

Multi-Source and Test-Time Domain Adaptation on Multi-variate Signals using Spatio-Temporal Monge Alignment

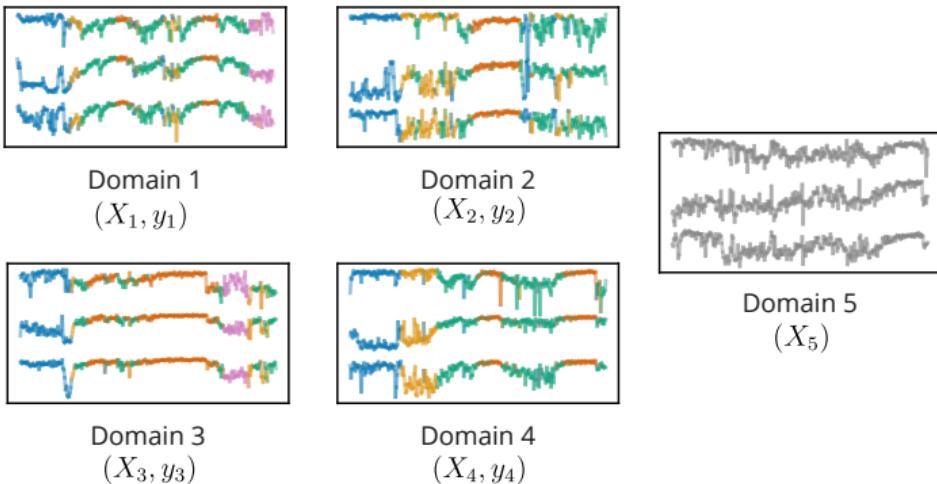
Théo Gnassounou, Antoine Collas, Rémi Flamary, Karim Lounici, Alexandre Gramfort

Huawei Seminar, 19-03-2025



Sleep stage classification from EEG signals

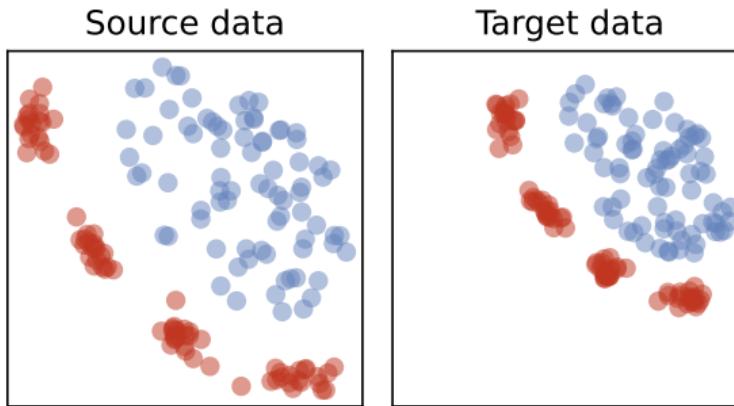
- **Multi-source** EEG signals from subjects/hospitals
- **Target** EEG signals from a new subject/hospital
- **No** access to the target labels
- **Shift** between the domains



→ **Goal: Adapt** the source to the target to **classify** the target signals

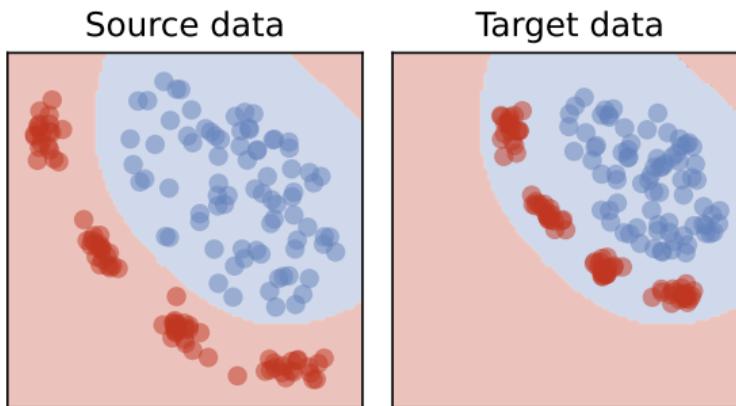
What is Domain Adaptation (DA)?

- Two type of domains: **Source** and **Target**.
- **Source** domains **with label** and **Target** domains **without label**.
- Assumption → **shift** between the distribution of the domain's data



