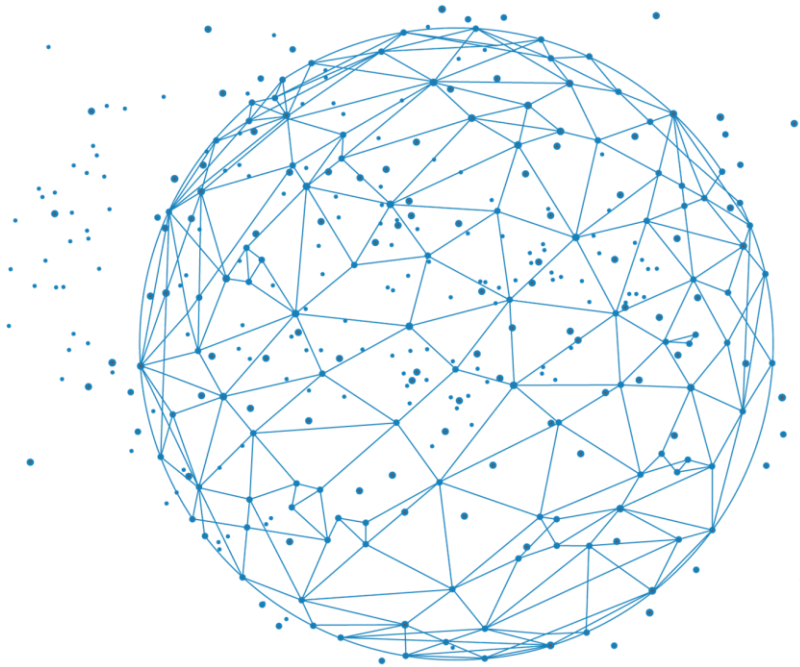


Second edition 2024 in Fréjus

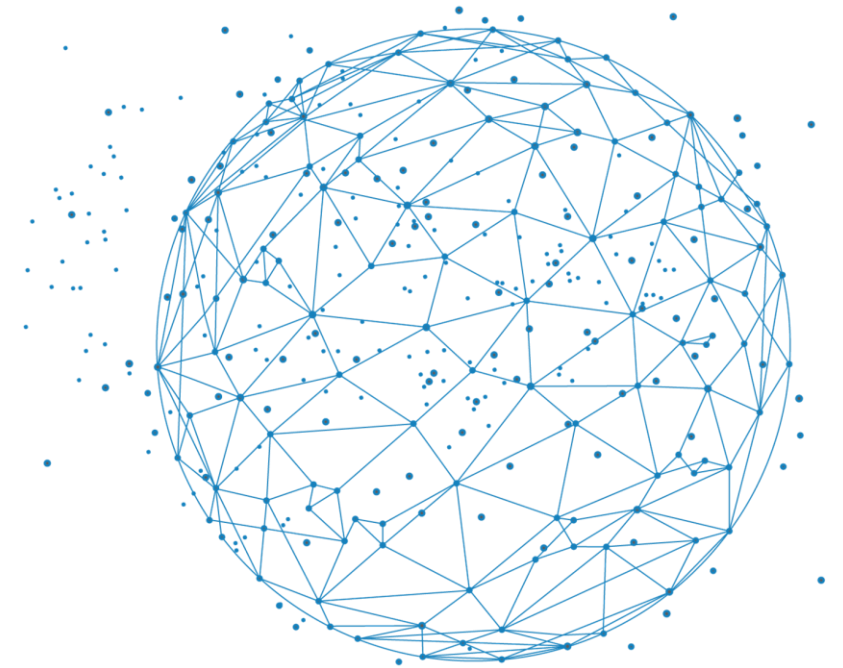


Regularized Generalized Canonical Correlation Analysis (RGCCA)

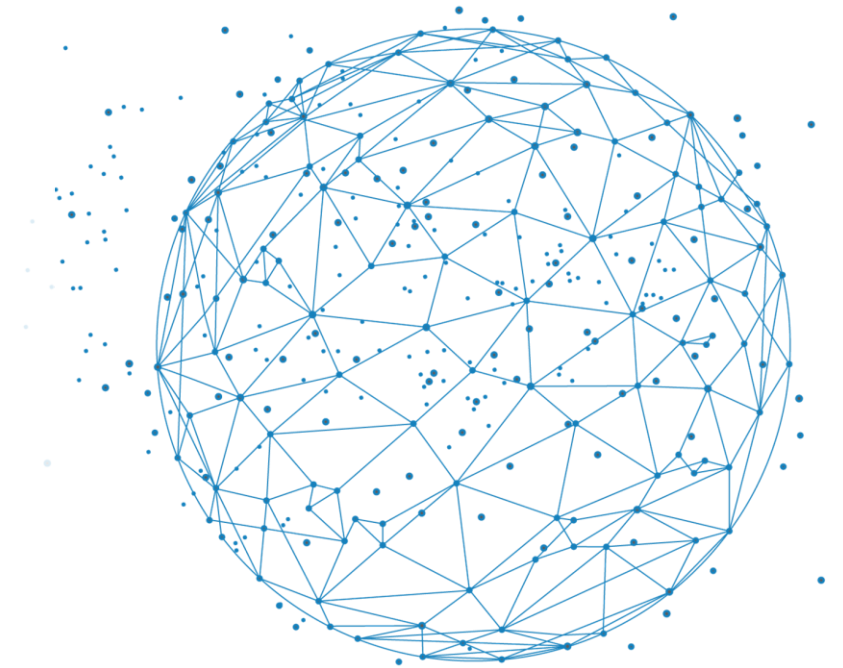
Jimmy Vandel (Plateforme Lilloise en Biologie & Santé)
Arnaud Gloaguen (CNRGH - CEA)
Vincent Guillemot (Institut Pasteur)

DOI version final

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2. Unsupervised analysis with one-block: Principal Component Analysis (PCA)
3. Unsupervised analysis with two-blocks:
Partial Least Squares (PLS) and Canonical Correlation Analysis (CCA)
4. Unsupervised analysis with L -blocks:
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Case Study: Major Depressive Disorder (MDD)



Data from this case study comes from Amazigh et. al 2024 [Sex-specific and multiomic integration enhance accuracy of peripheral blood biomarkers of major depressive disorder.](#)

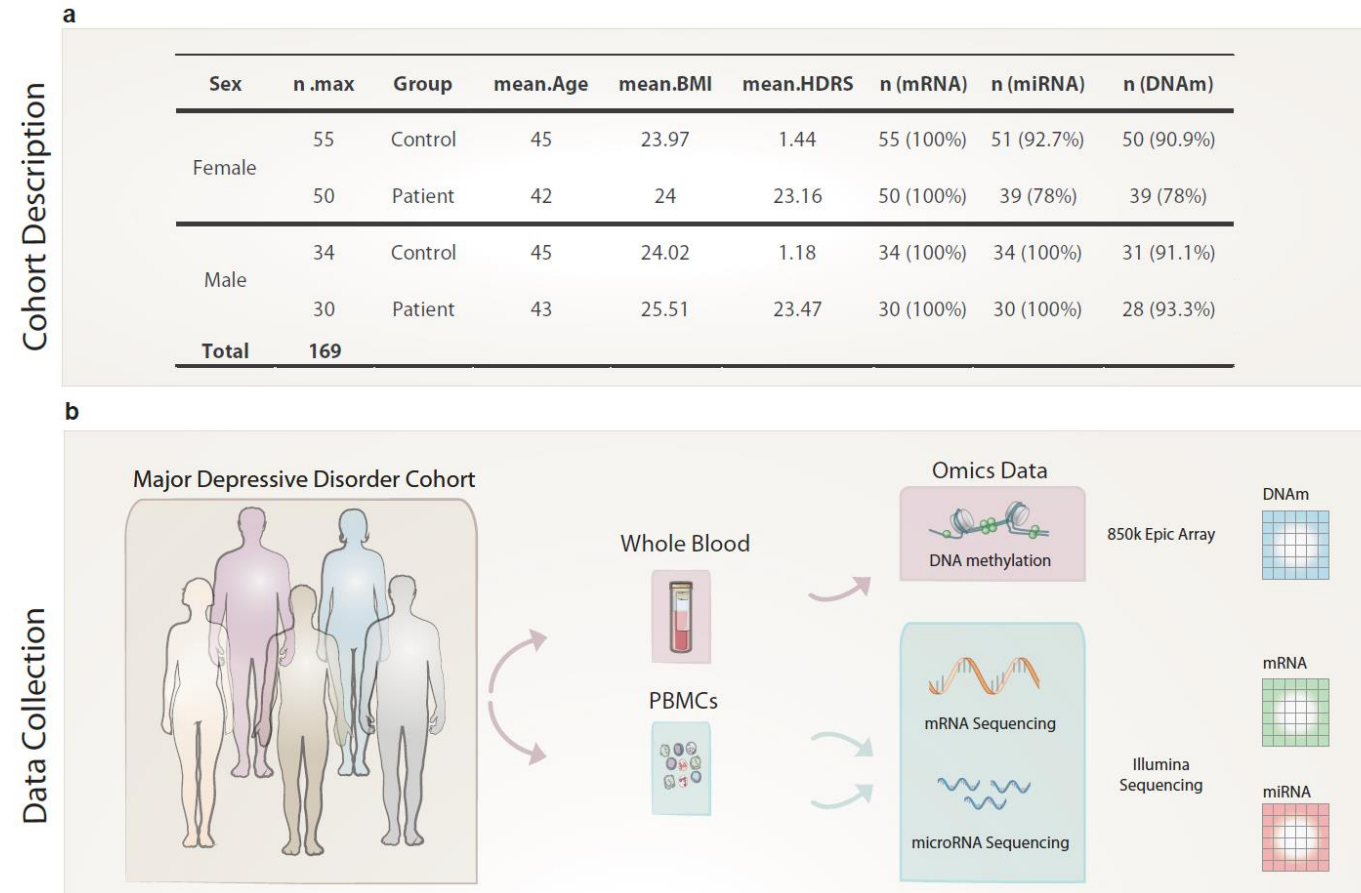


Figure taken from Amazigh Mokhtari's PhD manuscript.



```
> summary(DNAM_covariates_explored_female)
```

Sample_Group	BMI	BMI.bin	Age	Age.bin	Age_bin	Array	Slide
control:50	Min. :16.37	low :64	Min. :21.00	<20 : 0	2:21	R04C01 :19	204668820053: 3
mdd :37	1st Qu.:21.42	medium:19	1st Qu.:32.00	20-30:21	3:11	R05C01 :18	204679630043: 3
	Median :23.23	high : 4	Median :45.00	30-40:11	4:20	R06C01 :12	204564460100: 2
	Mean :23.83		Mean :43.52	40-50:20	5:26	R07C01 :12	204564470040: 2
	3rd Qu.:25.24		3rd Qu.:53.50	50-60:26	6: 8	R03C01 :10	204564470092: 2
	Max. :39.54		Max. :71.00	60-70: 8	7: 1	R02C01 : 8	204564470101: 2
				>70 : 1		(Other): 8	(Other) :73
	CD4	CD8	MO	B	NK	GR	
Min. :0.08709	Min. :0.02919	Min. :0.04979	Min. :0.00000	Min. :0.00000	Min. :0.00000	Min. :0.3883	
1st Qu.:0.15202	1st Qu.:0.08095	1st Qu.:0.07906	1st Qu.:0.01484	1st Qu.:0.01484	1st Qu.:0.03505	1st Qu.:0.5122	
Median :0.19110	Median :0.10843	Median :0.08997	Median :0.02433	Median :0.02433	Median :0.05053	Median :0.5982	
Mean :0.18577	Mean :0.10527	Mean :0.09208	Mean :0.02922	Mean :0.02922	Mean :0.05556	Mean :0.5862	
3rd Qu.:0.21439	3rd Qu.:0.12263	3rd Qu.:0.10495	3rd Qu.:0.03967	3rd Qu.:0.03967	3rd Qu.:0.07699	3rd Qu.:0.6446	
Max. :0.30672	Max. :0.19381	Max. :0.14454	Max. :0.13657	Max. :0.13657	Max. :0.14684	Max. :0.7691	



Low (≤ 25), High (≥ 30).

```
> summary(DNAM_covariates_explored_female)
```

Sample_Group	BMI	BMI.bin	Age	Age.bin	Age_bin	Array	Slide
control:50	Min. :16.37	low :64	Min. :21.00	<20 : 0	2:21	R04C01 :19	204668820053: 3
mdd :37	1st Qu.:21.42	medium:19	1st Qu.:32.00	20-30:21	3:11	R05C01 :18	204679630043: 3
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Case Study: Covariates



Low (≤ 25), High (≥ 30).

Relative to position on the DNAm chip.

```
> summary(DNAM_covariates_explored_female)
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Sample_Group	BMI	BMI.bin	Age	Age.bin	Age_bin	Array	slide
control:50	Min. :16.37	low :64	Min. :21.00	<20 : 0	2:21	R04C01 :19	204668820053: 3
mdd :37	1st Qu.:21.42	medium:19	1st Qu.:32.00	20-30:21	3:11	R05C01 :18	204679630043: 3
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Relative to position on the DNAm chip.

```
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```

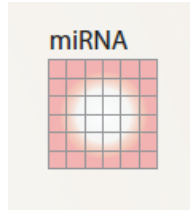
Sample_Group	BMI	BMI.bin	Age	Age.bin	Age_bin	Array	slide
control:50	Min. :16.37	low :64	Min. :21.00	<20 : 0	2:21	R04C01 :19	204668820053: 3
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	Median :23.23	high : 4	Median :45.00	30-40:11	4:20	R06C01 :12	204564460100: 2
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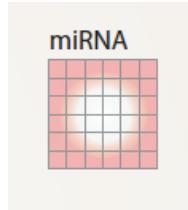
Relative to blood cell composition (T cells subsets, monocytes, B cells, NK cells and granulocytes) inferred from DNAm.

Case Study: Pre-processing

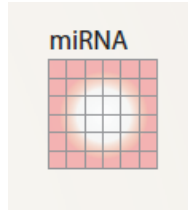


Case Study: Pre-processing

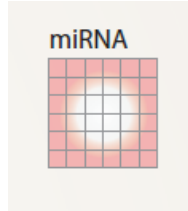




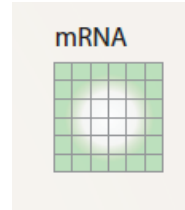
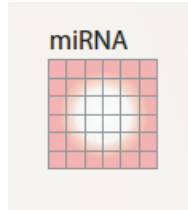
1. Remove miRNA with Nas.



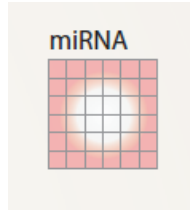
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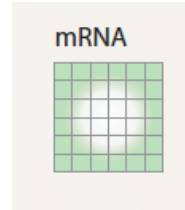
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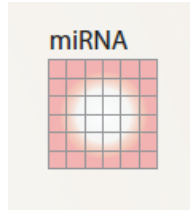
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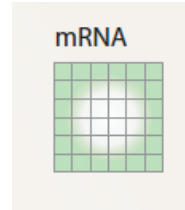
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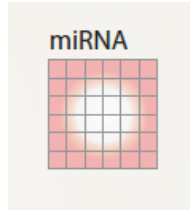
1. Normalization with Variance Stabilizing Transformations (VST; package DESeq2).



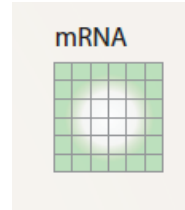
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2. Keep only genes both present in males and females.

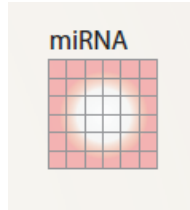


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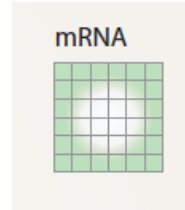


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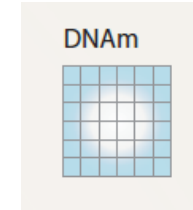
$MAD = \text{median}(|x_i - \text{median}(\mathbf{x})|)$, it is a robust estimation of the standard deviation.



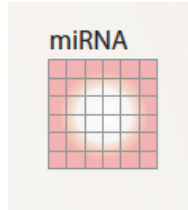
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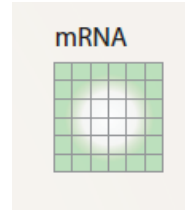
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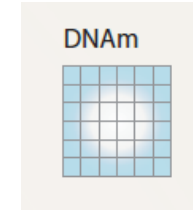
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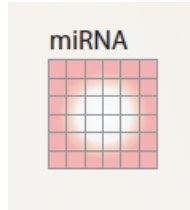


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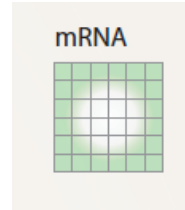


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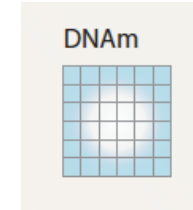
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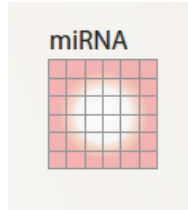


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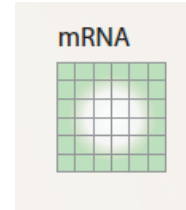


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2. Remove duplicated samples.

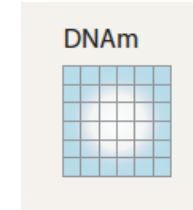
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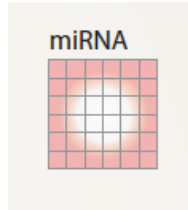


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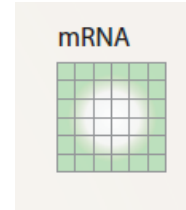


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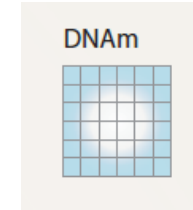
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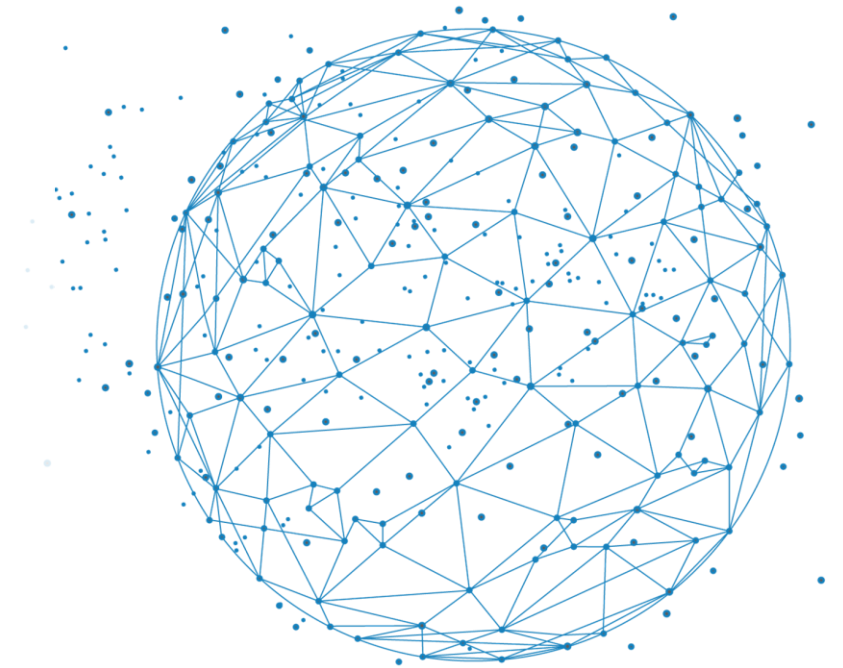


1. Normalization with Beta-Mixture Quantile (BMIQ) Normalization method (package ChAMP).
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➔ Finally: individuals common to **ALL** omics data are kept.

$MAD = \text{median}(|x_i - \text{median}(\mathbf{x})|)$, it is a robust estimation of the standard deviation.

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ChAMP's representation: Kruskal-Wallis test



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The Wilcoxon-Mann-Whitney proposes to test the association between a continuous (ex: age) and a discrete variable (ex: sex).

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$$\left\{ \begin{array}{l} H_0: (x_1, \dots, x_n) \text{ and } (y_1, \dots, y_m) \text{ comes from the same distribution.} \end{array} \right.$$



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The test is likely to be rejected.

