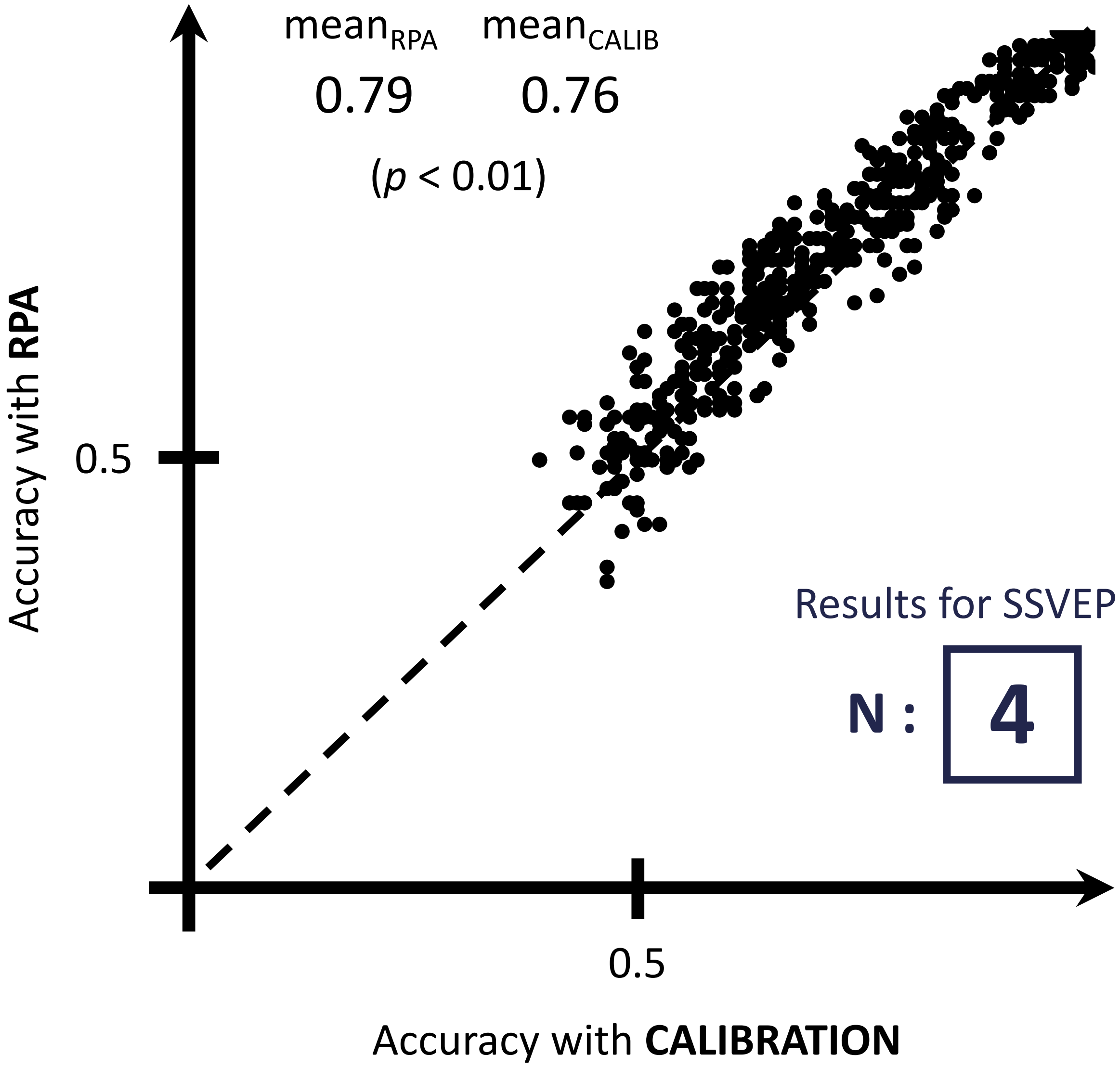
(Consider an **increasing** number of available points in the target dataset)

Use the Wilcoxon Paired statistical test to check if one method is **superior** to the other in **average** (for all pairs of subjects)



Results on the GIGADB dataset (Motor Imagery, Two classes)