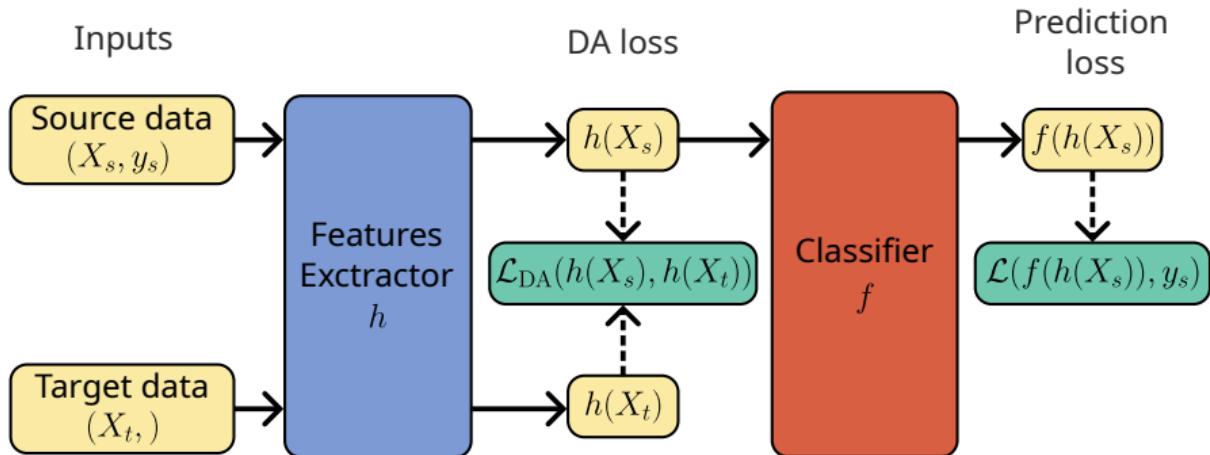
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→ **Problem:** **Drop in performance** when applying a model trained on the source to the target.

Traditional DA methods: Deep Learning

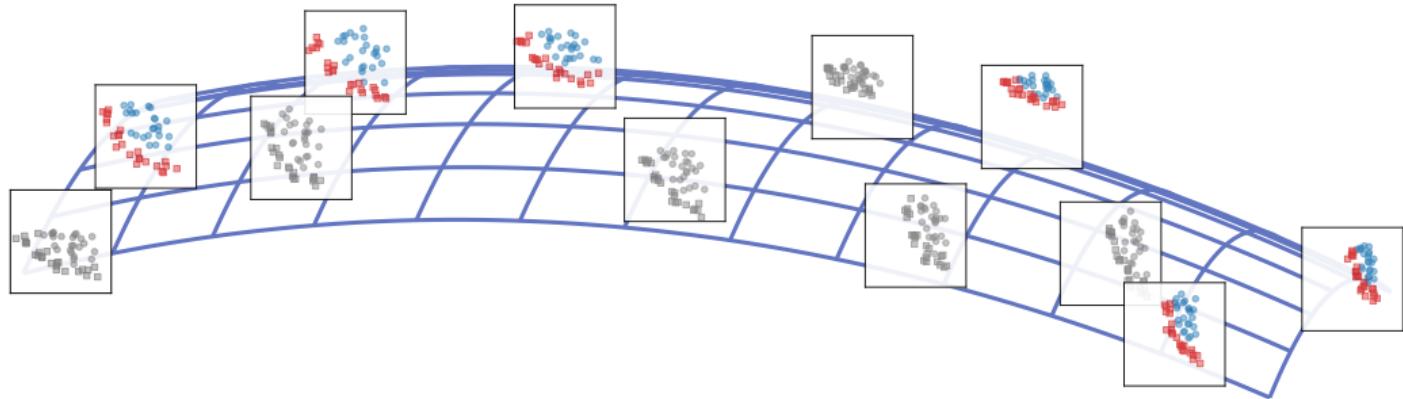


- Reduce the **divergence** between the source and target features with:
 - Correlation Alignment¹
 - Domain Adversarial Neural Network²
 - Joint Distribution Optimal Transport³
 - ...

¹Sun et. al., 2016 ²Ganin et. al., 2016 ³Damodaran et. al., 2018

Multi-source multi-target Domain Adaptation

Domain manifold



→ Multiple **subjects** and **hospitals** with **different** EEG signals

Source-free Domain Adaptation (or Test-Time DA)

1. Train-time

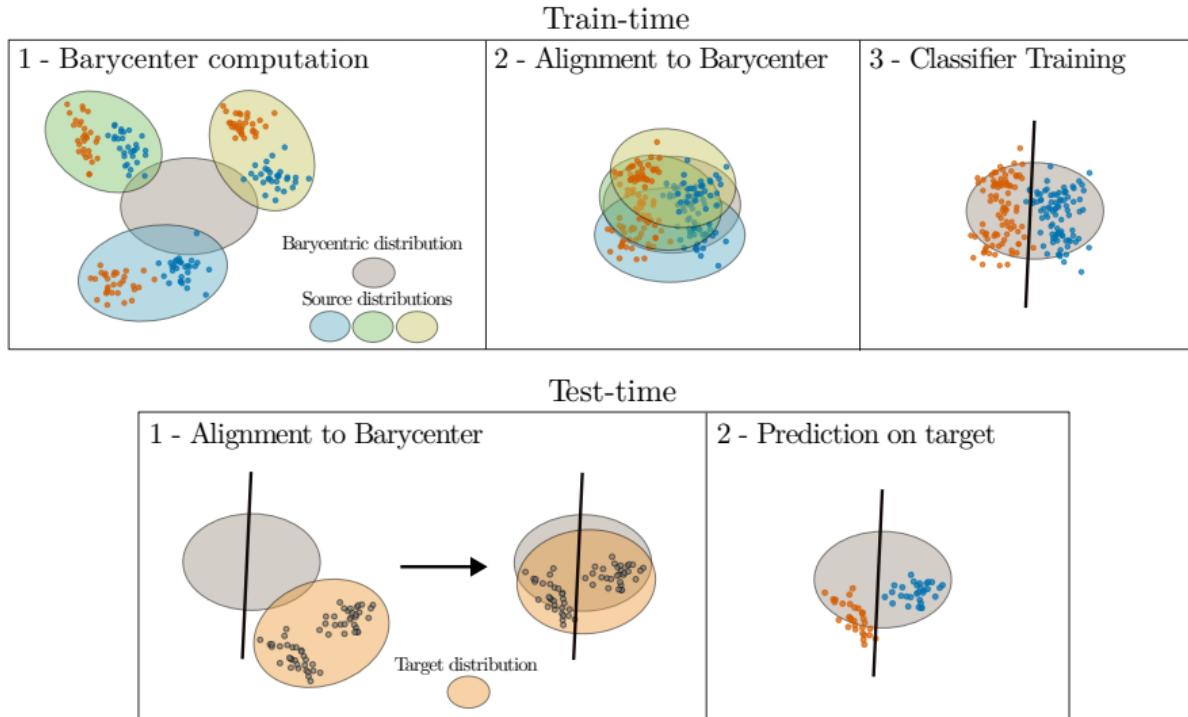
- Acces to **Source** domains with labels
- **No** access to **Target** domains
- **Train** a model on the source domains with labels