ChAMP's representation: F-test





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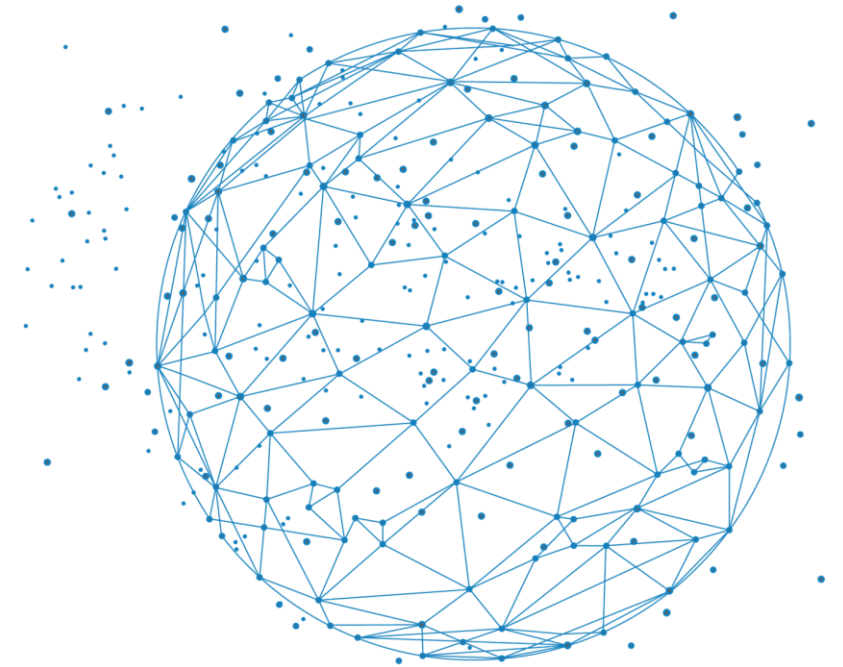
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If the variables are strongly linked $\rightarrow RSS_0 \gg RSS_1 \rightarrow F \sim \frac{RSS_0}{RSS_1} \times (n - 2) \gg n - 2 \rightarrow$ The test is likely to be rejected.

If the variables are NOT strongly linked $\rightarrow RSS_0 \sim RSS_1 \rightarrow F \sim 0 \rightarrow$ The test is likely to be accepted.

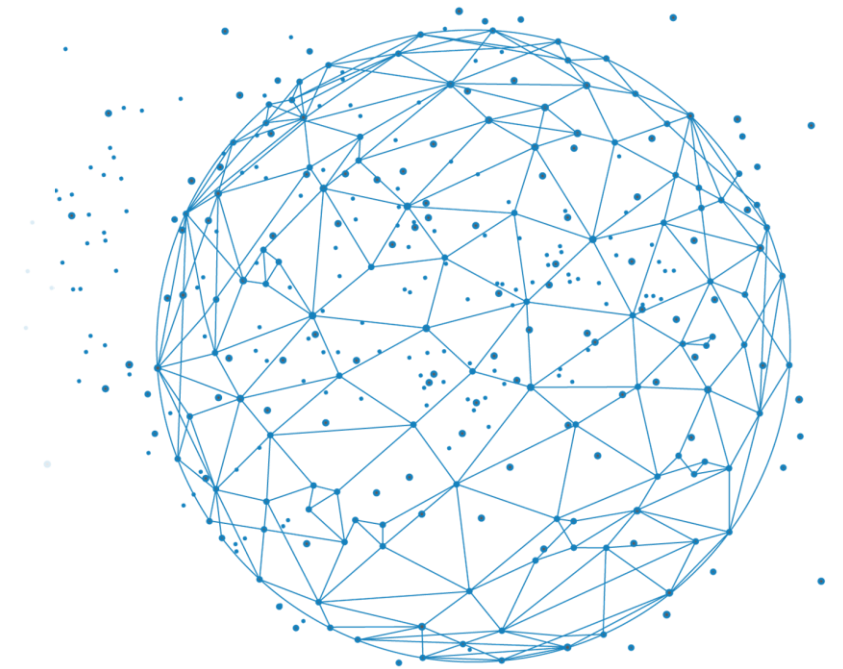
Now with this 2 tests, let us see what are the results of PCA on the MDD case study

→ See section 1 on the Rmarkdown `MDD_case_study_RGCCA`

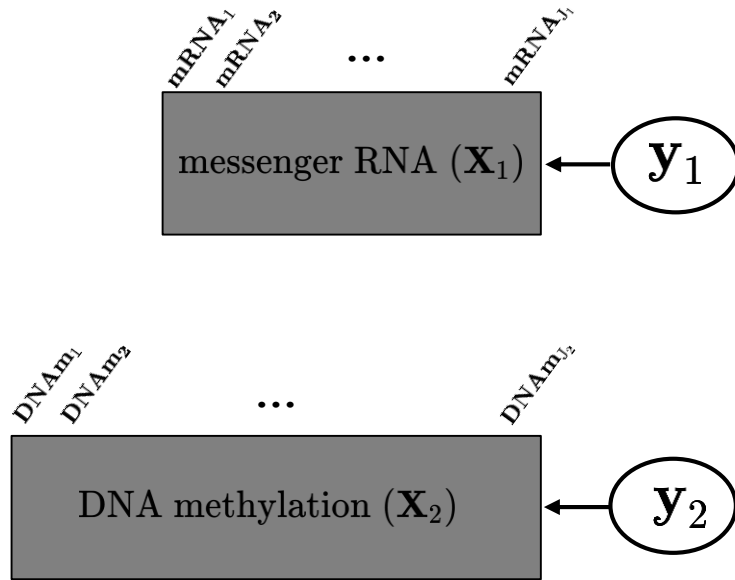


1. Introduction of the case study
2. Unsupervised analysis with one-block: Principal Component Analysis (PCA)
- 3. Unsupervised analysis with two-blocks:
Partial Least Squares (PLS) and Canonical Correlation Analysis (CCA)**
4. Unsupervised analysis with L -blocks:
Regularized Generalized Canonical Correlation Analysis (RGCCA)
5. Supervised analysis with RGCCA
6. Variable selection in RGCCA:
Sparse Generalized Canonical Correlation Analysis (SGCCA)
7. The flexible Optimization Framework of RGCCA

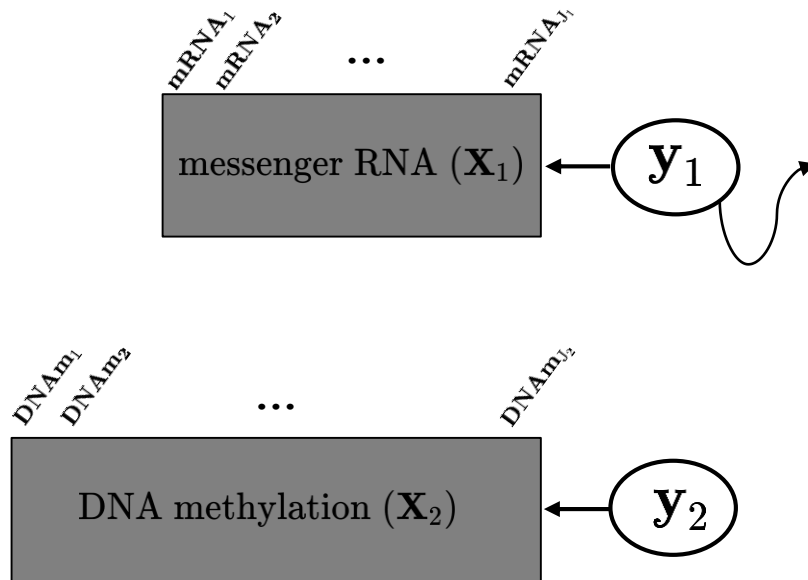
- ❖ The general principal
- ❖ Extension to multi-way analysis
- ❖ From Sequential to Global



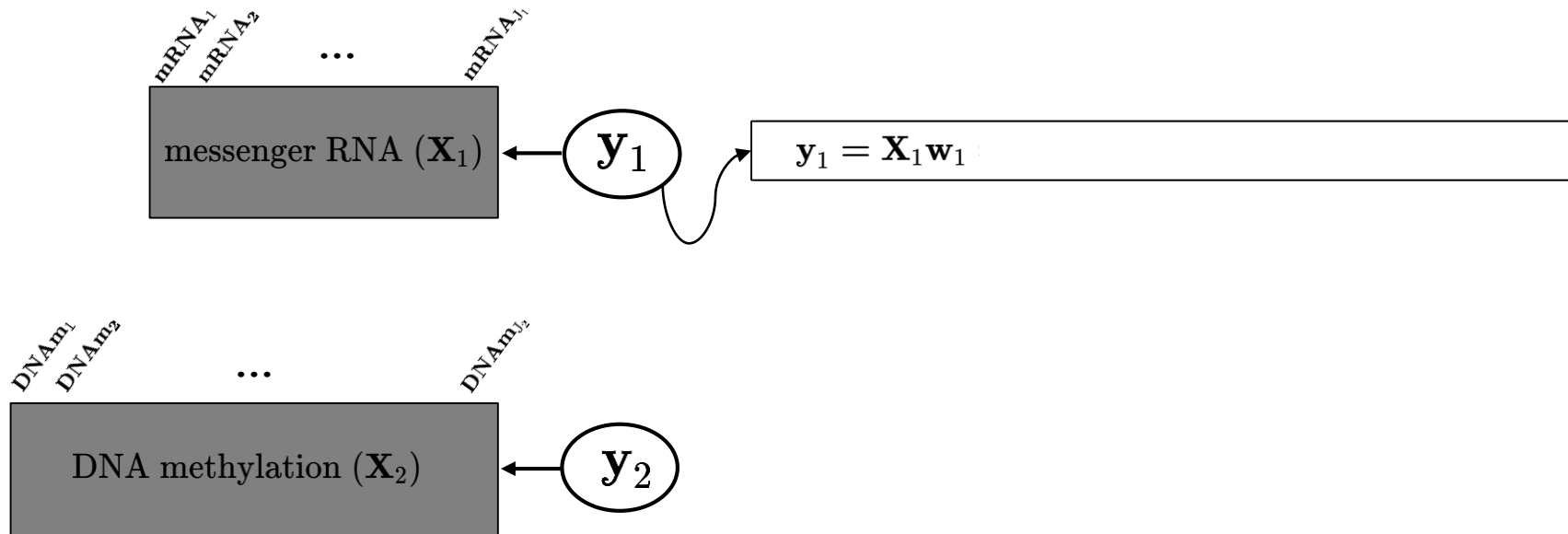
The philosophy of multiblock component methods



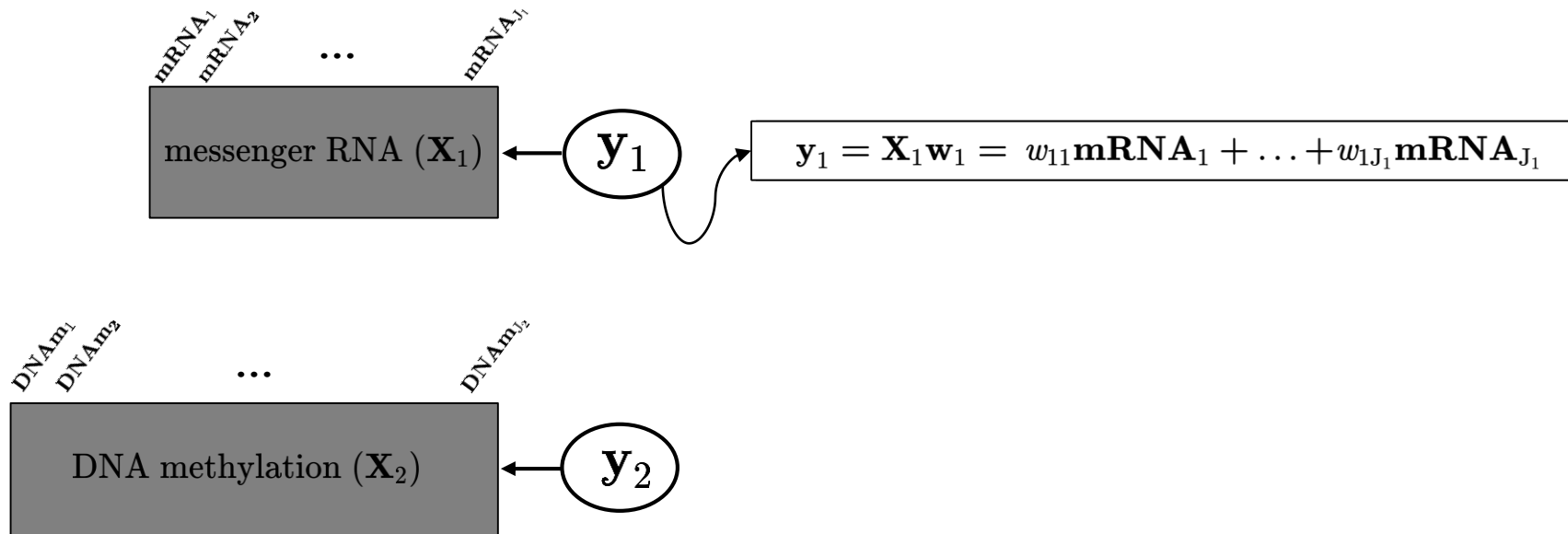
The philosophy of multiblock component methods



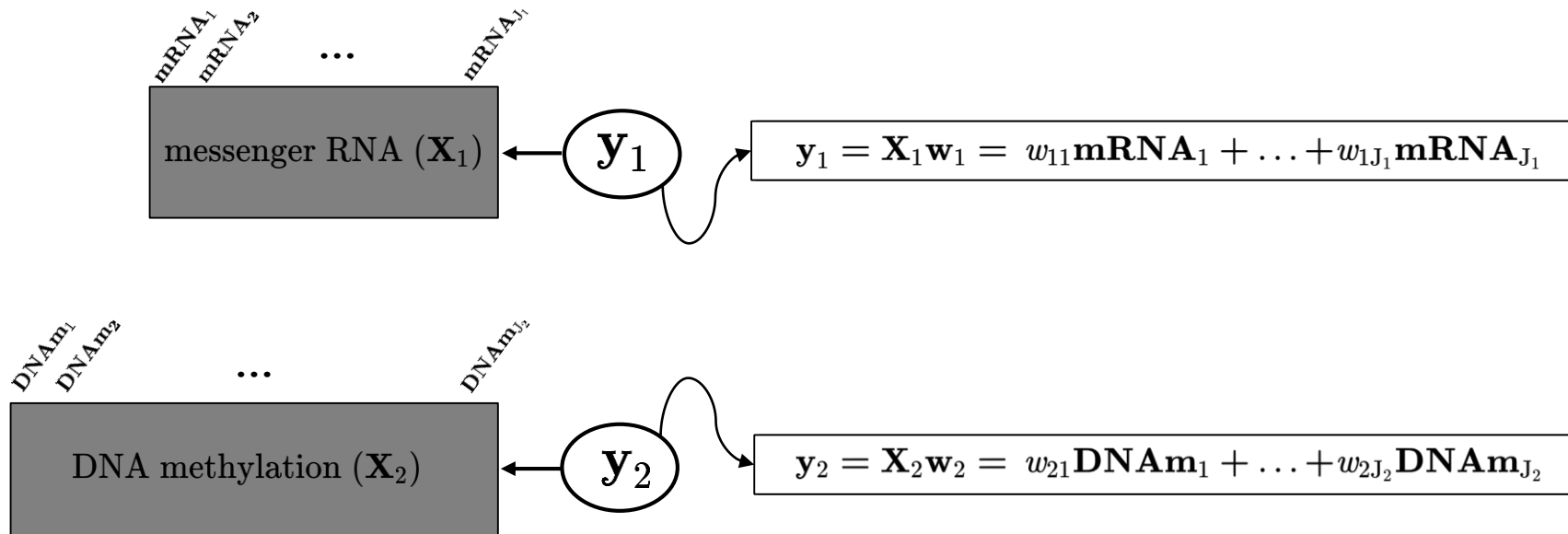
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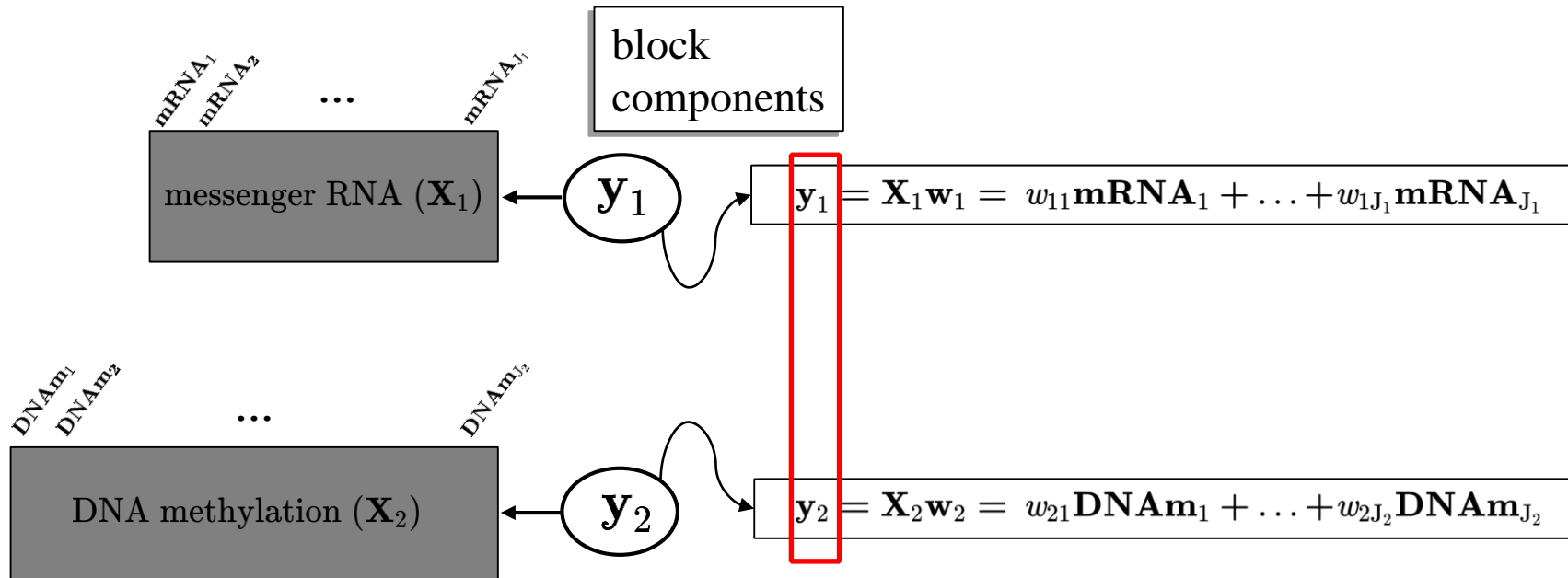
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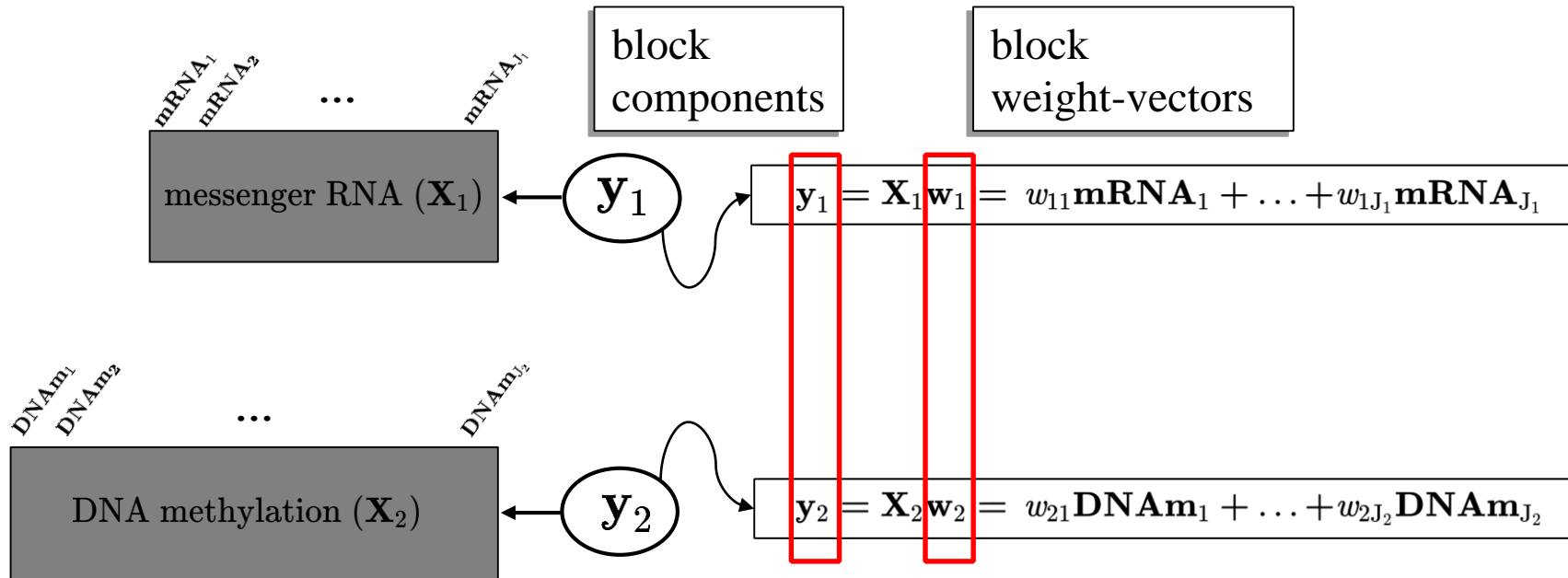
The philosophy of multiblock component methods

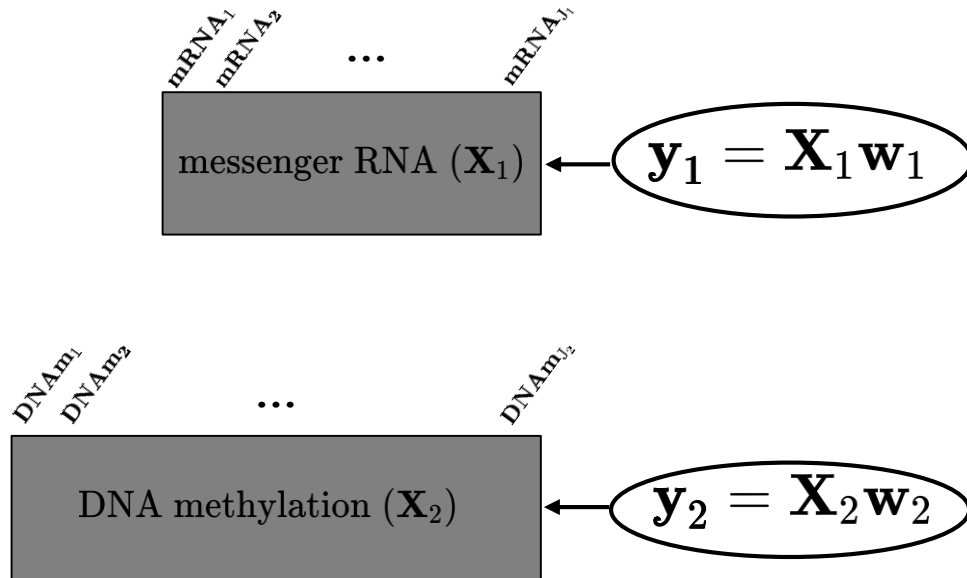


The philosophy of multiblock component methods



The philosophy of multiblock component methods

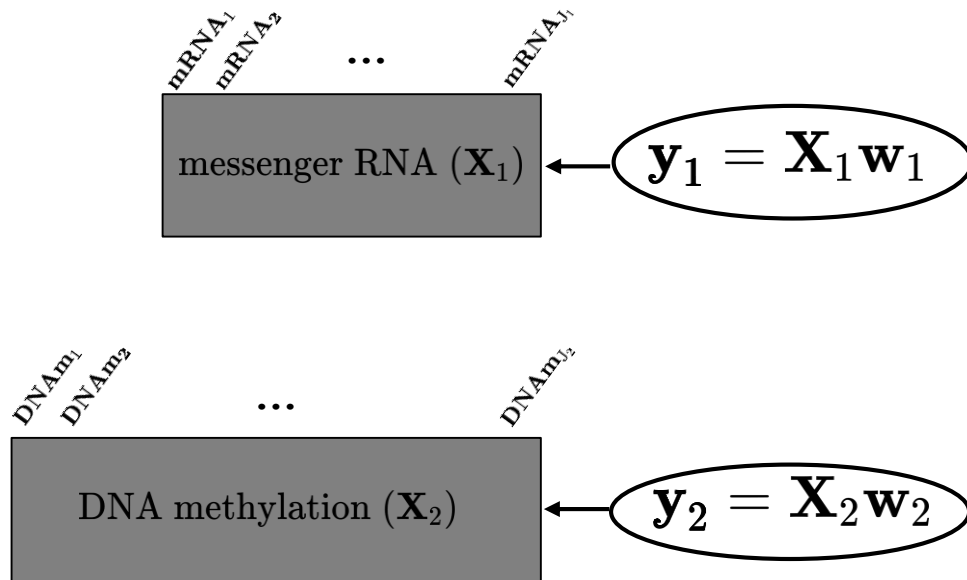




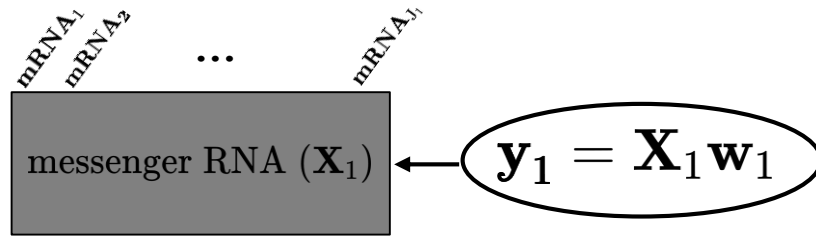
Block components should be verified for two properties at the same time:

1. Block components well explain their own block.
1. Block components are as correlated as possible for connected blocks.

The philosophy of multiblock component methods

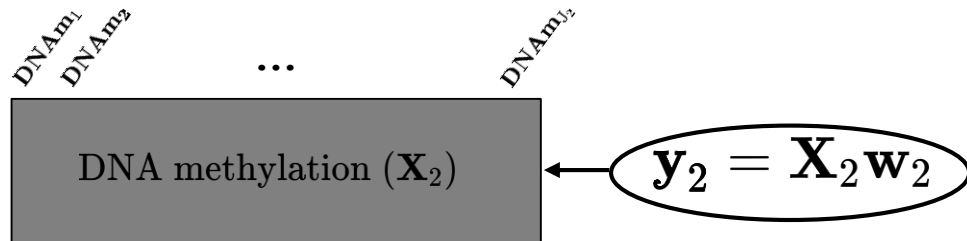


The philosophy of multiblock component methods



Correlation based methods

Find block-weight vectors $\mathbf{w}_1, \dots, \mathbf{w}_J$ maximizing a function of $\Phi = \{\text{cor}(\mathbf{X}_j \mathbf{w}_j, \mathbf{X}_k \mathbf{w}_k)\}$.



Covariance based methods

Find block-weight vectors $\mathbf{w}_1, \dots, \mathbf{w}_J$ maximizing a function of $\Psi = \{\text{cov}(\mathbf{X}_j \mathbf{w}_j, \mathbf{X}_k \mathbf{w}_k)\}$.

Courtesy to Arthur Tenenhaus.



Principal Component Analysis (PCA)

$$\max_{\mathbf{w}} \text{Var}(\mathbf{X}\mathbf{w})$$
$$\|\mathbf{w}\|_2^2 = 1$$



How can we “adapt” PCA for two-blocks analysis ?

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$$\max_{\mathbf{w}_1, \mathbf{w}_2} \text{Var}(\mathbf{X}_1 \mathbf{w}_1) \text{Var}(\mathbf{X}_2 \mathbf{w}_2)$$
$$\|\mathbf{w}_i\|_2^2 = 1$$



How can we “adapt” PCA for two-blocks analysis ?

$$\max_{\mathbf{w}_1, \mathbf{w}_2} \text{Var}(\mathbf{X}_1 \mathbf{w}_1) \quad \text{Var}(\mathbf{X}_2 \mathbf{w}_2)$$
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How can we “adapt” PCA for two-blocks analysis ?

$$\max_{\mathbf{w}_1, \mathbf{w}_2} \text{Var}(\mathbf{X}_1 \mathbf{w}_1) \text{Cor}(\mathbf{X}_1 \mathbf{w}_1, \mathbf{X}_2 \mathbf{w}_2) \text{Var}(\mathbf{X}_2 \mathbf{w}_2)$$
$$\|\mathbf{w}_i\|_2^2 = 1$$



How can we “adapt” PCA for two-blocks analysis ?

$$\max_{\mathbf{w}_1, \mathbf{w}_2} \sqrt{\text{Var}(\mathbf{X}_1 \mathbf{w}_1)} \text{Cor}(\mathbf{X}_1 \mathbf{w}_1, \mathbf{X}_2 \mathbf{w}_2) \sqrt{\text{Var}(\mathbf{X}_2 \mathbf{w}_2)}$$
$$\|\mathbf{w}_i\|_2^2 = 1$$



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$$\max_{\substack{\mathbf{w}_1, \mathbf{w}_2 \\ \|\mathbf{w}_i\|_2^2 = 1}} \underbrace{\sqrt{\text{Var}(\mathbf{X}_1 \mathbf{w}_1)} \text{Cor}(\mathbf{X}_1 \mathbf{w}_1, \mathbf{X}_2 \mathbf{w}_2) \sqrt{\text{Var}(\mathbf{X}_2 \mathbf{w}_2)}}_{\text{Cov}(\mathbf{X}_1 \mathbf{w}_1, \mathbf{X}_2 \mathbf{w}_2)}$$



How can we “adapt” PCA for two-blocks analysis ?

$$\begin{aligned} & \max_{\mathbf{w}_1, \mathbf{w}_2} \text{Cov}(\mathbf{X}_1 \mathbf{w}_1, \mathbf{X}_2 \mathbf{w}_2) \\ & \|\mathbf{w}_i\|_2 = 1 \end{aligned}$$



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How can we “adapt” PCA for two-blocks analysis ?

$$\max_{\substack{\mathbf{w}_1, \mathbf{w}_2 \\ \text{Var}(\mathbf{X}_i \mathbf{w}_i) = 1}} \text{Cov}(\mathbf{X}_1 \mathbf{w}_1, \mathbf{X}_2 \mathbf{w}_2) = \max_{\substack{\mathbf{w}_1, \mathbf{w}_2 \\ \text{Var}(\mathbf{X}_i \mathbf{w}_i) = 1}} \text{Cor}(\mathbf{X}_1 \mathbf{w}_1, \mathbf{X}_2 \mathbf{w}_2)$$

From PCA to PLS/CCA





Partial Least Squares (PLS2)

$$\max_{\mathbf{w}_1, \mathbf{w}_2} \text{Cov}(\mathbf{X}_1 \mathbf{w}_1, \mathbf{X}_2 \mathbf{w}_2)$$
$$\|\mathbf{w}_i\|_2^2 = 1$$

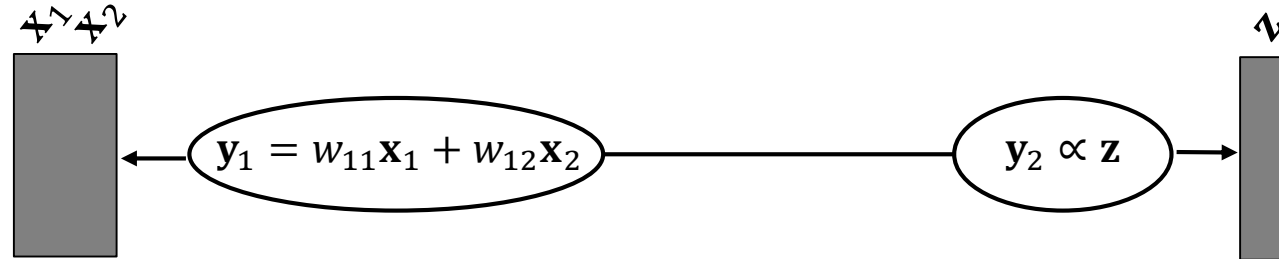


Canonical Correlation Analysis (CCA)

$$\max_{\mathbf{w}_1, \mathbf{w}_2} \text{Cov}(\mathbf{X}_1 \mathbf{w}_1, \mathbf{X}_2 \mathbf{w}_2)$$
$$\text{Var}(\mathbf{X}_i \mathbf{w}_i) = 1$$

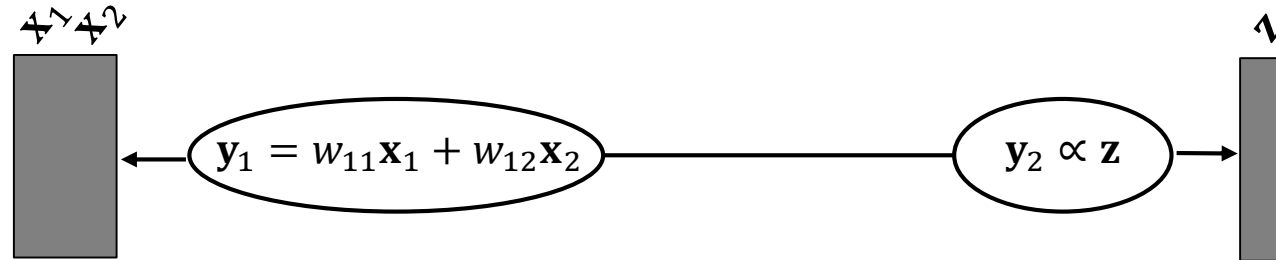
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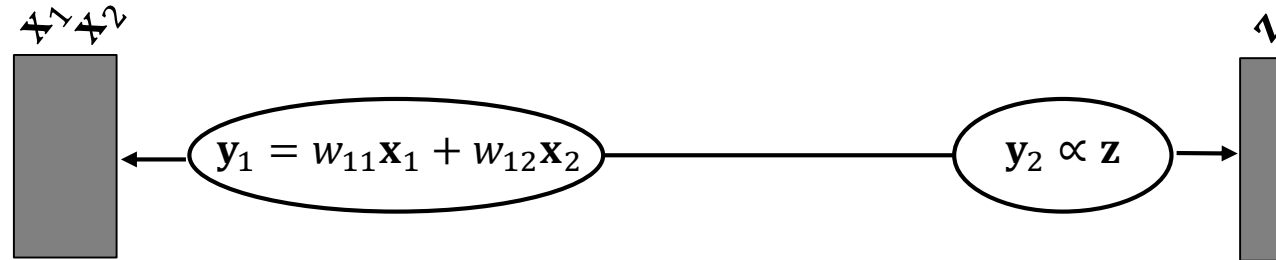
$$[\mathbf{x}_1 \ \mathbf{x}_2] \sim \mathcal{N}\left((0,0), \begin{pmatrix} 1 & 0.5 \\ 0.5 & 1 \end{pmatrix}\right)$$





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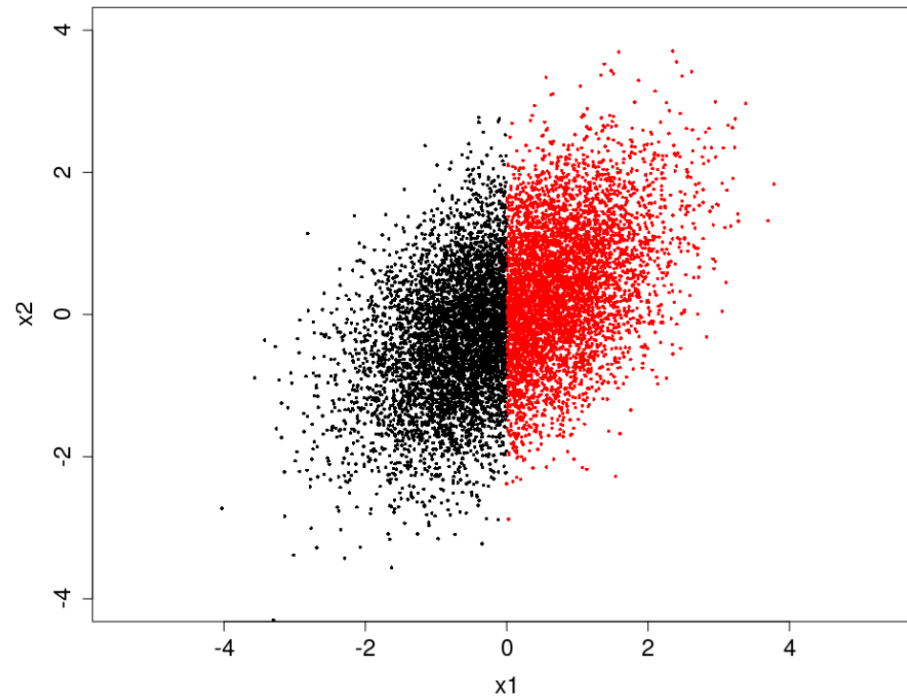
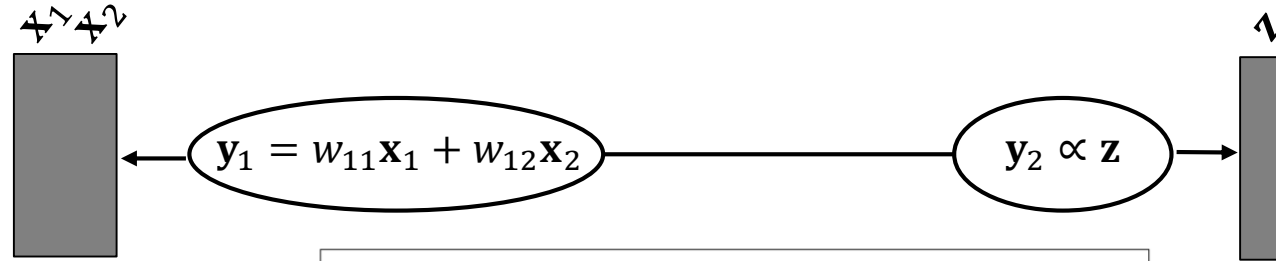
$$(\mathbf{z})_i = \begin{cases} 0 & \text{if } (\mathbf{x})_i < 0 \\ 1 & \text{otherwise} \end{cases}$$