2. Test-time

- **No** access to **Source** domains
- Acces to **Target** domains **without** labels
- **Finetune** the model on the target domains without access to the target labels

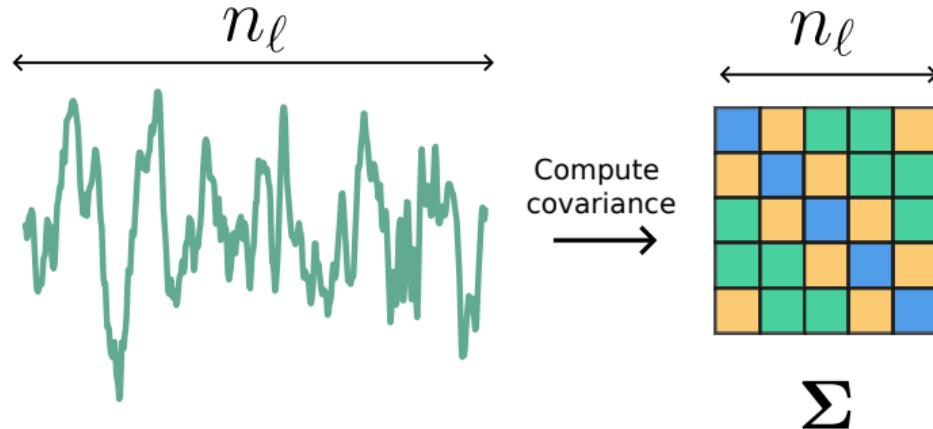
→ Practitioners **only** have access to the target data at test-time

Distribution alignment to barycenter to tackle domain shift



Assumptions on the signals

- Centered **Gaussian** distributions $\rightarrow \mathbf{X} \sim \mathcal{N}(\mathbf{0}, \Sigma)$ with $\Sigma \in \mathcal{S}_{n_\ell}^{++}$
- Σ is the "auto-covariance", computed with time-lagged. $\Sigma_{i,j} = \mathbf{X}_i \mathbf{X}_j$
- **Stationarity+Periodicity** \rightarrow Covariance matrices are **Toeplitz circulant** matrices.

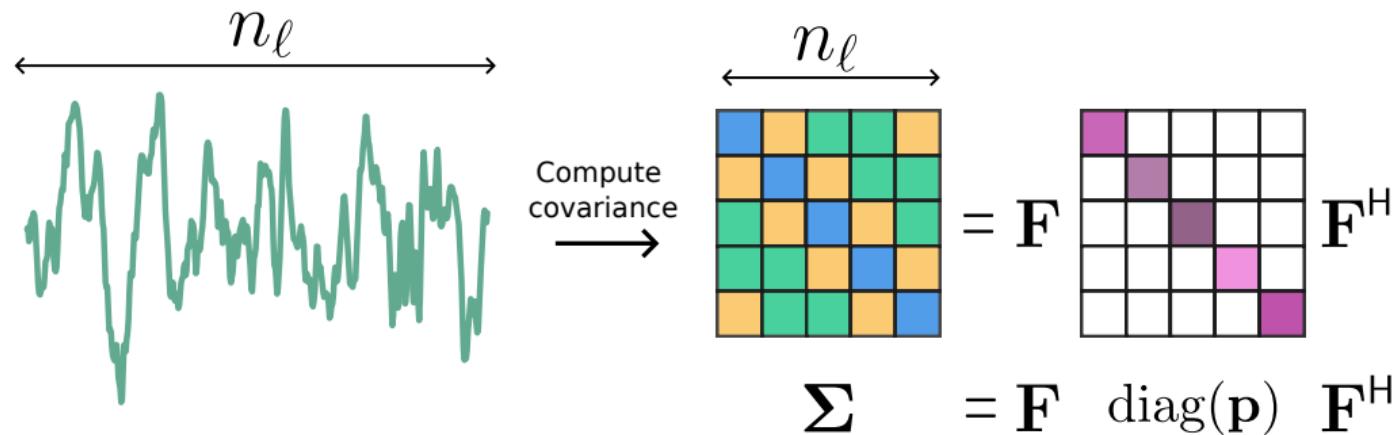


Assumptions on the signals

The Discrete Fourier Transform (DFT) can diagonalize the circulant matrix

$$\Sigma = \mathbf{F} \text{diag}(\mathbf{p}) \mathbf{F}^*,$$

with \mathbf{F} and \mathbf{F}^* the Fourier transform operator and its inverse, and \mathbf{p} the Power Spectral Density (PSD) of the signal.



Monge mapping for Gaussian distributions

Let consider Gaussian distributions $\mu_d = \mathcal{N}(\mathbf{0}, \Sigma_d)$ with $d \in \{s, t\}$. The OT cost, also called the **Bures-Wasserstein distance** when using a quadratic ground metric, is

$$\mathcal{W}_2^2(\mu_s, \mu_t) = \text{Tr} \left(\Sigma_s + \Sigma_t - 2 \left(\Sigma_t^{\frac{1}{2}} \Sigma_s \Sigma_t^{\frac{1}{2}} \right)^{\frac{1}{2}} \right). \quad (1)$$

The OT mapping, also called **Monge mapping**, can be expressed as the following affine function :

$$m(x) = \mathbf{A}x, \quad \text{with} \quad \mathbf{A} = \Sigma_s^{-\frac{1}{2}} \left(\Sigma_s^{\frac{1}{2}} \Sigma_t \Sigma_s^{\frac{1}{2}} \right)^{\frac{1}{2}} \Sigma_s^{-\frac{1}{2}} = \mathbf{A}^T. \quad (2)$$

The diagram shows the components of the mapping matrix \mathbf{A} with arrows indicating their source. The first arrow, labeled "Map", points from the term $\mathbf{A}x$ to the left side of the equation. The second arrow, labeled "Source Covariance", points from the term $\Sigma_s^{-\frac{1}{2}}$ to the term $\Sigma_s^{\frac{1}{2}}$ in the matrix. The third arrow, labeled "Target Covariance", points from the term Σ_t to the term Σ_t in the matrix.

Wasserstein barycenter between Gaussian distributions

Considering multiple Gaussian distributions μ_k . The barycenter $\bar{\mu}$ is expressed as

$$\bar{\mu} = \arg \min_{\mu} \frac{1}{K} \sum_{k=1}^K \mathcal{W}_2^2(\mu, \mu_k) . \quad (3)$$

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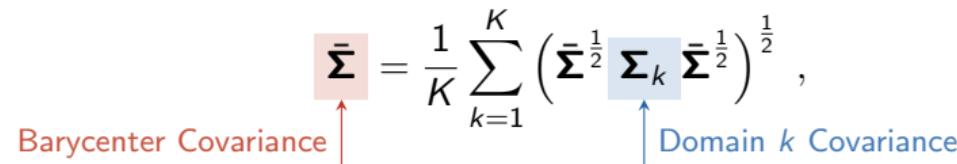
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The barycenter is still a Gaussian distribution $\bar{\mu} = \mathcal{N}(\mathbf{0}, \bar{\Sigma})$.

⇒ **No closed-form** for computing the covariance $\bar{\Sigma}$.

One uses the following optimality condition from¹:

$$\bar{\Sigma} = \frac{1}{K} \sum_{k=1}^K \left(\bar{\Sigma}^{\frac{1}{2}} \Sigma_k \bar{\Sigma}^{\frac{1}{2}} \right)^{\frac{1}{2}}, \quad (4)$$



¹ Agueh et. al., 2011

Previously for Univariate Gaussian stationary signals

- **Stationary** Gaussian signals with **PSD** \mathbf{p}_s and \mathbf{p}_t
- **Monge mapping** between the two **univariate** signals
- After **diagonalization** of the covariance matrix, the mapping is expressed as a **convolution**¹:

$$m(\mathbf{x}) = \mathbf{h} * \mathbf{x}, \quad \text{with} \quad \mathbf{h} = \mathbf{F}^* \left(\mathbf{p}_t^{\odot \frac{1}{2}} \odot \mathbf{p}_s^{\odot -\frac{1}{2}} \right). \quad (5)$$

The diagram shows the components of the convolution equation. The filter \mathbf{h} is highlighted in blue. The target power spectral density $\mathbf{p}_t^{\odot \frac{1}{2}}$ is highlighted in yellow. The source power spectral density $\mathbf{p}_s^{\odot -\frac{1}{2}}$ is highlighted in red. Arrows from the labels 'Filter', 'Target PSD', and 'Source PSD' point to their respective highlighted components in the equation.

¹Flamary et. al., 2018

Wasserstein barycenter between Gaussian stationary signals

Lemma from¹

Consider K centered stationary Gaussian signals of PSD \mathbf{p}_k with $k \in [K]$, the Wasserstein barycenter of the K signals is a centered stationary Gaussian signal of PSD $\bar{\mathbf{p}}$ with:

$$\bar{\mathbf{p}} = \left(\frac{1}{K} \sum_{k=1}^K \mathbf{p}_k^{\odot \frac{1}{2}} \right)^{\odot 2}. \quad (6)$$

Barycenter PSD ↑ Domain k PSD ↑

Sketch of proof: the proof directly applies the optimality condition (7) of the barycenter. With factorized covariances, the matrix square root and the inverse can be simplified as element-wise square root and inverse.