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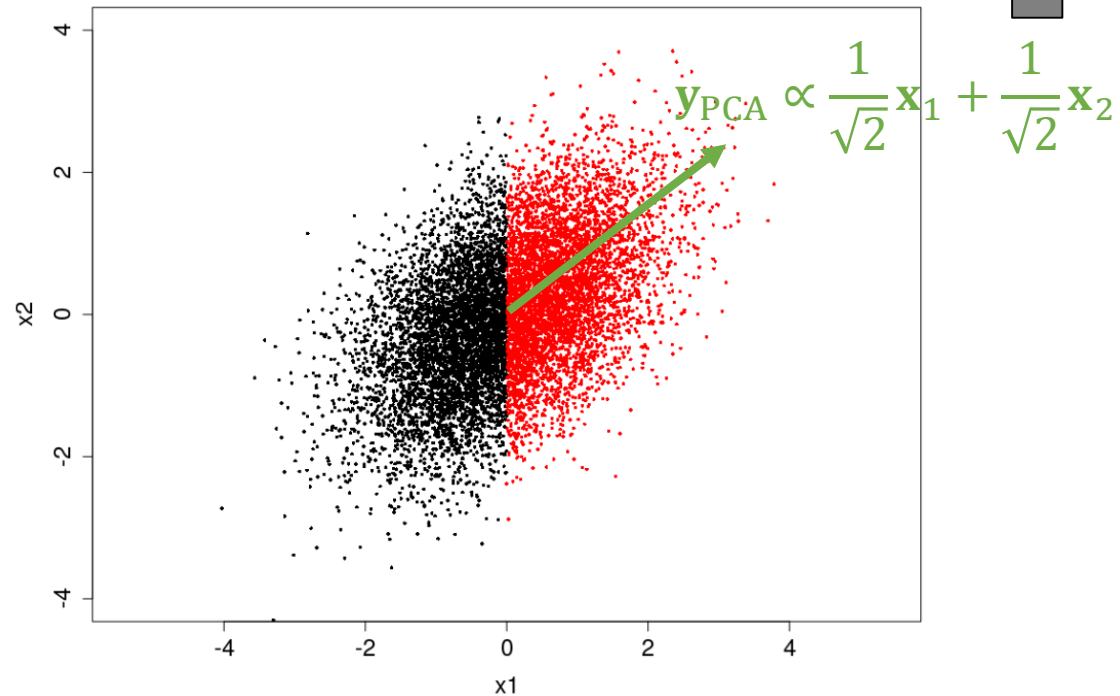
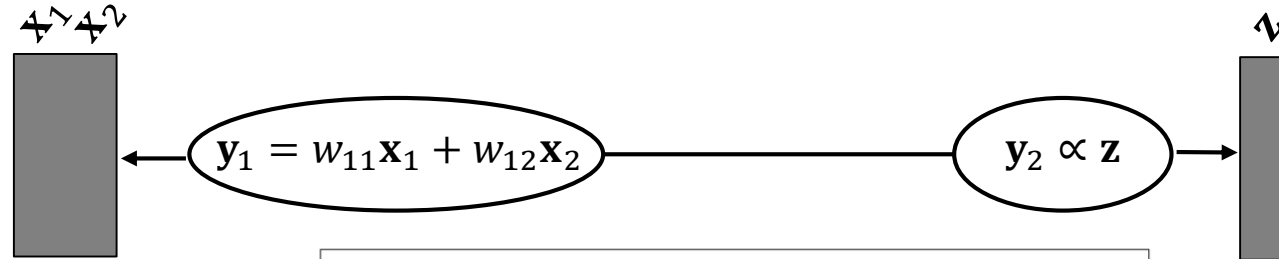
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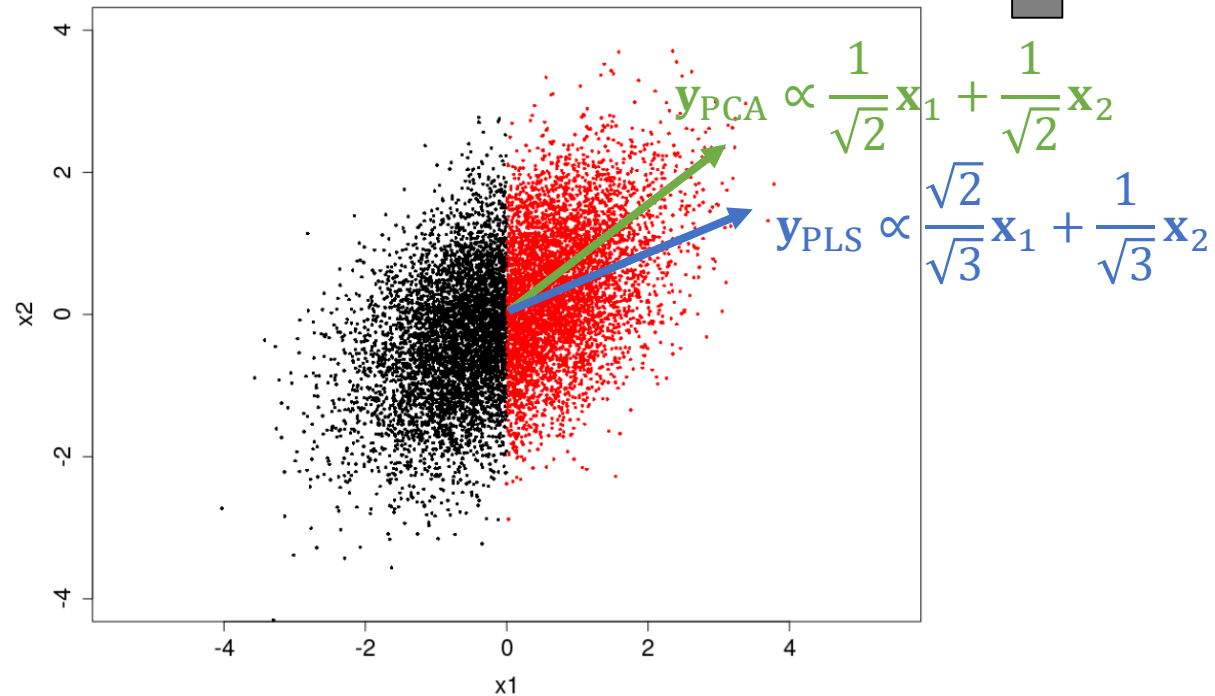
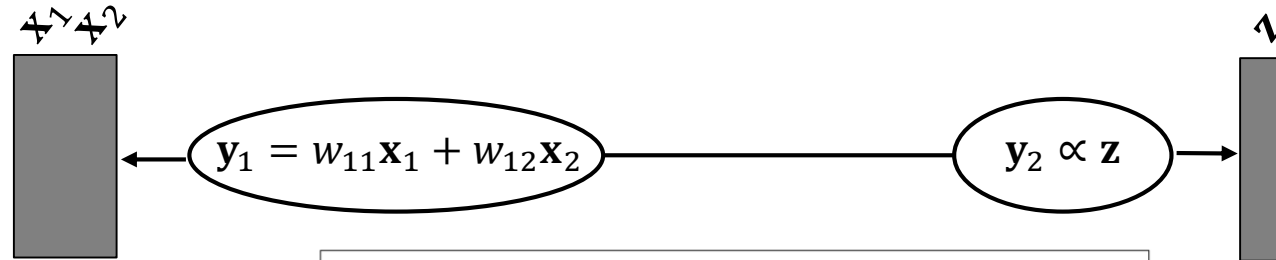
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PLS & CCA with a figure

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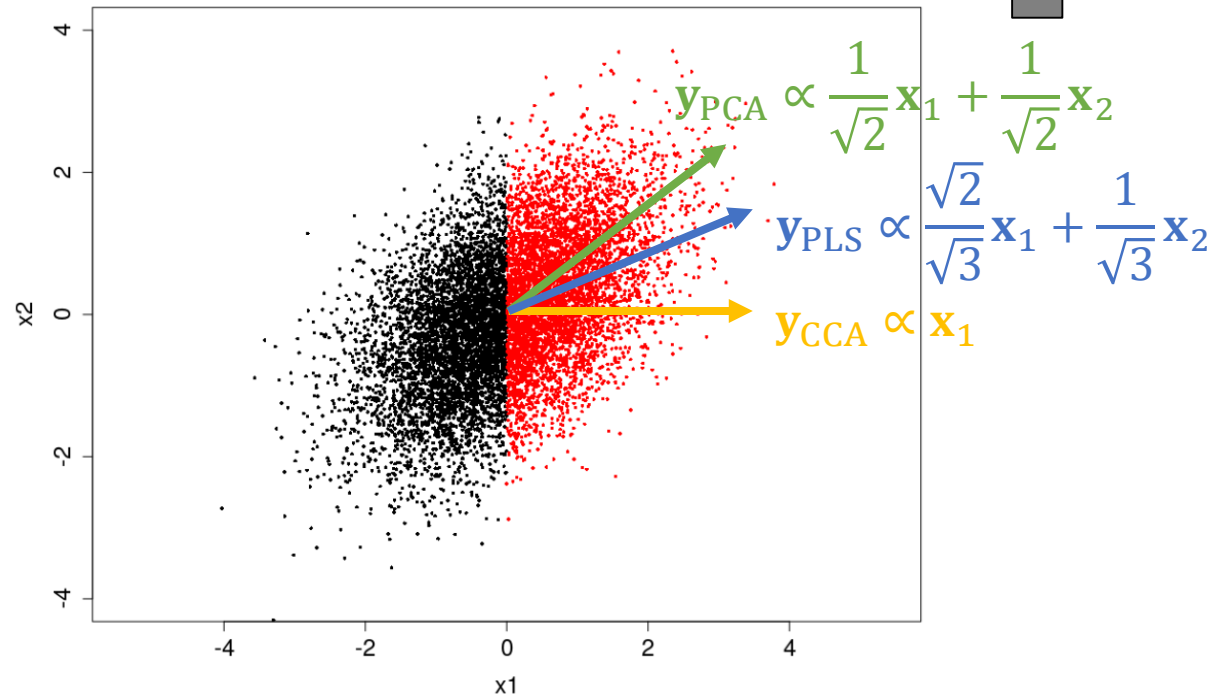
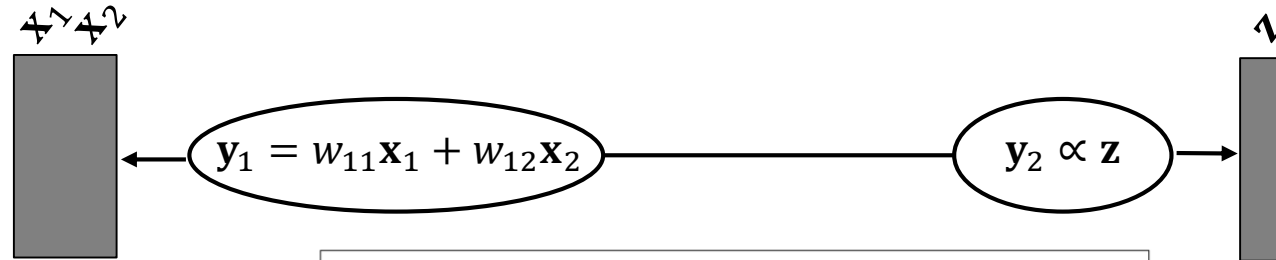
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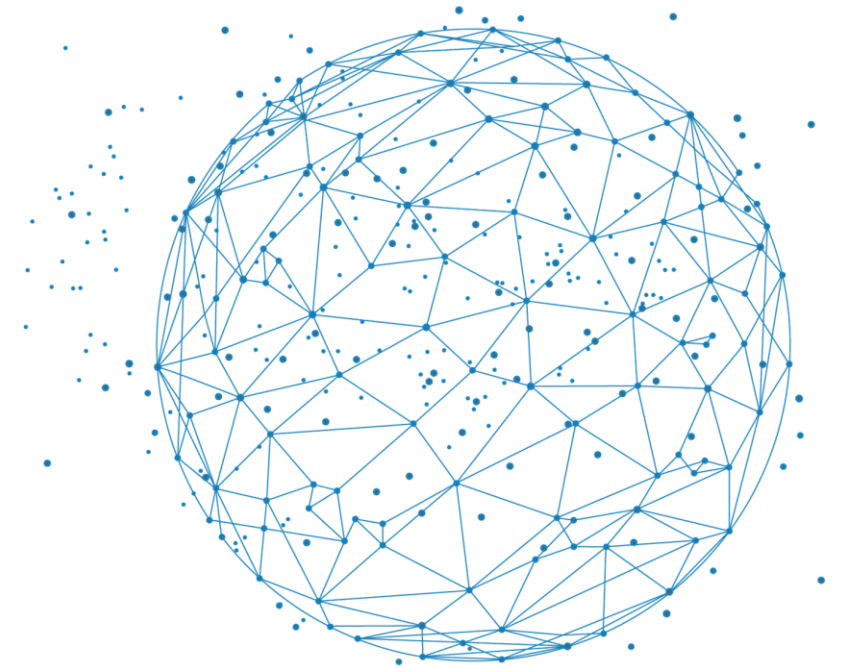
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Let us see what are the results of PLS/CCA on the MDD case study

→ See section 2.2 & 2.3 on the Rmarkdown `MDD_case_study_RGCCA`



Overfitting



Overfitting



	x_1	x_2	x_3	x_4	y
	Intercept	Age	Nb_sisters	Neighbor'weight (kg)	Subject's Height (cm)
Subj1	1	5	1	1	90
Subj2	1	10	2	50	125
Subj3	1	15	1	80	160
Subj4	1	20	2	90	180

Overfitting



	x_1	x_2	x_3	x_4	y
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We are looking for $\beta_1, \beta_2, \beta_3$ and β_4 that minimizes $J_{TRAIN} = \sum_{i=2}^4 (y_i - \beta_1 x_{i1} - \beta_2 x_{i2} - \beta_3 x_{i3} - \beta_4 x_{i4})^2$.

Overfitting



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Overfitting



	x ₁	x ₂	x ₃	x ₄	y
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Here, we are in “high-dimension” as $n < p$. The problem is ill-posed (more unknown parameters than equations).

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Overfitting



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	β_1	β_2	β_3	β_4	J_{train}	J_{test}
Solution 1	43.75	0	1.375	6.25	8.4e-22	1491.891
Solution 2	-7456.25	-1000	251.375	2506.25	1.1e-19	95817179
⋮						

Overfitting



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OVERFITTING

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Cross-Validation & Regularization



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Cross-Validation allows to evaluate the generalization power of a model and realize if the model overfits or not.

Cross-Validation & Regularization



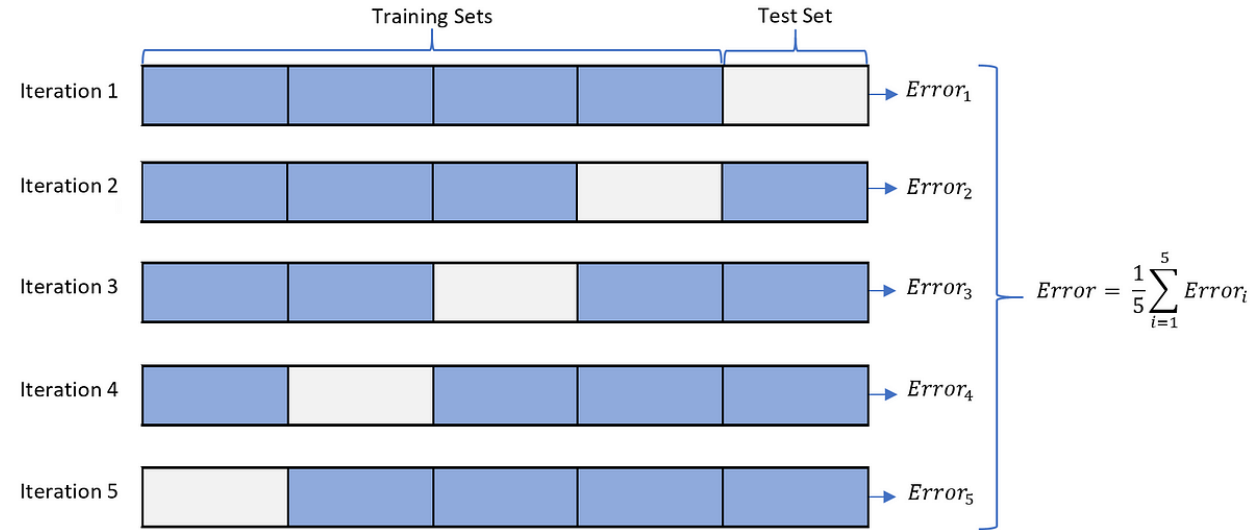
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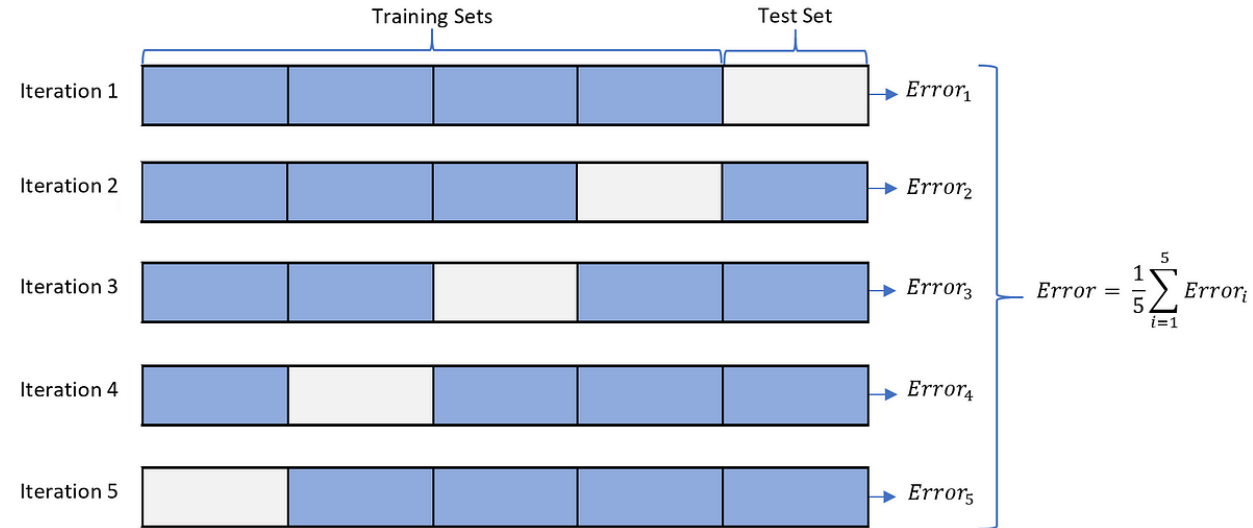
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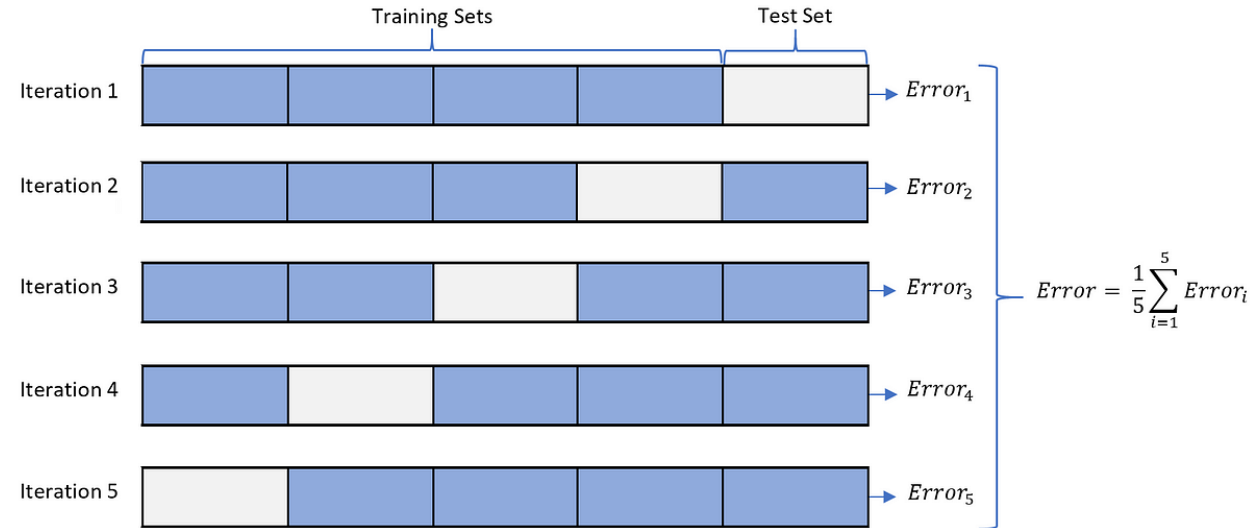