¹ Gnassounou et. al., 2023

New assumption on the signals

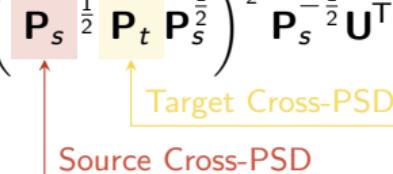
- **Multivariate** signals with cross covariance $\Sigma \in \mathcal{S}_{n_\ell n_c}^{++}$
 - Reduction of parameters from $(\mathbf{n}_\ell \times \mathbf{n}_c)^2 \rightarrow \mathbf{n}_\ell \times \mathbf{n}_c^2$
 - **P** is the cross-PSD matrix of the signal

$$\left(\begin{array}{c|ccc} & n_c & & \\ \hline \Sigma & \left(\begin{array}{c|cc} \text{Block 1} & \text{Block 2} & \text{Block 3} \\ \text{Block 4} & \text{Block 5} & \text{Block 6} \\ \text{Block 7} & \text{Block 8} & \text{Block 9} \end{array} \right) & \text{...} & \text{...} \\ \hline & n_\ell & & \end{array} \right) = F \left(\begin{array}{c|ccc} & n_c & & \\ \hline \text{F}^H & \left(\begin{array}{c|cc} \text{Block 1} & \text{Block 2} & \text{Block 3} \\ \text{Block 4} & \text{Block 5} & \text{Block 6} \\ \text{Block 7} & \text{Block 8} & \text{Block 9} \end{array} \right) & \text{...} & \text{...} \\ \hline & n_\ell & & \end{array} \right) F^H = F U \left(\begin{array}{c|ccc} & n_c & & \\ \hline P & \left(\begin{array}{c|cc} \text{Block 1} & \text{Block 2} & \text{Block 3} \\ \text{Block 4} & \text{Block 5} & \text{Block 6} \\ \text{Block 7} & \text{Block 8} & \text{Block 9} \end{array} \right) & \text{...} & \text{...} \\ \hline & n_\ell & & \end{array} \right) U^T F^H$$

Monge mapping for Multivariate Gaussian stationary signals

- Let consider Gaussian distributions $\mu_d = \mathcal{N}(\mathbf{0}, \Sigma_d)$ with $d \in \{s, t\}$ and $\Sigma_d = \mathbf{F}\mathbf{U}\mathbf{Q}_d\mathbf{U}^T\mathbf{F}^H$

$$\begin{pmatrix} \text{diag}(\mathbf{p}_{1,1}) & \dots & \text{diag}(\mathbf{p}_{1,n_c}) \\ \dots & \dots & \dots \\ \text{diag}(\mathbf{p}_{n_c,1}) & \dots & \text{diag}(\mathbf{p}_{n_c,n_c}) \end{pmatrix} \triangleq \mathbf{U}\mathbf{P}_s^{-\frac{1}{2}} \begin{pmatrix} \mathbf{P}_s^{\frac{1}{2}} & \mathbf{P}_t & \mathbf{P}_s^{\frac{1}{2}} \end{pmatrix}^{\frac{1}{2}} \mathbf{P}_s^{-\frac{1}{2}} \mathbf{U}^T \in \mathcal{H}_{n_c f}^{++}$$



- Given a signal $\mathbf{X} = [\mathbf{x}_1, \dots, \mathbf{x}_{n_c}]^T \in \mathbb{R}^{n_c \times n_\ell}$ the Monge mapping is a sum of convolutions

$$m(\mathbf{X}) = \left[\sum_{j=1}^{n_c} \mathbf{h}_{1,j} * \mathbf{x}_j, \dots, \sum_{j=1}^{n_c} \mathbf{h}_{n_c,j} * \mathbf{x}_j \right]^T$$

where $\mathbf{h}_{i,j} = \frac{1}{\sqrt{f}} \mathbf{F}^H \mathbf{p}_{i,j} \in \mathbb{R}^f$.



Wasserstein barycenter for Multivariate Gaussian stationary signals

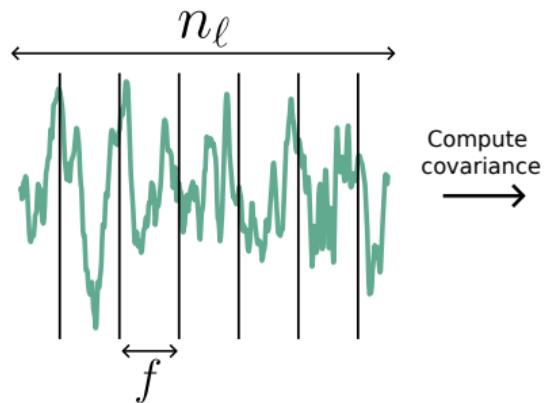
- No more closed form for the barycenter covariance $\bar{\Sigma}$.
- The barycenter PSD $\bar{\mathbf{P}}$ is expressed as

$$\bar{\mathbf{P}} = \frac{1}{K} \sum_{k=1}^K \left(\bar{\mathbf{P}}^{\frac{1}{2}} \mathbf{P}_k \bar{\mathbf{P}}^{\frac{1}{2}} \right)^{\frac{1}{2}}, \quad (7)$$

Barycenter cross-PSD Domain k cross-PSD

How to reduce the the number of parameters of the filter?