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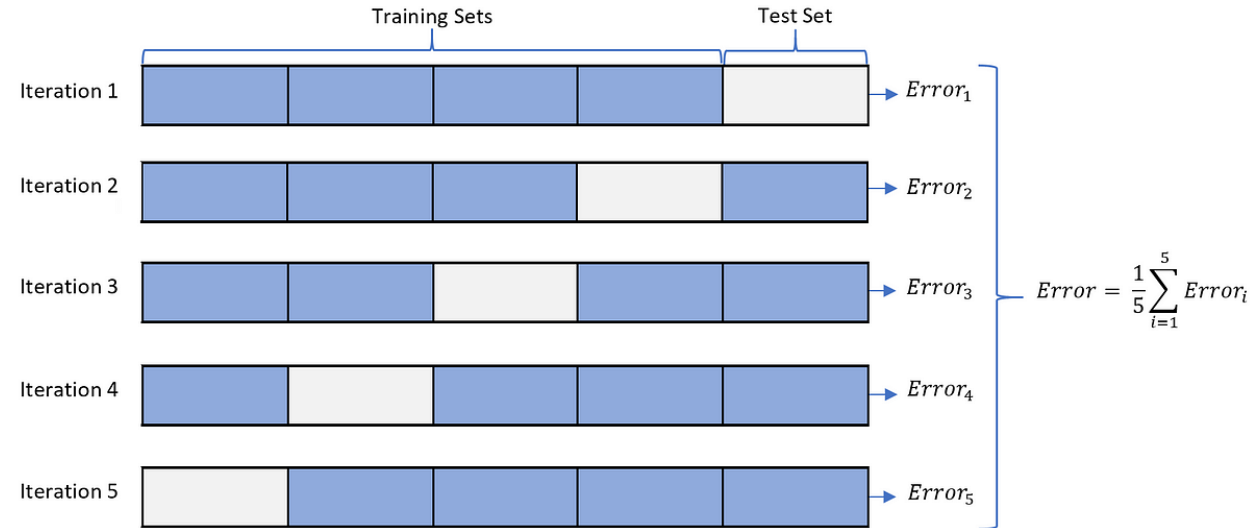
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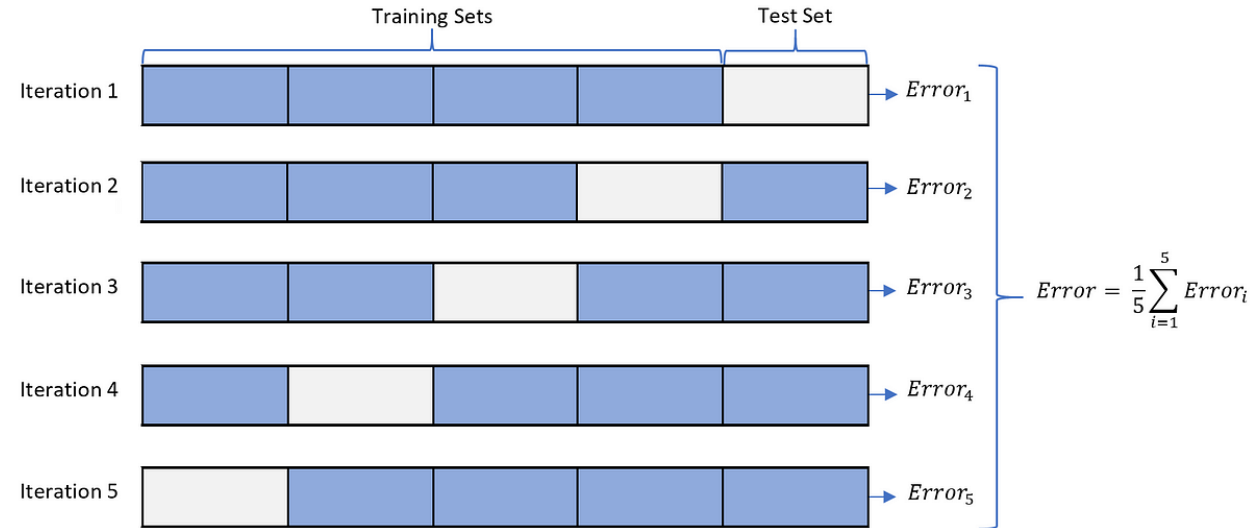
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Regularization consists in adding more constraints to the model in order to reduce the space of solutions.

Multiple regularizations are available such as Ridge or LASSO regularizations.

Here, we choose to regularize the model by forcing it to have a low number of variables.

Application on the example



Application on the example



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Variables considered	J_{TRAIN}	J_{TEST}
(x_1, x_2)	3.750000e+01	100
(x_1, x_3)	2.403846e+01	959.8081
(x_1, x_4)	1.512500e+03	4900
(x_1, x_2, x_3)	1.831567e-22	203.0625
(x_1, x_2, x_4)	6.464166e-24	225
(x_1, x_3, x_4)	8.664767e-22	1491.8906

Application on the example

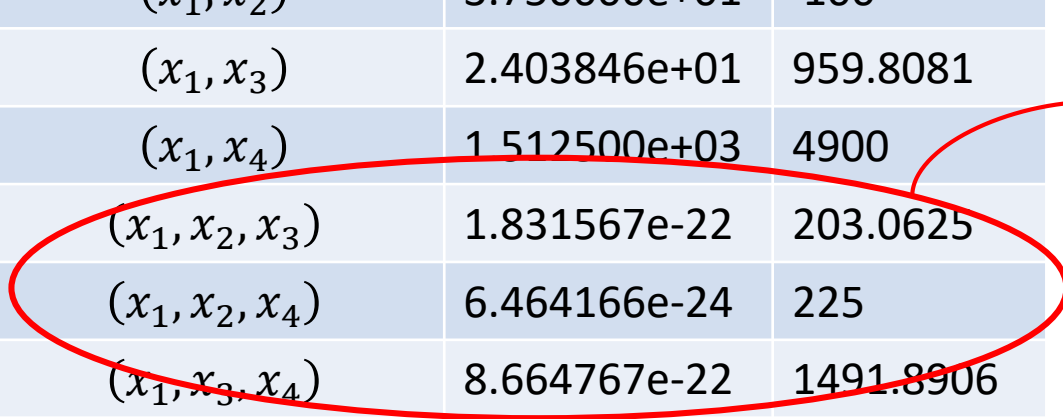
So let us consider all models with either 2 or 3 variables (with at least the intercept each time).

By doing so, we add respectively 2 (ex: $\beta_2 = 0$ and $\beta_4 = 0$) or 1 constraint (idem).

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Best model

OVERFITTING

CV was also used here so set an hyper-parameter: «the number of variables to keep in the model».

Here apparently, keeping only 2 variables leads to the best model with the variable «Age», which was expected.

Overfitting, Cross-Validation & Regularization





Overfitting can be handled with regularization.



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Cross-Validation can both help to:



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Cross-Validation can both help to:

- 1. realize if the model overfits or not**



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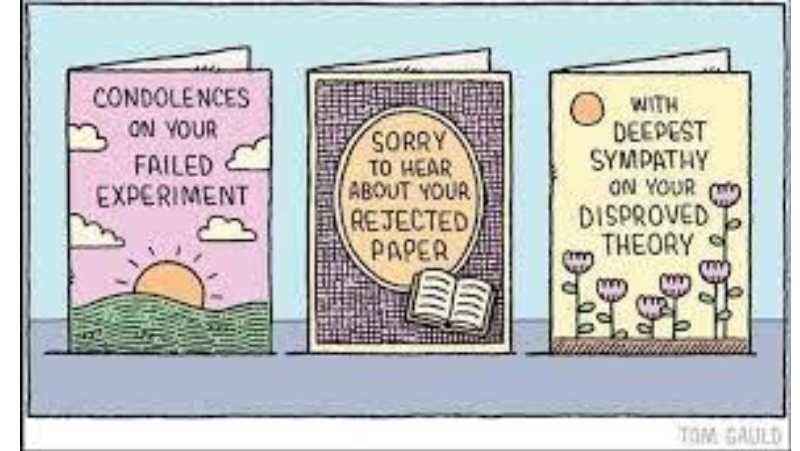
- 1. realize if the model overfits or not**
- 2. tune the hyper-parameters (associated with the regularization).**



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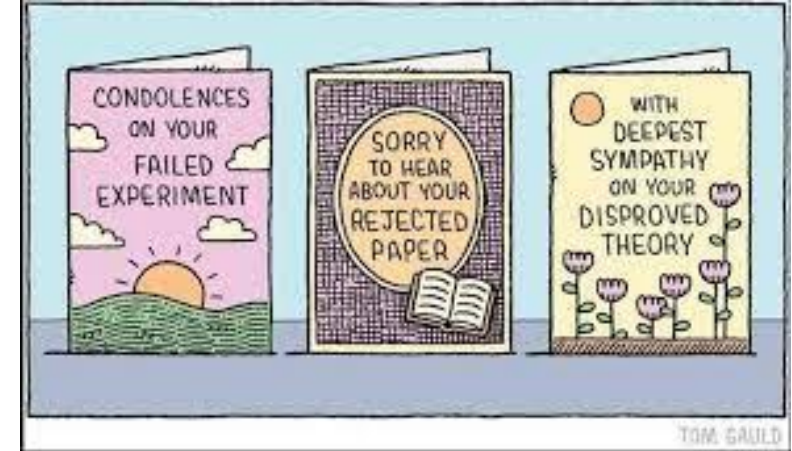




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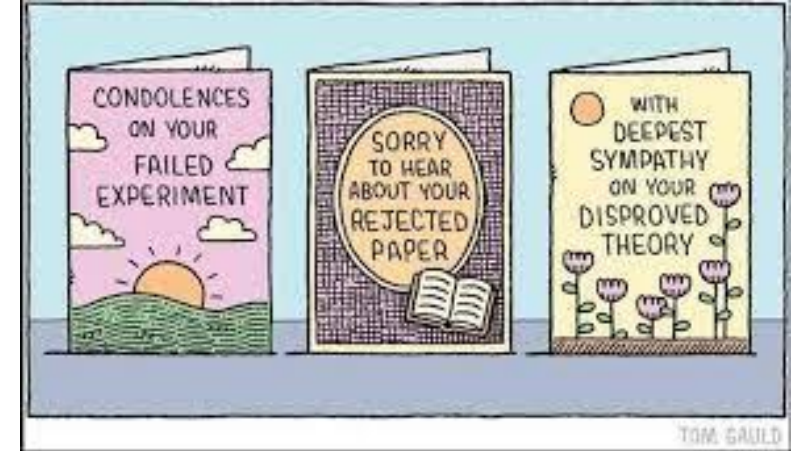
Classical mistake to avoid with Cross-Validation: «**Double Dipping**».



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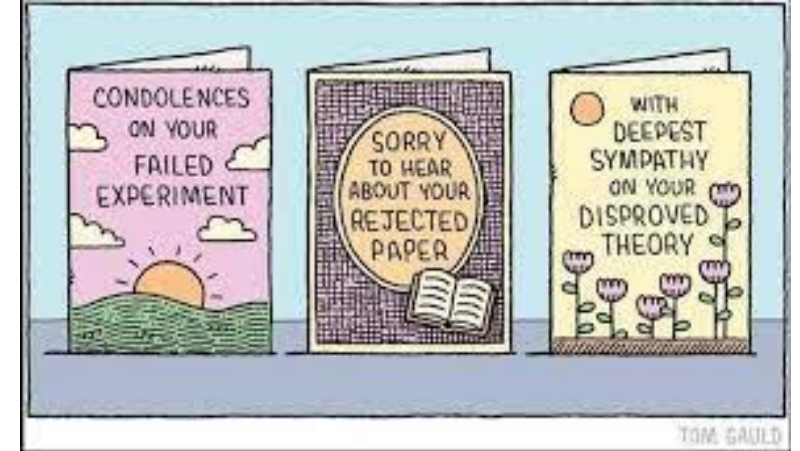
➔ The whole point of Cross-Validation is to keep the train and the test sets **independant** from each other.



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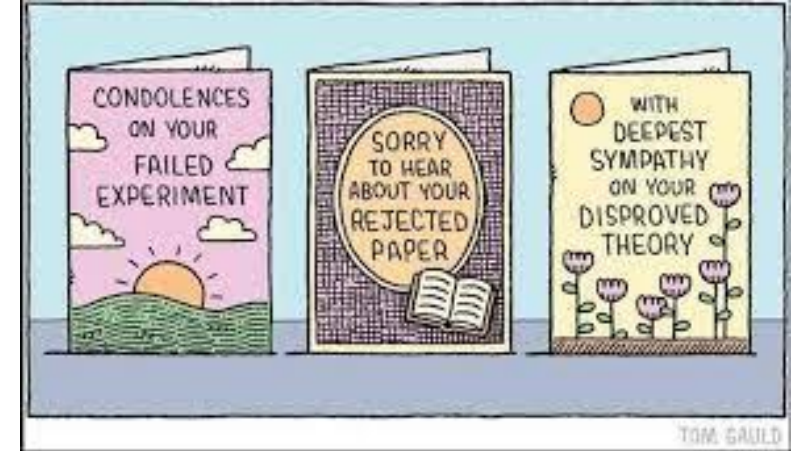
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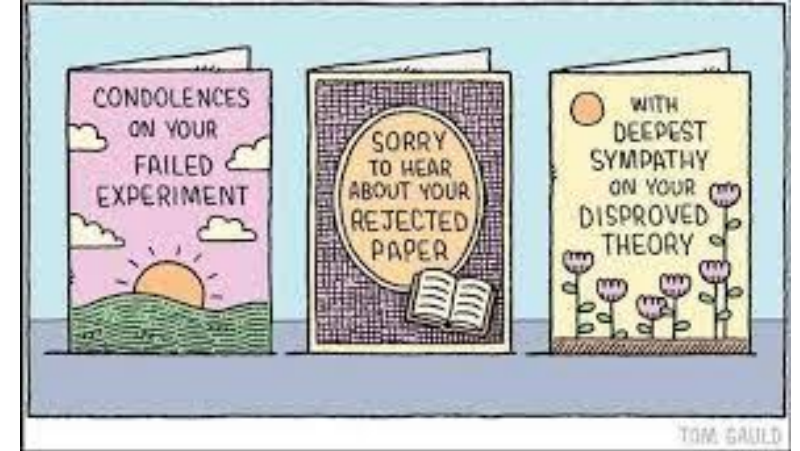
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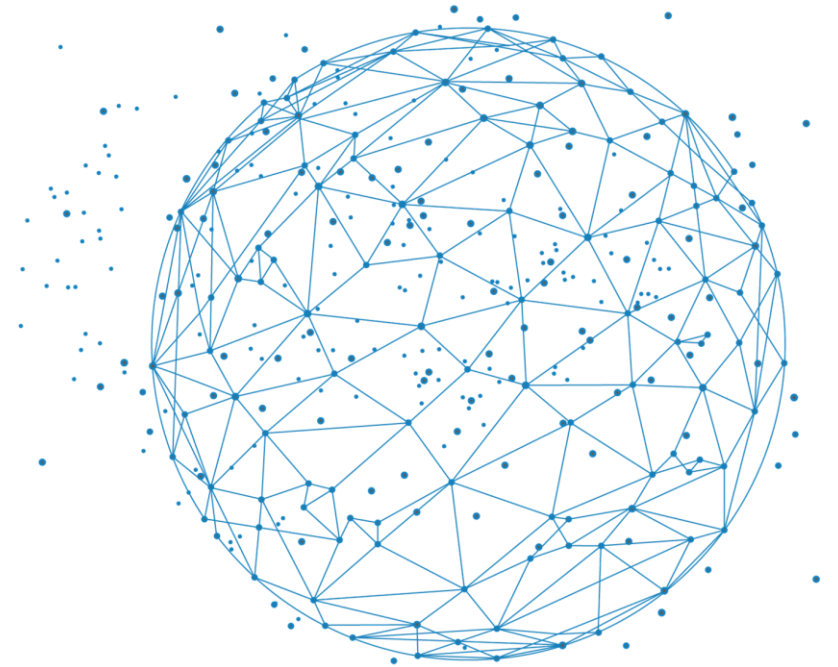
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This is no longer the case when for example:

1. Normalization accross subjects is performed on the whole data-set.
2. Variable selection is performed on the whole data-set (ex: differentially expressed genes)

How do we regularize CCA ?





Canonical Correlation Analysis (CCA)

$$\max_{\mathbf{w}_1, \mathbf{w}_2} \text{Cov}(\mathbf{X}_1 \mathbf{w}_1, \mathbf{X}_2 \mathbf{w}_2)$$
$$\text{Var}(\mathbf{X}_i \mathbf{w}_i) = 1$$

Partial Least Squares (PLS2)

$$\max_{\mathbf{w}_1, \mathbf{w}_2} \text{Cov}(\mathbf{X}_1 \mathbf{w}_1, \mathbf{X}_2 \mathbf{w}_2)$$
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Regularized-CCA

$$\max_{\mathbf{w}_1, \mathbf{w}_2} \text{Cov}(\mathbf{X}_1 \mathbf{w}_1, \mathbf{X}_2 \mathbf{w}_2)$$

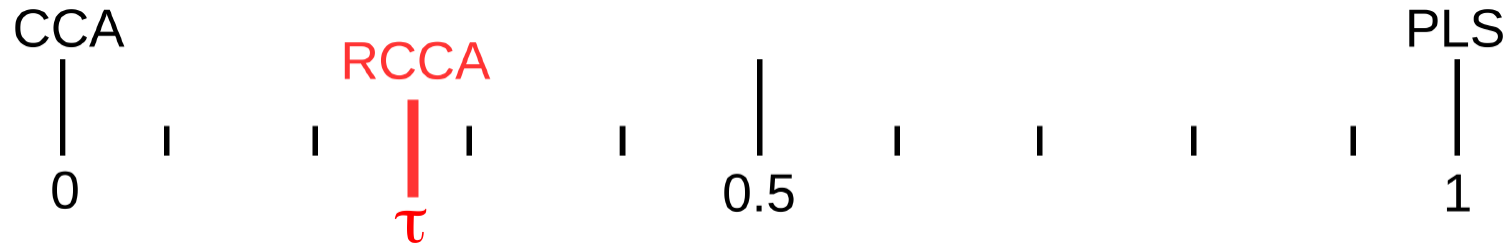
$$\text{s. t. } (1 - \tau_i) \text{Var}(\mathbf{X}_i \mathbf{w}_i) + \tau_i \|\mathbf{w}_i\|_2^2 = 1.$$

Canonical Correlation Analysis (CCA)

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Regularized-CCA

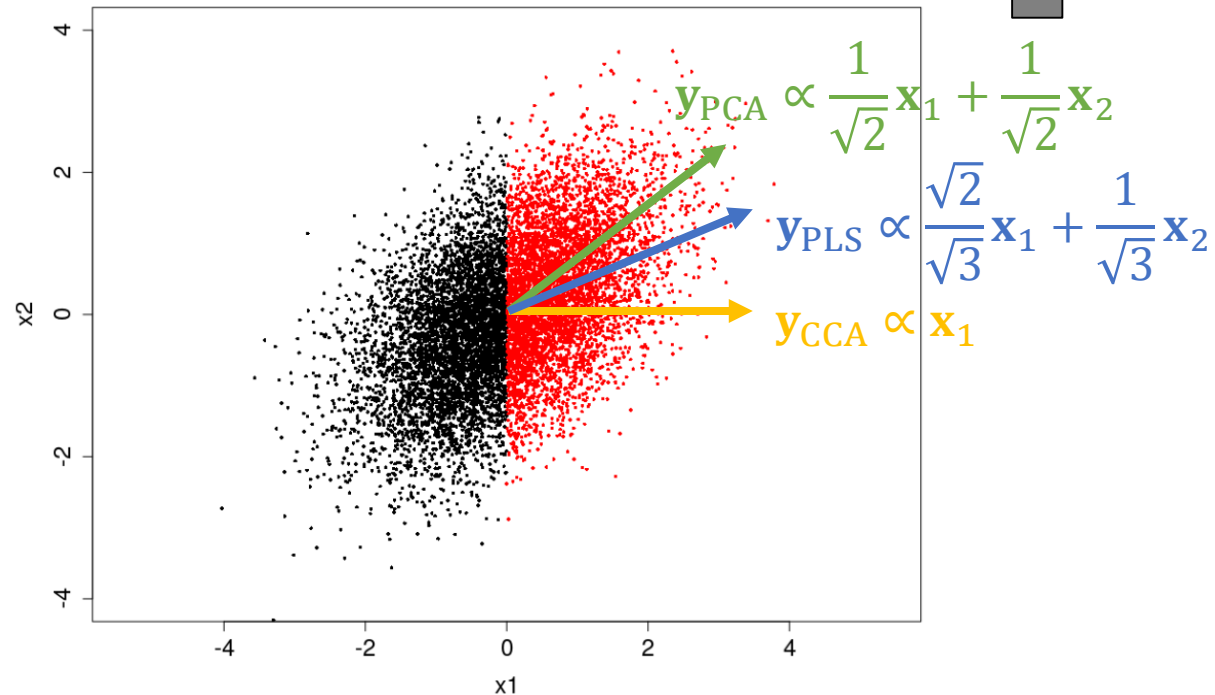
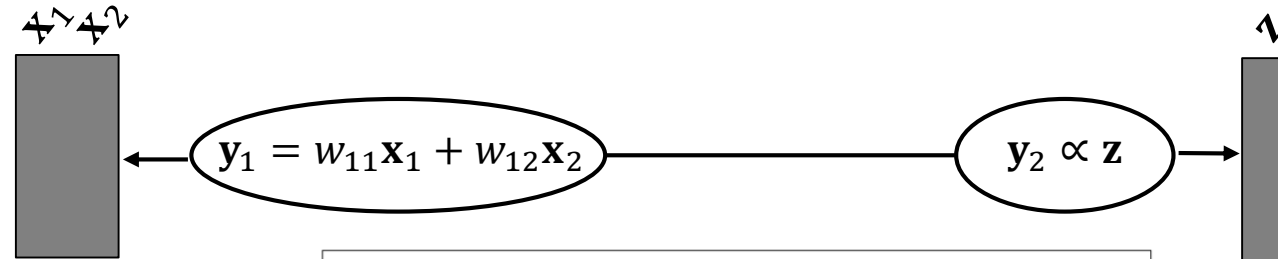
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PLS & CCA with a figure

$$[\mathbf{x}_1 \ \mathbf{x}_2] \sim \mathcal{N}\left((0,0), \begin{pmatrix} 1 & 0.5 \\ 0.5 & 1 \end{pmatrix}\right)$$

$$(\mathbf{z})_i = \begin{cases} 0 & \text{if } (\mathbf{x})_i < 0 \\ 1 & \text{otherwise} \end{cases}$$