- $n_\ell \times n_c^2$ parameters for \mathbf{h} still highlight
- $n_\ell \rightarrow f$
- Use **Welch** method to estimate the PSD
 - Cut the signal into segments
 - Compute the PSD of each segment
 - Average the PSD



$$\mathbf{P} = \left(\begin{array}{c|ccccc} & & & & & \\ \hline & \textcolor{brown}{\square} & \textcolor{blue}{\square} & \textcolor{red}{\square} & \textcolor{green}{\square} & \textcolor{purple}{\square} \\ & \textcolor{blue}{\square} & \textcolor{brown}{\square} & \textcolor{red}{\square} & \textcolor{green}{\square} & \textcolor{purple}{\square} \\ & \textcolor{red}{\square} & \textcolor{blue}{\square} & \textcolor{brown}{\square} & \textcolor{green}{\square} & \textcolor{purple}{\square} \\ & \textcolor{green}{\square} & \textcolor{red}{\square} & \textcolor{blue}{\square} & \textcolor{brown}{\square} & \textcolor{purple}{\square} \\ & \textcolor{purple}{\square} & \textcolor{green}{\square} & \textcolor{red}{\square} & \textcolor{blue}{\square} & \textcolor{brown}{\square} \\ \hline & & & & & \\ \end{array} \right)$$

n_c
 $n_\ell \rightarrow f$

$$\Sigma = \mathbf{F} \quad \mathbf{F}^H$$
$$\Sigma = \mathbf{F} \quad \text{diag}(\mathbf{p}) \quad \mathbf{F}^H$$

Convolutional Monge Mapping Normalization (CMMN)

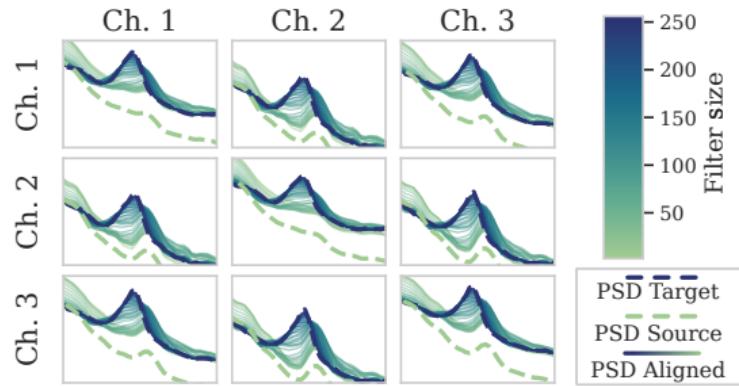
1. Train-time: Access to source domains

- Compute **cross-PSD** $\hat{\mathbf{P}}_k$ for each source domain.
- Compute **barycenter** $\hat{\mathbf{p}}$ with the PSD $\hat{\mathbf{P}}_k$.
- Compute the **convolutional filters** \mathbf{h}
- **Train a predictor** g on the normalized source data.

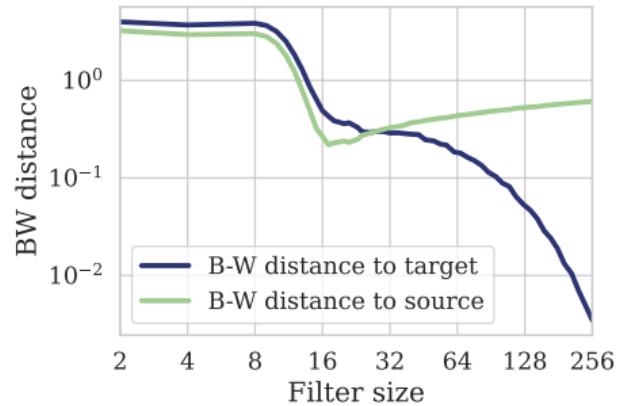
2. Test-time: Access to unseen target data

- Compute the **cross-PSD** $\hat{\mathbf{P}}_t$ for the target domain.
- Compute the **convolutional filter** \mathbf{h} between target domain and the barycenter $\hat{\mathbf{P}}$.
- Predict target labels with trained predictor g .

Illustration of the monge mapping for two signals

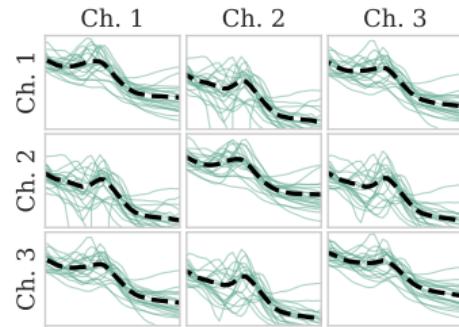


(a) Cross-PSD alignment

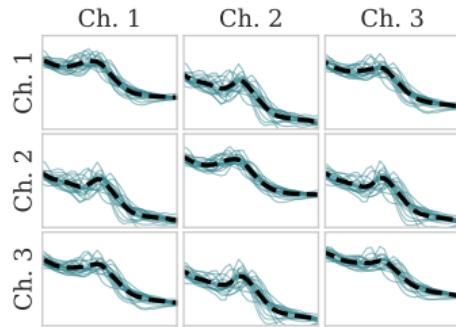


(b) Bures-Wasserstein distance

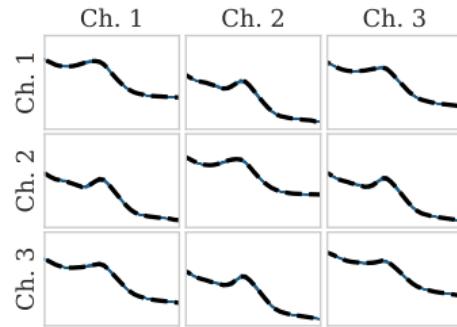
Cross-PSD alignment to barycenter for different filters size