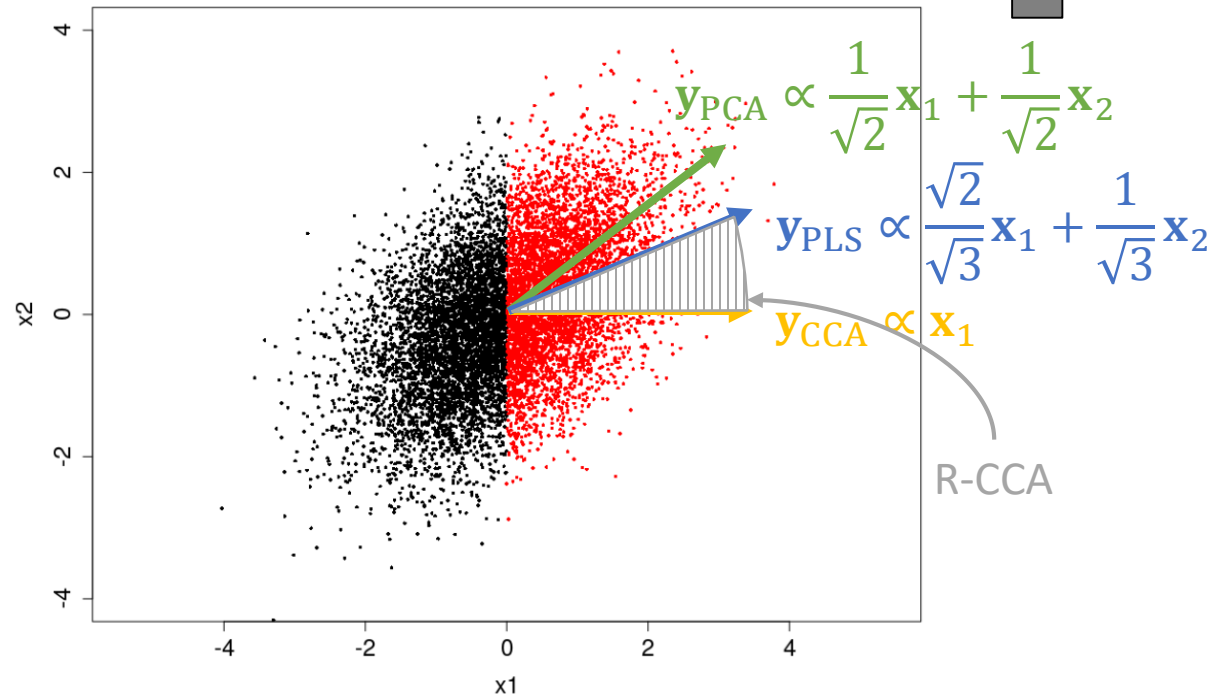
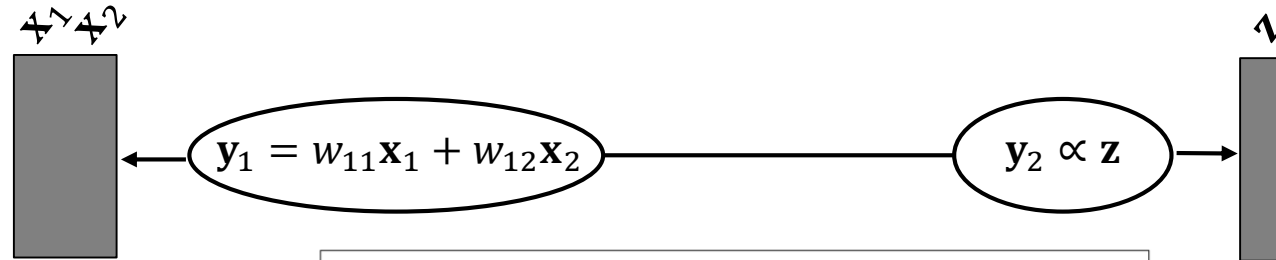


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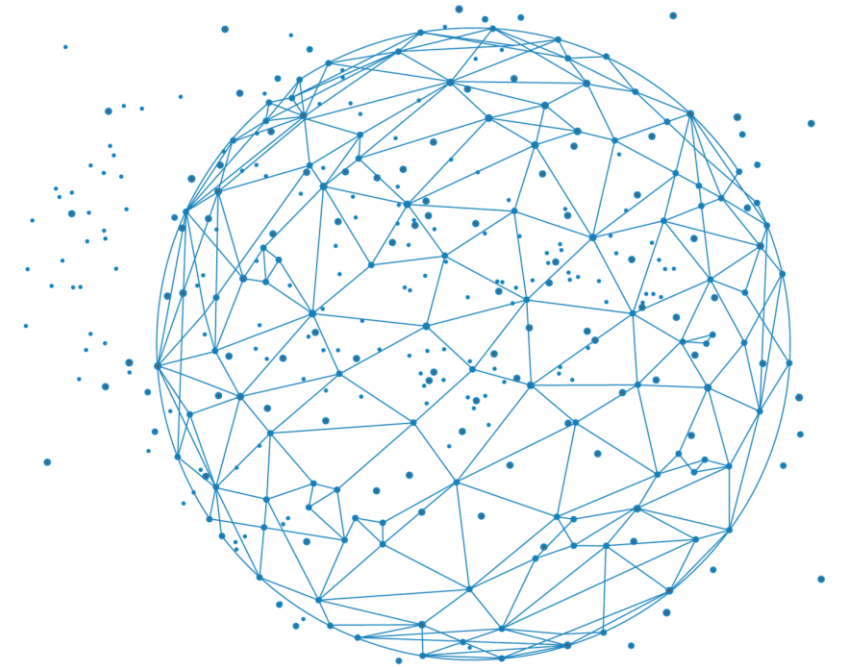
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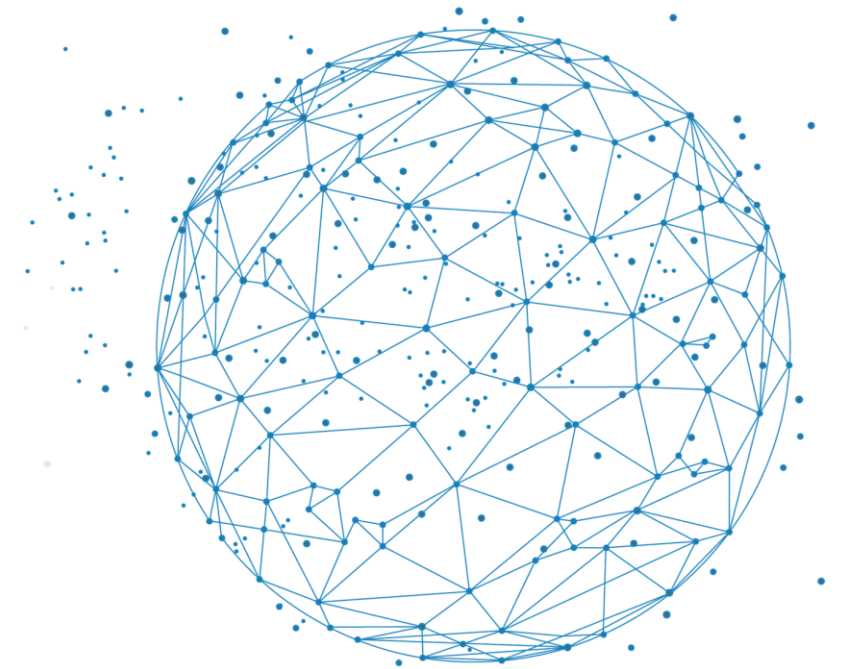


Let us see how Regularize CCA performs on the MDD case study

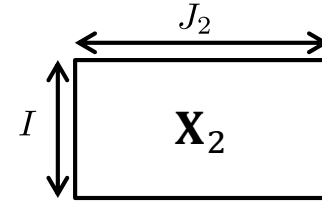
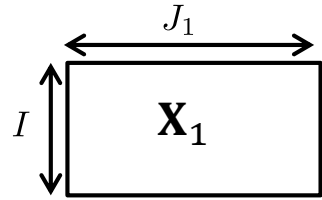
→ See section 2.4 & 2.5 on the Rmarkdown ``MDD_case_study_RGCCA``



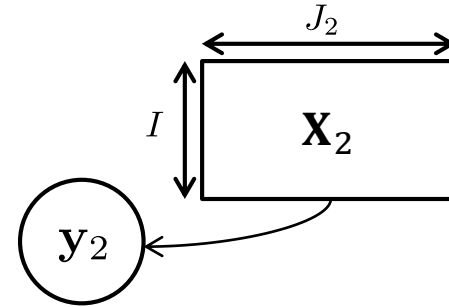
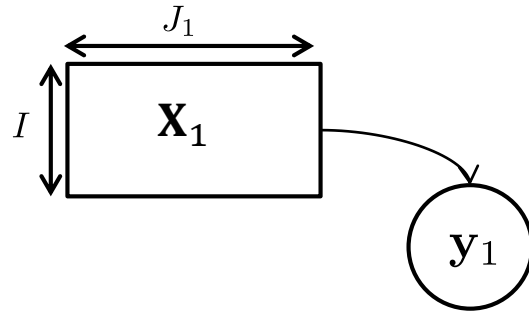
1. Introduction of the case study
2. Unsupervised analysis with one-block: Principal Component Analysis (PCA)
3. Unsupervised analysis with two-blocks:
Partial Least Squares (PLS) and Canonical Correlation Analysis (CCA)
4. **Unsupervised analysis with L -blocks:**
Regularized Generalized Canonical Correlation Analysis (RGCCA)
5. Supervised analysis with RGCCA
6. Variable selection in RGCCA:
Sparse Generalized Canonical Correlation Analysis (SGCCA)
7. The flexible Optimization Framework of RGCCA
 - ❖ The general principal
 - ❖ Extension to multi-way analysis
 - ❖ From Sequential to Global



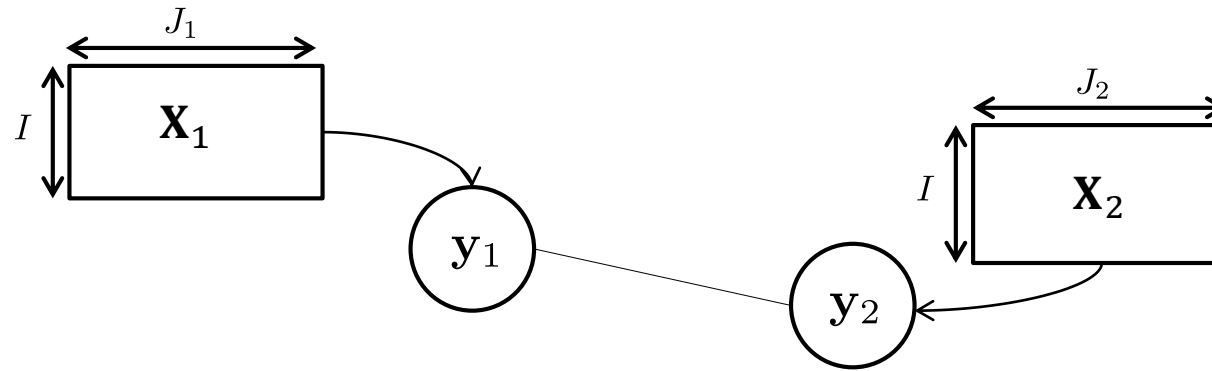
Regularized Generalized Canonical Correlation Analysis (RGCCA)



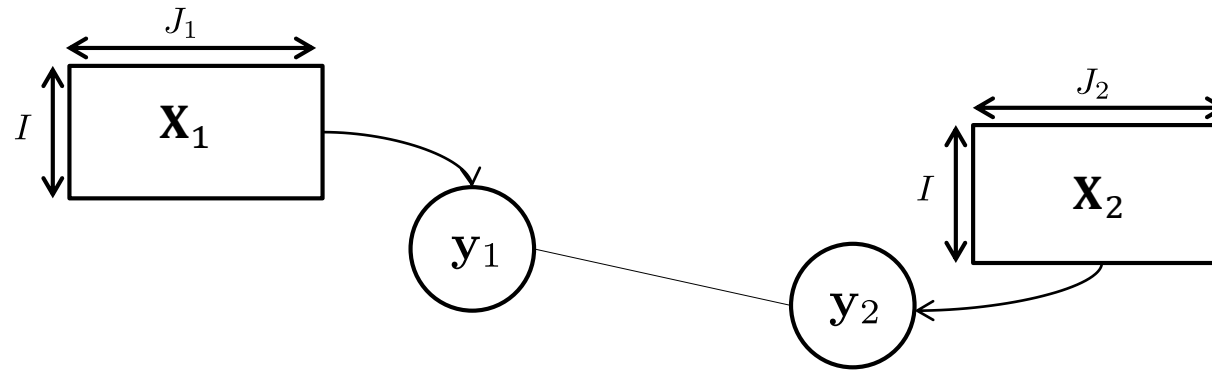
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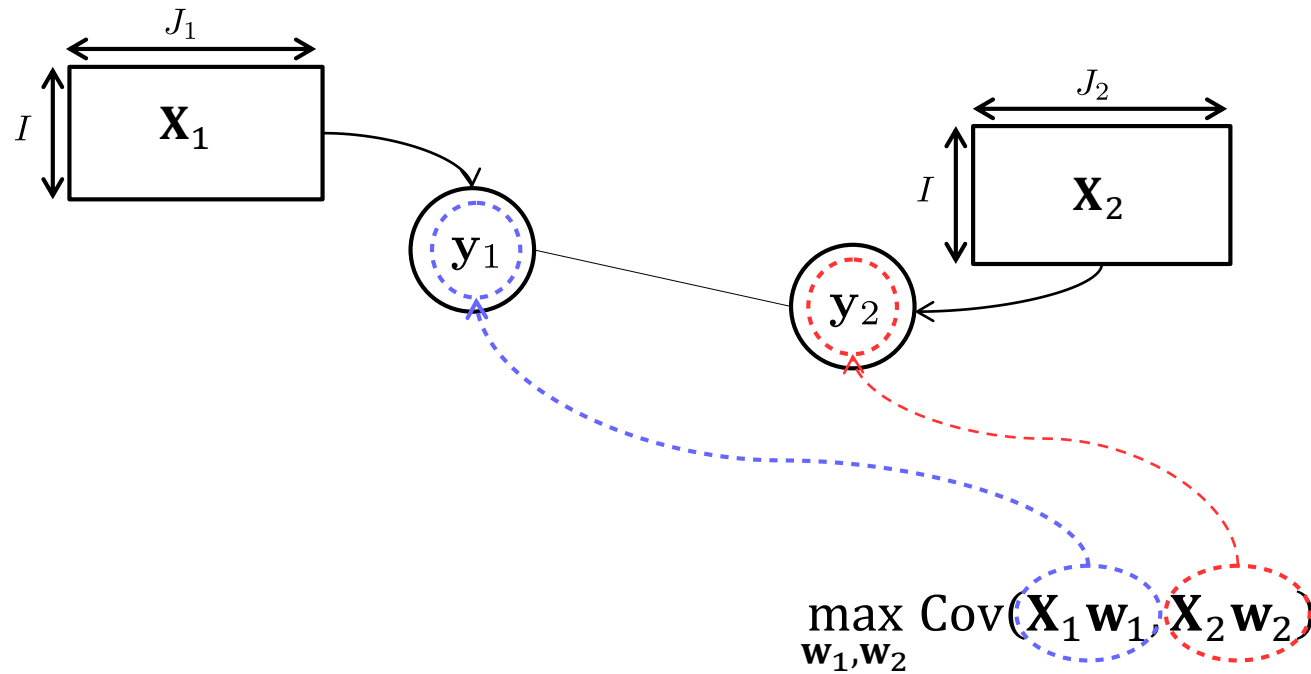


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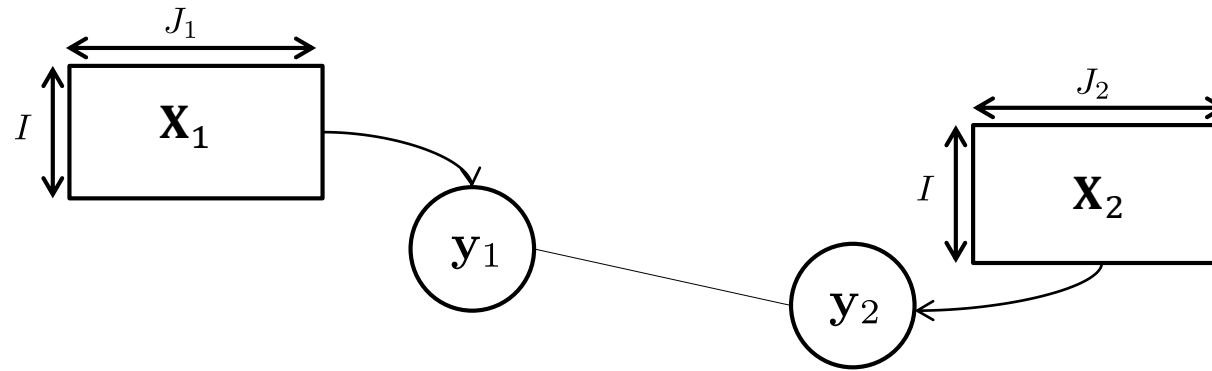


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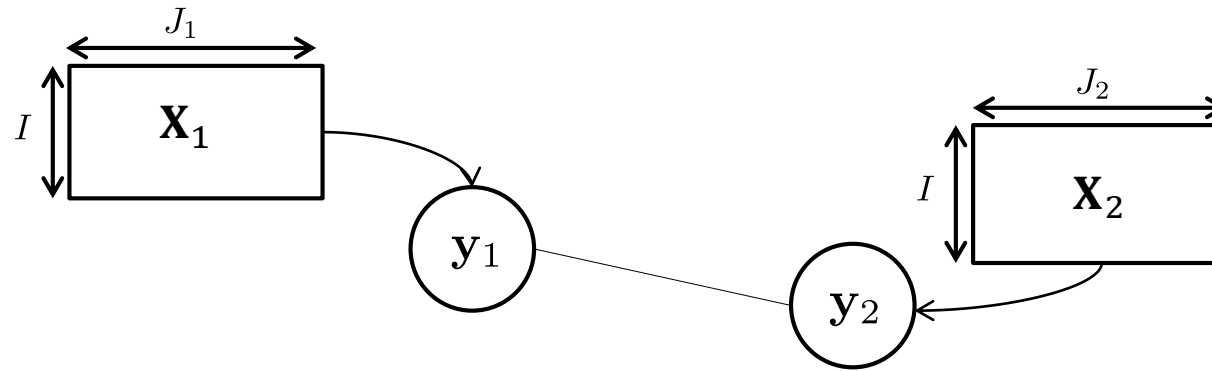