(a) Source cross-PSD



(b) Alignment with $f = 32$



(c) Alignment with $f = 256$

Domain adaptation in biosignals

Possible variability in biosignals:

- Variability in the **patient population** : age, gender, height, diseased or healthy, different sleep stage proportion.

Domain adaptation in biosignals

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- Variability in **data interpretation by specialist** : different scoring criteria, subjectivity, tiredness.

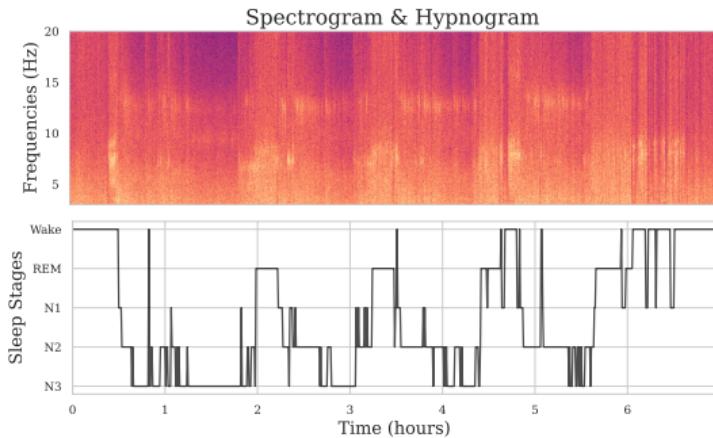
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→ **Domain Adaptation** problem.

Sleep Staging



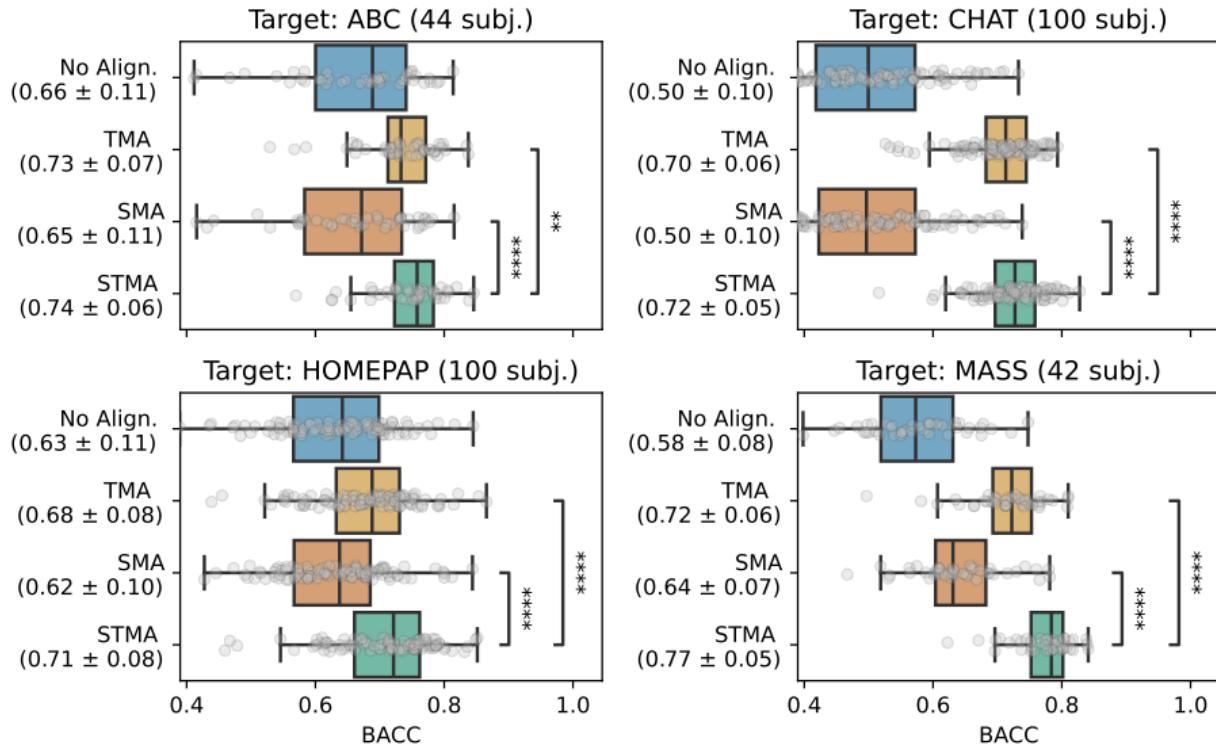
- **Classification** problem with **five** classes:
Wake, N1, N2, N3, REM
- **Frequency** helps to classify sleep stage