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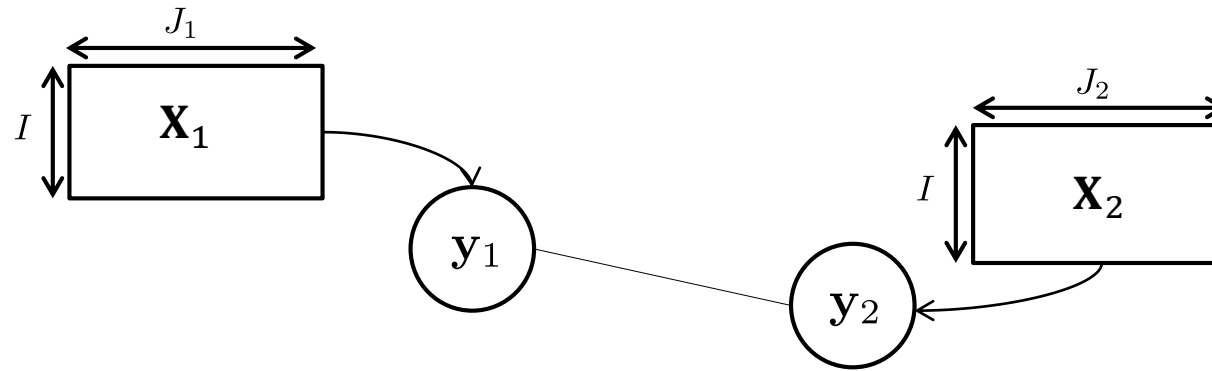
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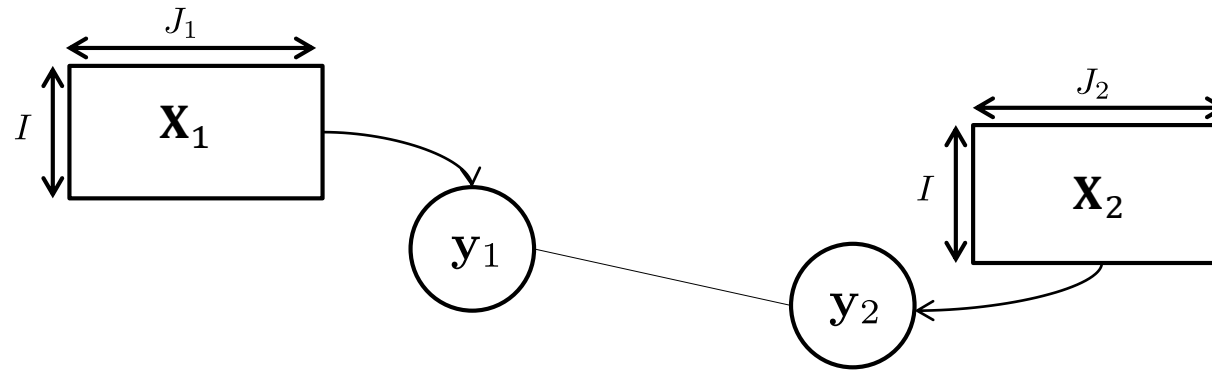
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Canonical Correlation Analysis

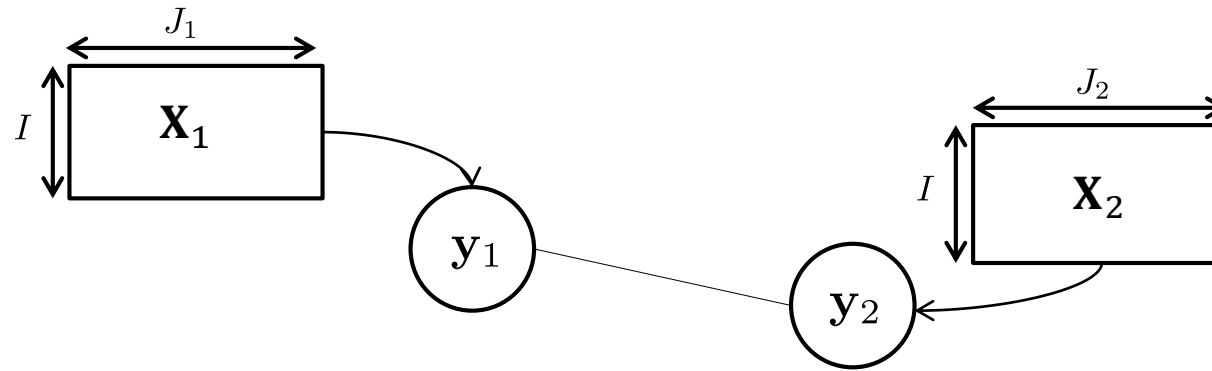
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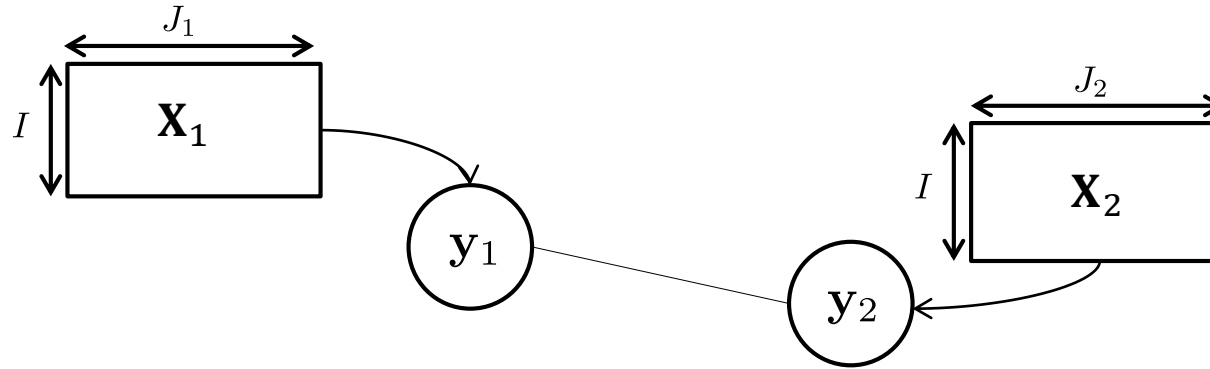
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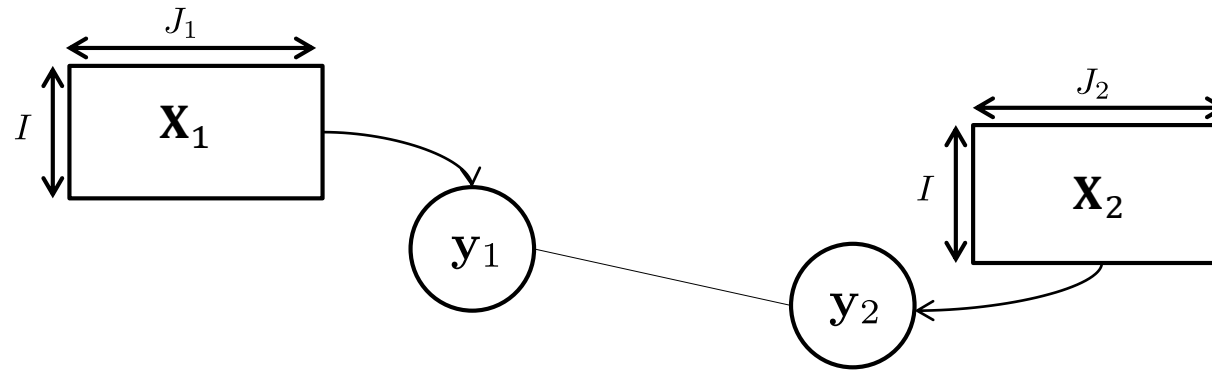


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➔ Partial Least Squares 2

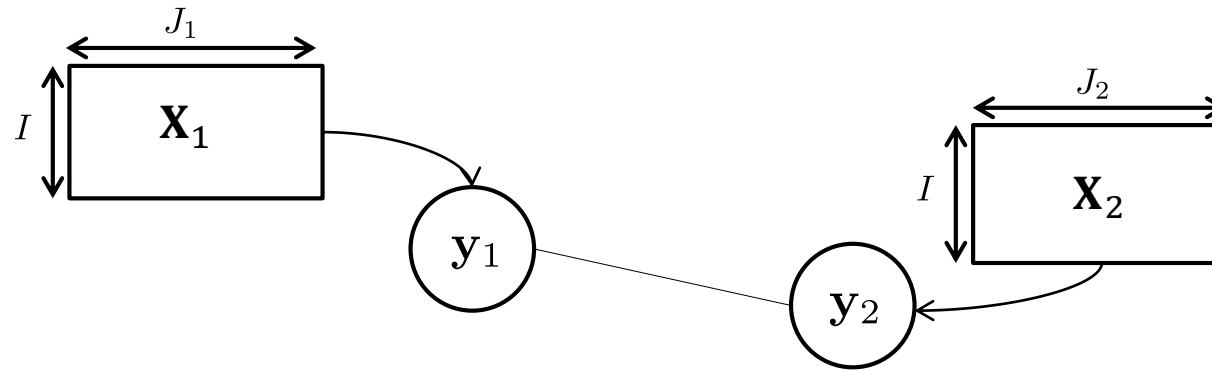
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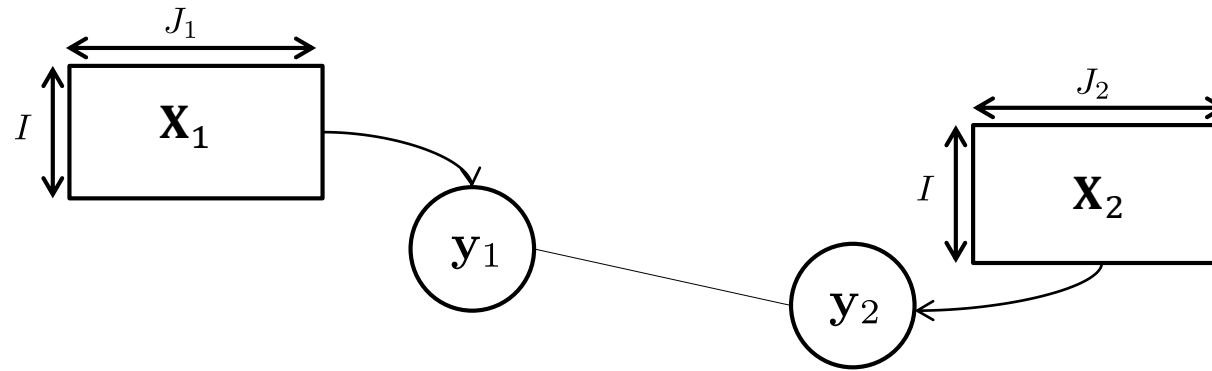
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$$\text{s. t. } \mathbf{w}_l^\top \mathbf{M}_l \mathbf{w}_l = 1, \quad l = 1, 2.$$

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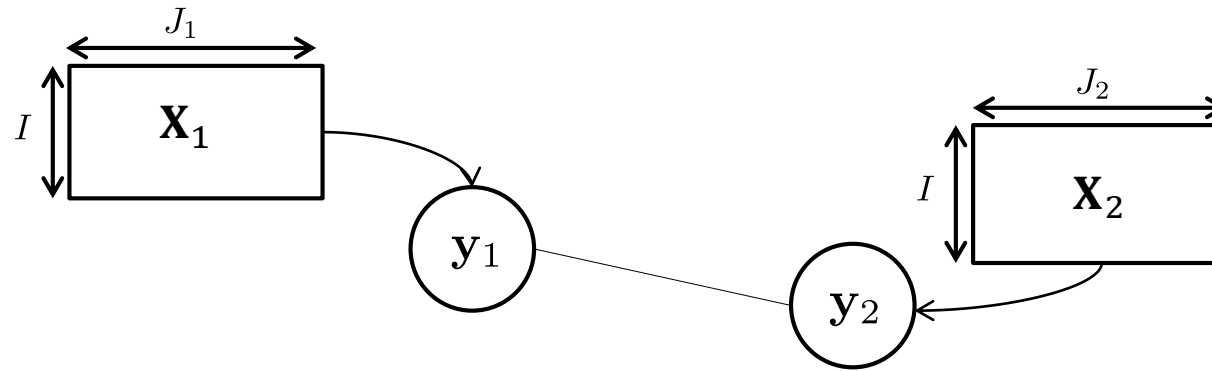


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➔ where \mathbf{M}_l is any $J_l \times J_l$ positive definite matrix

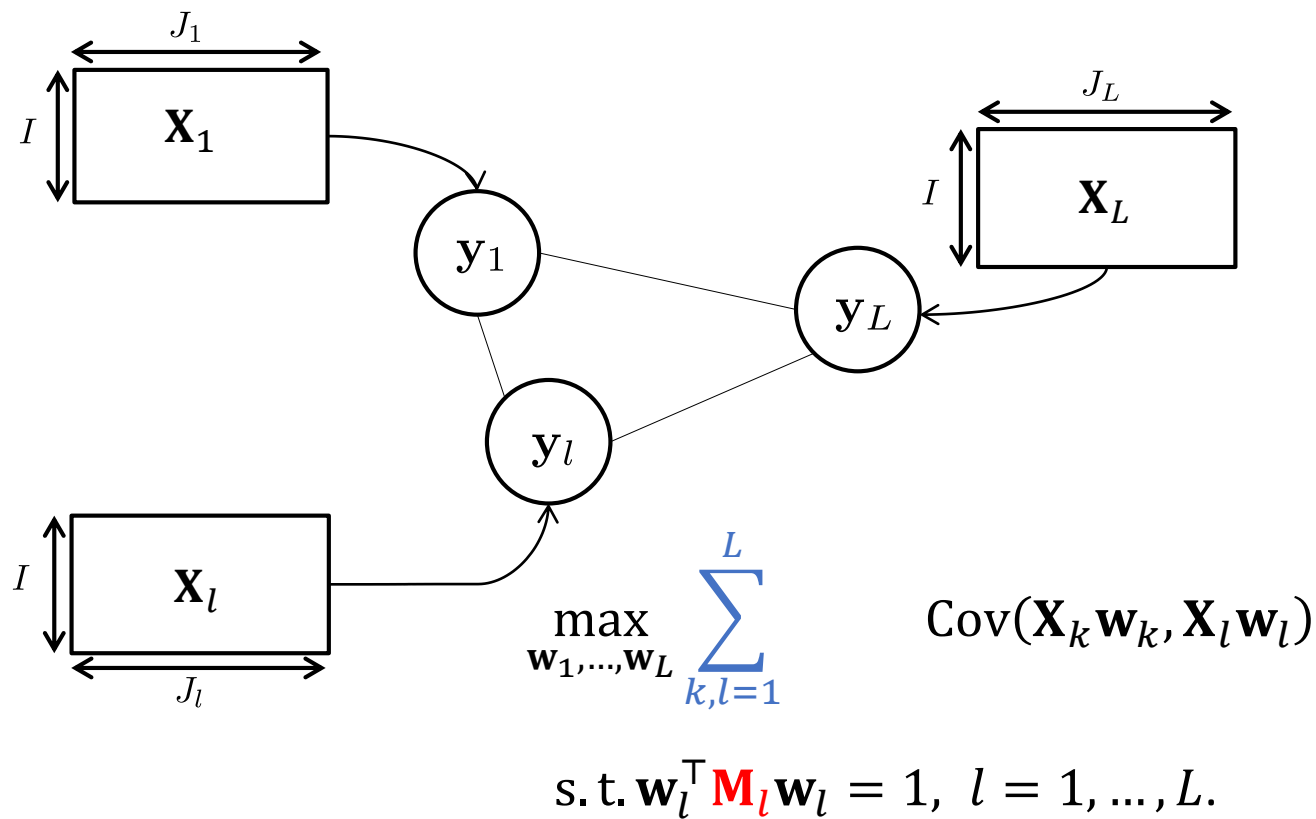
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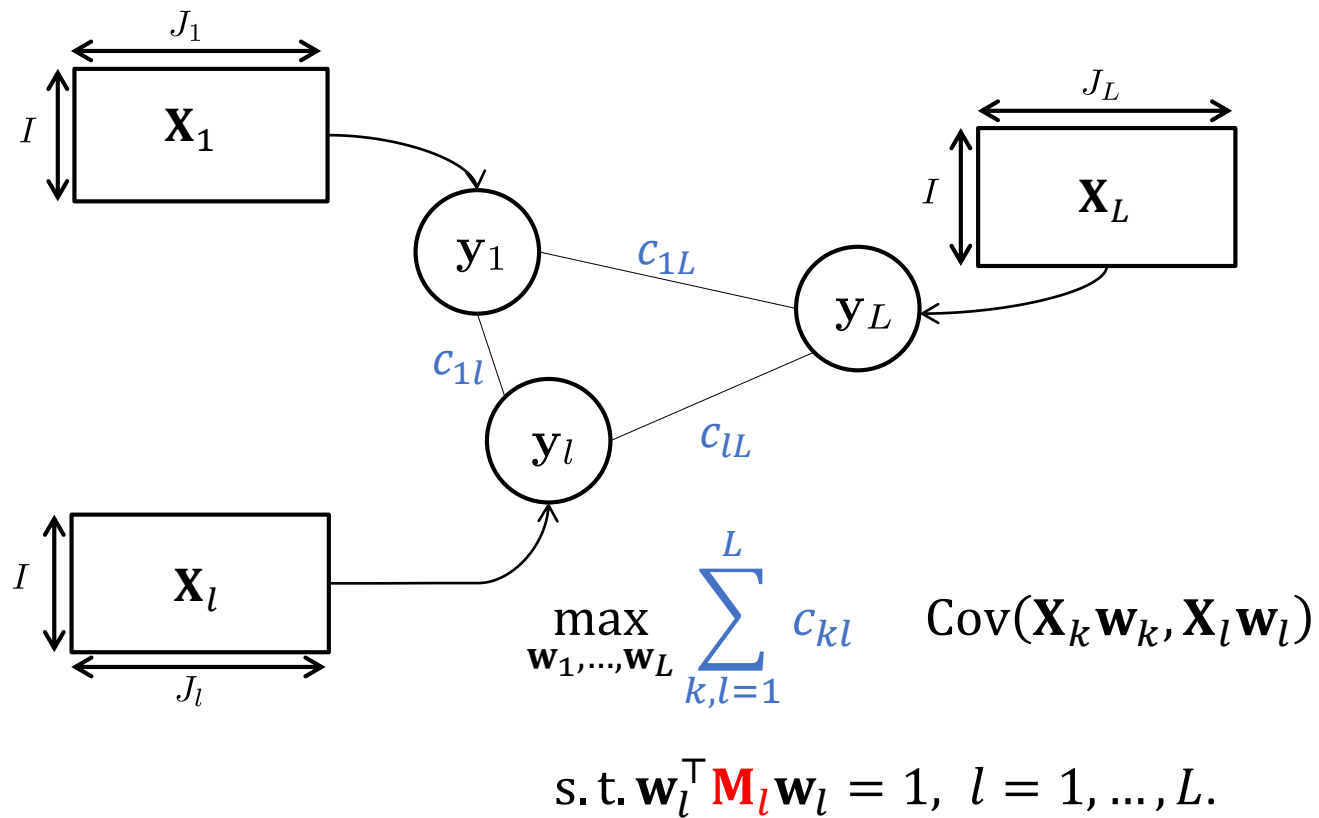
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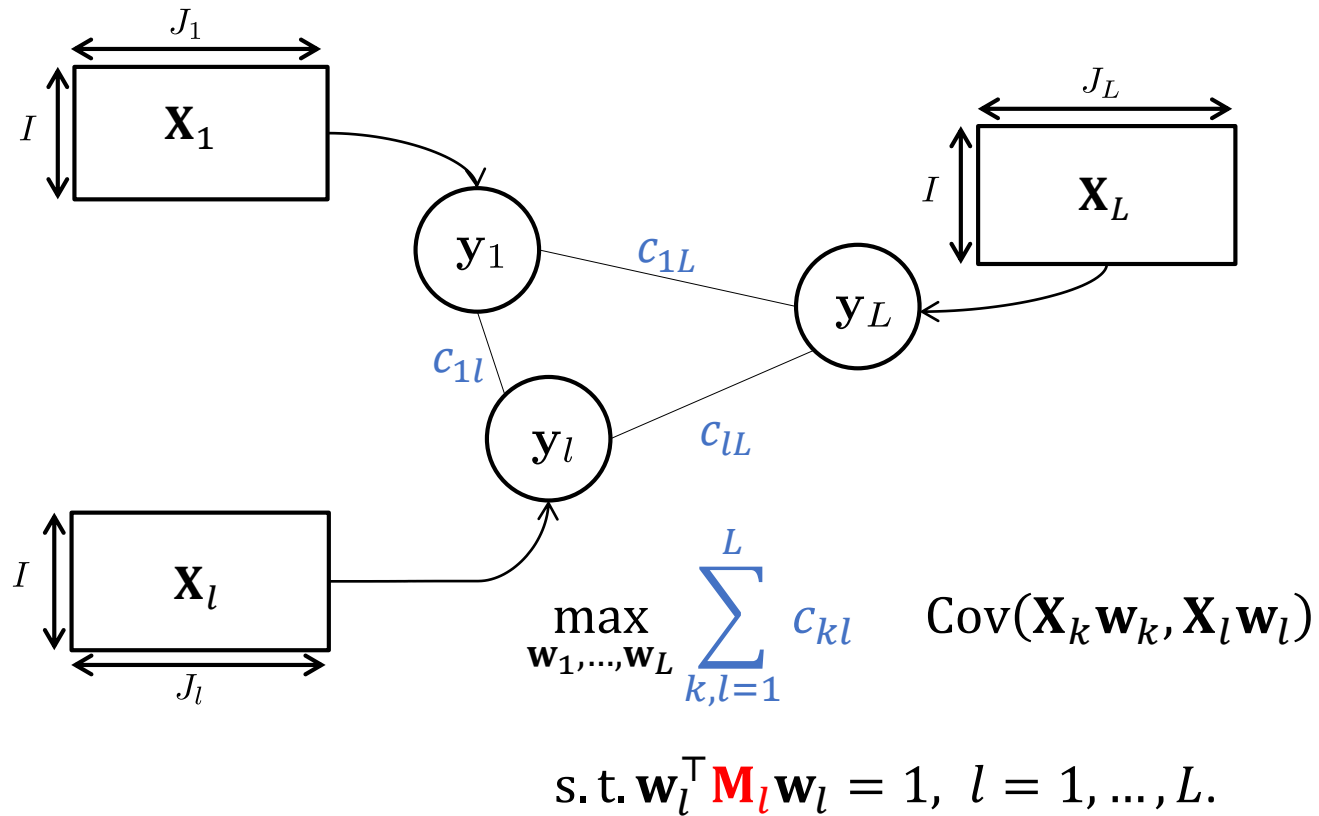
Regularized Generalized Canonical Correlation Analysis (RGCCA)