Experimental setup

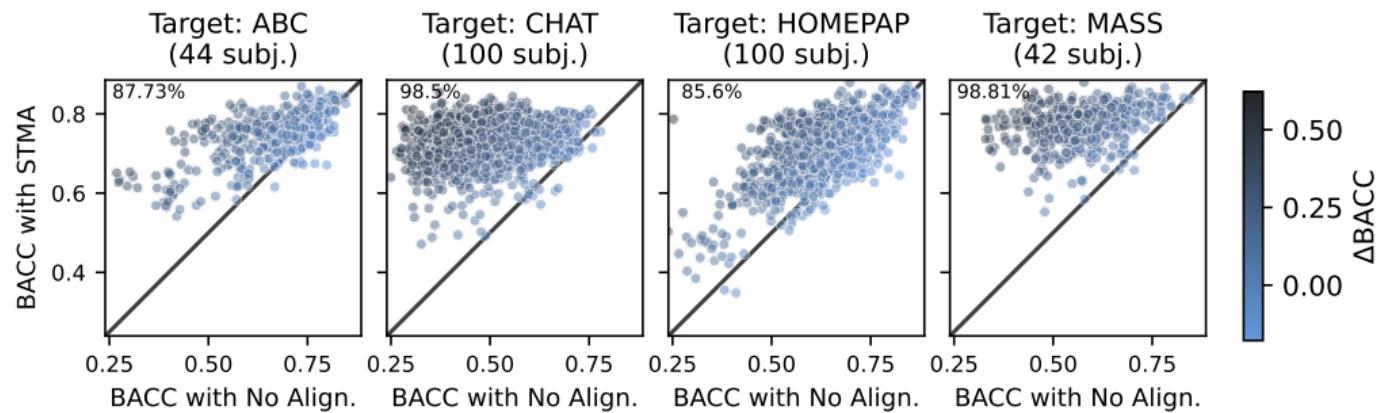
- Four different datasets: **ABC** , **CHAT** , **HOMEPA**P and **MASS**
- Around **300** subjects in total
- One **domain** = One **subject**
- **Seven** EEG channels
- Use **CNN** architecture from¹

¹ Chambon et. al., 2018

Results on Sleep data



Results on Sleep data



How to use DA?

Skada¹ is a **Python** library to **easily** use DA methods.

- **Homogeneous API** for all DA methods (Shallow and Deep learning).
- **Sklearn-like API** with estimator class (.fit, .predict, ...), pipeline, grid search ...
- **DA scorer** to validate hyper-parameters without using target label.



¹ *Gnassounou et. al., 2024*

Data format in Skada

- $X \rightarrow$ 2D array of shape ($n_samples$, $n_features$)
- $y \rightarrow$ 1D array of shape ($n_samples$,)
- $sample_domain \rightarrow$ 1D array of shape ($n_samples$,) giving the **domain** of each **sample**

```
1      from skada.datasets import make_shifted_datasets  
2  
3      X, y, sample_domain = make_shifted_datasets(  
4          20, 20, shift='covariate_shift', random_state=42  
5      )
```

- All shift are available in `make_shifted_datasets` function

Shallow DA in Skada

- Initialize the estimator
- Fit the model
- Don't forget to give the **sample domain**

```
1  from skada import LinOT  
2  
3  estimator = LinOT()  
4  estimator.fit(X, y, sample_domain=sample_domain)
```

- ~ 20 shallow methods available in Skada

Pipeline DA in Skada

- Can be used with **Pipeline**

```
1   from skada import make_da_pipeline
2   from skada import LinOTAdapter, GaussianReweightAdapter
3   from sklearn.linear_model import LogisticRegression
4
5   pipeline = Pipeline(
6       LinOTAdapter(),
7       LogisticRegression()
8   )
9   pipeline.fit(X, y, sample_domain=sample_domain)
```

- Possibility to mixed DA adapters

```
1   pipeline = Pipeline(
2       LinOTAdapter(),
3       GaussianReweightAdapter(),
4       LogisticRegression()
5   )
```

DA scorer in Skada

- Possibility to use `cross_val_score` with **DA scorers**
- DA scorers are used to **validate** the **hyperparameters** without using the target labels

```
1      from skada.scorers import ImportanceWeightedScorer  
2  
3      scorer = ImportanceWeightedScorer()  
4      score = cross_val_score(pipeline, X, y, sample_domain=sample_domain,  
→      scoring=scorer)
```

- 6 DA scorers available in Skada

Deep DA method in Skada

- Use **Skorch** → Pytorch wrapper for **Sklearn**
- Give an **architecture** and **hyperparameters**

```
1      from skada.deep import DeepCoral
2      from skada.deep.modules import ToyCNN
3
4      model = DeepCoral(
5          ToyCNN(),
6          batch_size=32,
7          max_epochs=5,
8          lr=1e-3,
9          reg=1,
10         layer_name="feature_extractor",
11         )
12         model.fit(X, y, sample_domain=sample_domain)
```

- ~ 10 Deep DA methods available in Skada

Conclusion

- Distribution shift is a **challenging** problem in **biosignals**
- Alignment of the **cross-PSD** is a **powerful** tool to tackle the problem
- Try **Skada** to easily use DA methods
- Don't hesitate to contribute to the library!