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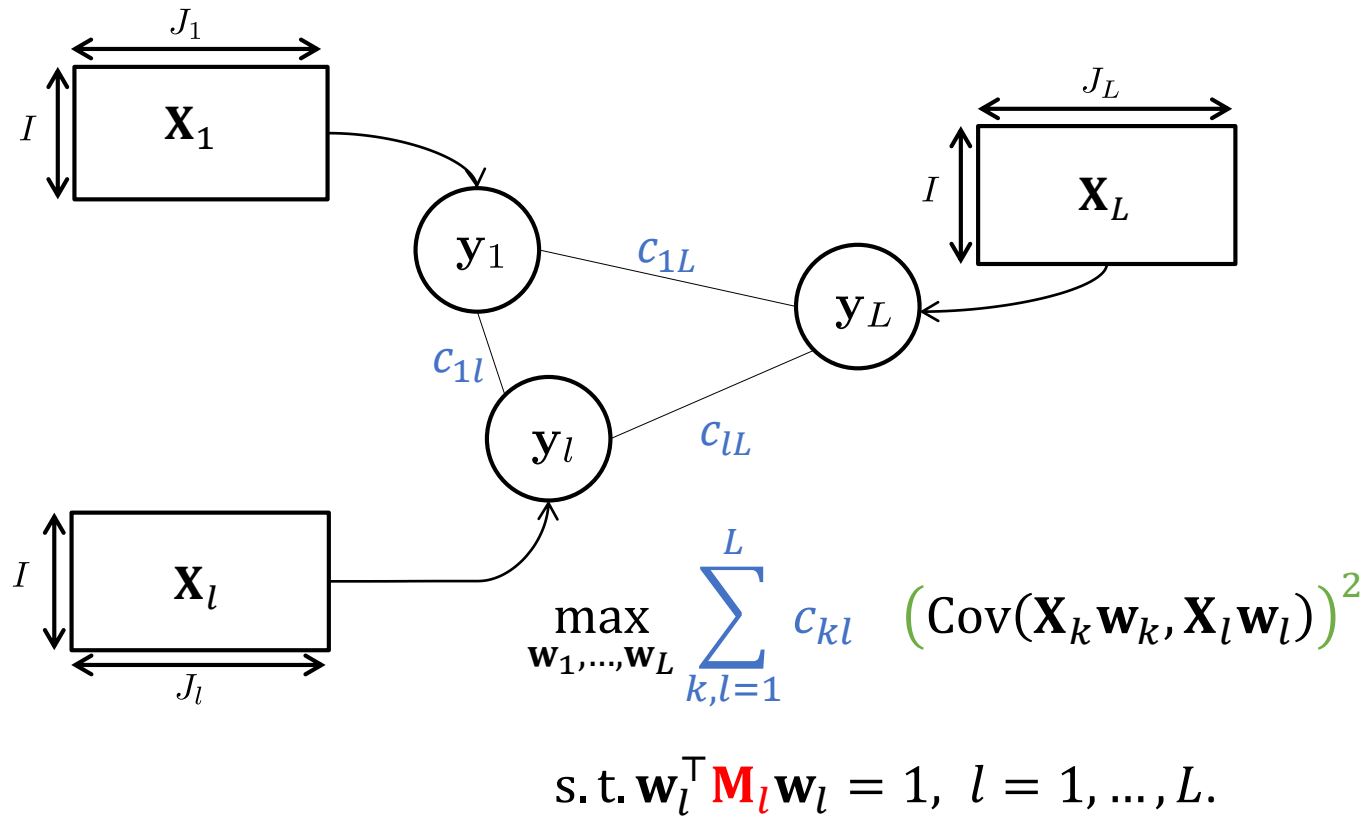


Regularized Generalized Canonical Correlation Analysis (RGCCA)



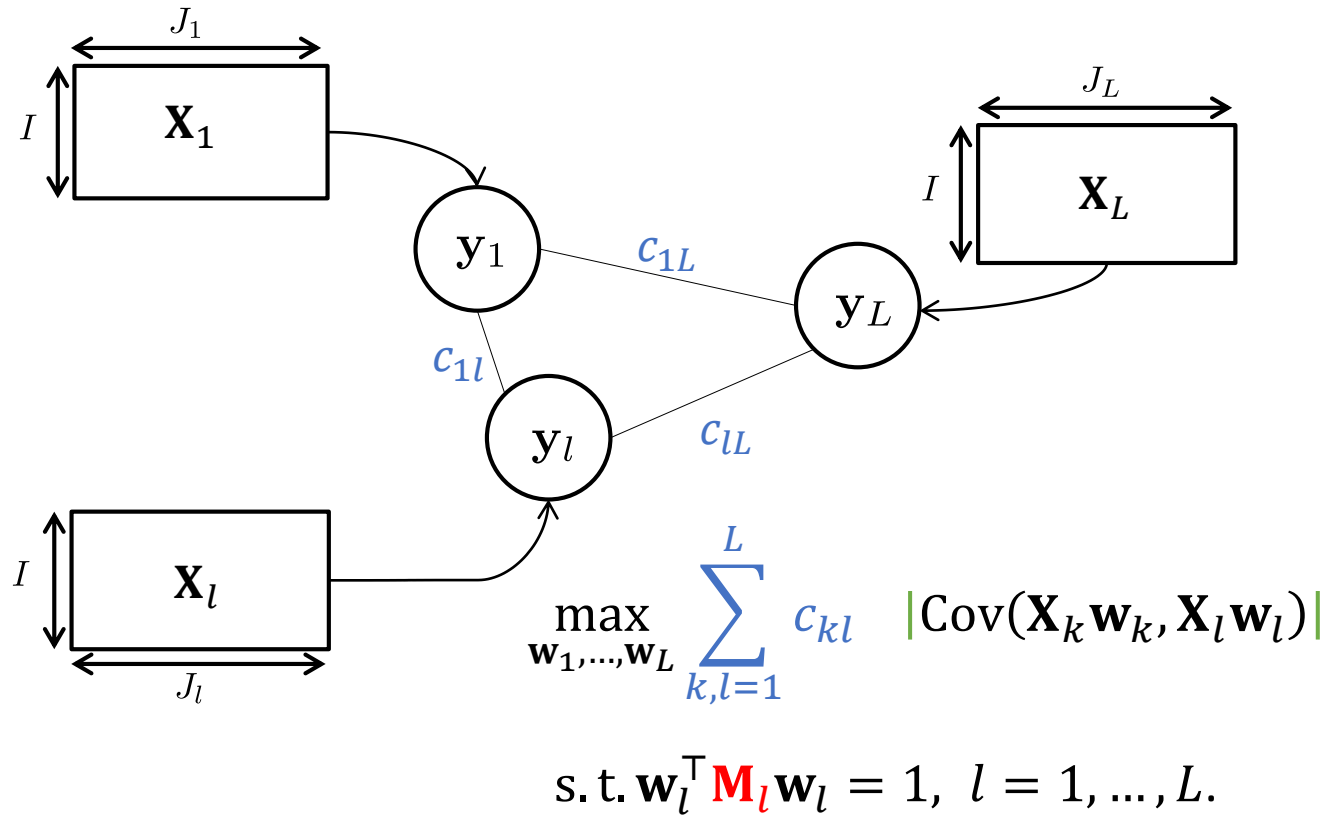
➡ if all blocks are connected and $\mathbf{M}_l = \mathbf{I}_l$ ➡ SUMCOV-2

Regularized Generalized Canonical Correlation Analysis (RGCCA)



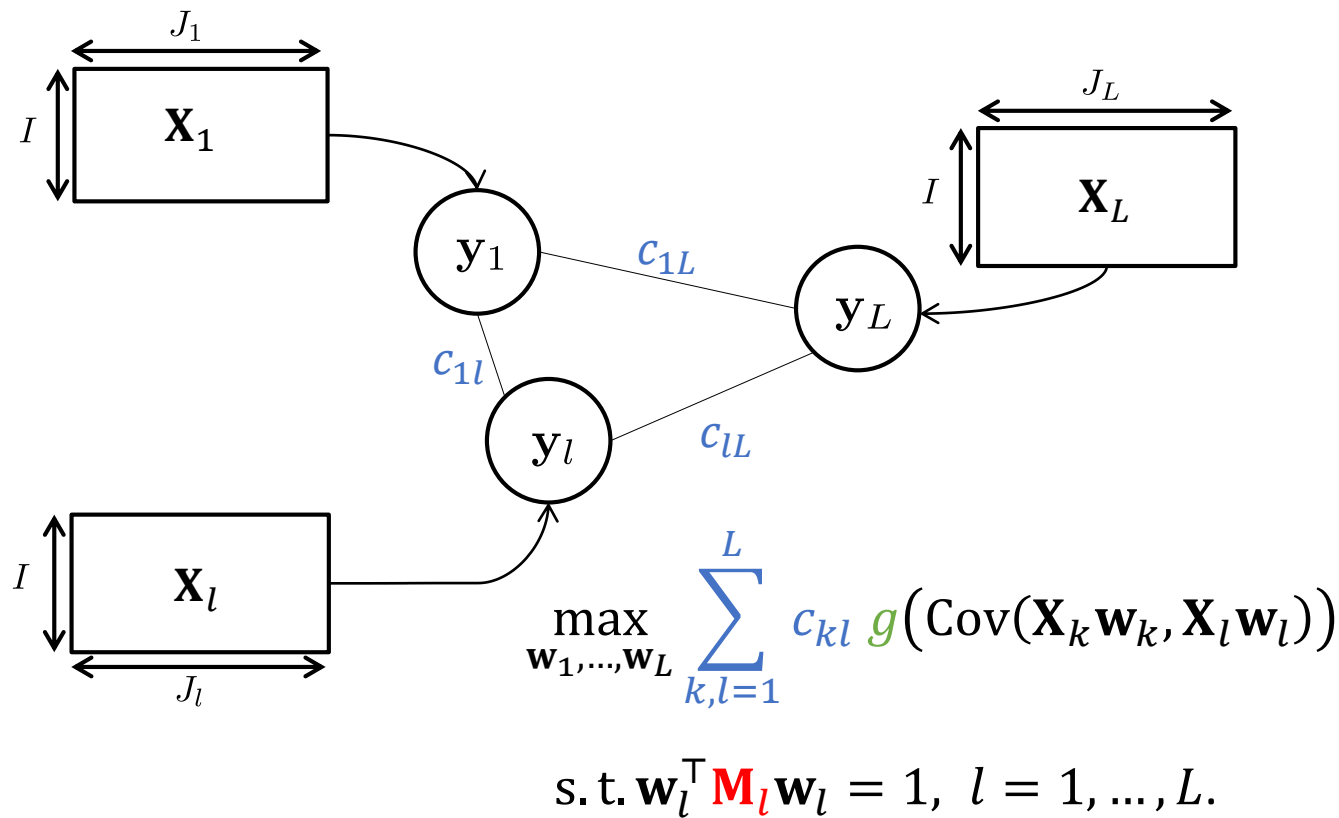
➡ if all blocks are connected and $\mathbf{M}_l = \mathbf{I}_l$ ➡ SSQCOV-2

Regularized Generalized Canonical Correlation Analysis (RGCCA)

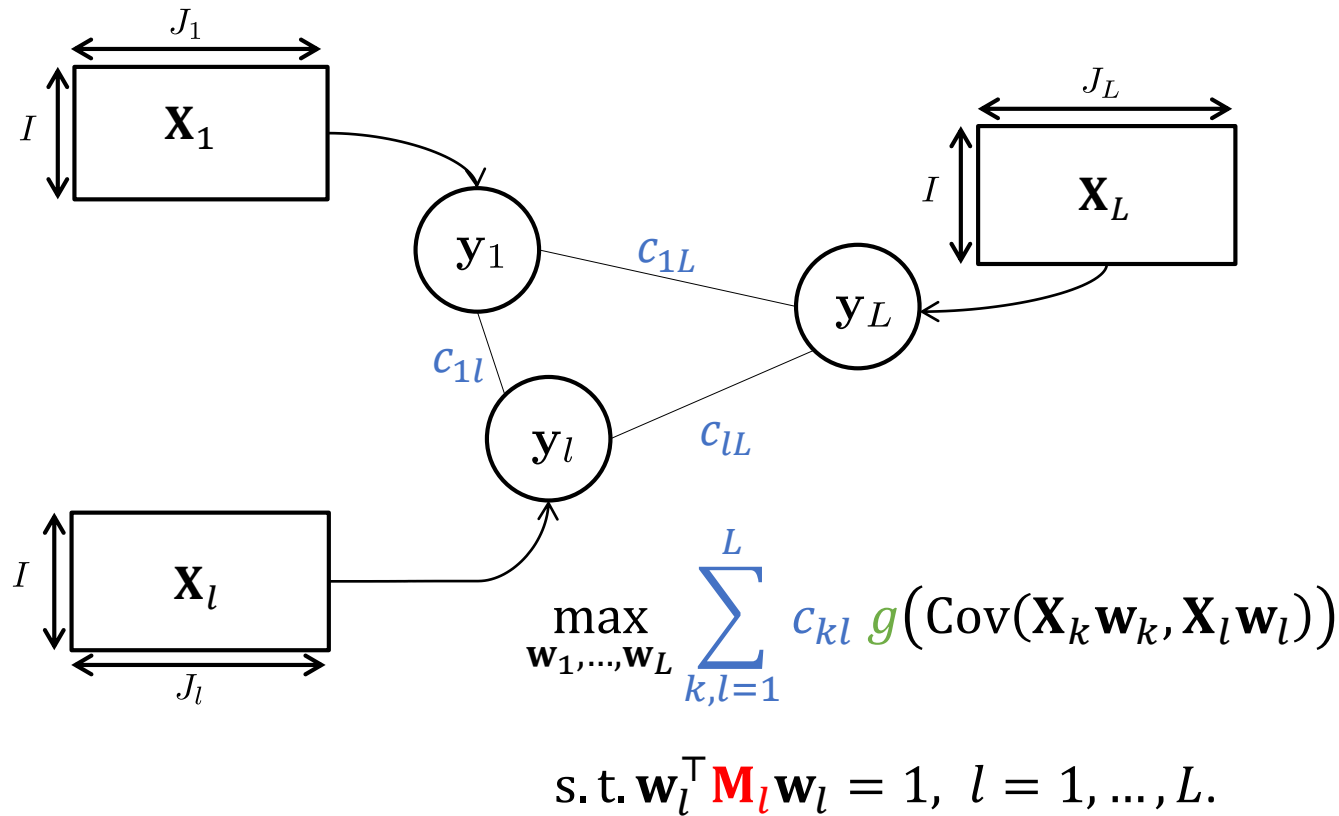


➡ if all blocks are connected and $\mathbf{M}_l = \mathbf{I}_l$ ➡ SABSCOV-2

Regularized Generalized Canonical Correlation Analysis (RGCCA)



Regularized Generalized Canonical Correlation Analysis (RGCCA)



➔ with g a continuous, convex and derivable function.



The Regularized Generalized Canonical Correlation Analysis (RGCCA) Optimization criterion :

$$\max_{\mathbf{w}_1, \dots, \mathbf{w}_L} \sum_{k,l=1}^L c_{kl} g(\text{Cov}(\mathbf{X}_k \mathbf{w}_k, \mathbf{X}_l \mathbf{w}_l))$$
$$\text{s. t. } \mathbf{w}_l^T \mathbf{M}_l \mathbf{w}_l = 1, \quad l = 1, \dots, L.$$



The Regularized Generalized Canonical Correlation Analysis (RGCCA) Optimization criterion :

$$\begin{aligned} \max_{\mathbf{w}_1, \dots, \mathbf{w}_L} \quad & \sum_{k,l=1}^L c_{kl} g(\text{Cov}(\mathbf{X}_k \mathbf{w}_k, \mathbf{X}_l \mathbf{w}_l)) \\ \text{s. t.} \quad & \mathbf{w}_l^T \mathbf{M}_l \mathbf{w}_l = 1, \quad l = 1, \dots, L. \end{aligned}$$

➔ With “ g ” a continuous, convex and derivable function.



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- ➔ With “ g ” a continuous, convex and derivable function.
- ➔ $c_{lk} = 1$ for two connected blocks and 0 otherwise.



The Regularized Generalized Canonical Correlation Analysis (RGCCA) Optimization criterion :

$$\begin{aligned} \max_{\mathbf{w}_1, \dots, \mathbf{w}_L} \quad & \sum_{k,l=1}^L c_{kl} g(\text{Cov}(\mathbf{X}_k \mathbf{w}_k, \mathbf{X}_l \mathbf{w}_l)) \\ \text{s. t.} \quad & \mathbf{w}_l^T \mathbf{M}_l \mathbf{w}_l = 1, \quad l = 1, \dots, L. \end{aligned}$$

- ➔ With “ g ” a continuous, convex and derivable function.
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Most of the time (this is the case today !) \mathbf{M}_l is chosen such that:

$$\mathbf{w}_l^T \mathbf{M}_l \mathbf{w}_l = (1 - \tau_l) \text{Var}(\mathbf{X}_l \mathbf{w}_l) + \tau_l \|\mathbf{w}_l\|_2^2 = 1.$$



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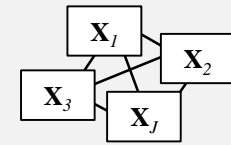
Most of the time (this is the case today !) \mathbf{M}_l is chosen such that:

$$\mathbf{w}_l^\top \mathbf{M}_l \mathbf{w}_l = \mathbf{w}_l^\top \underbrace{\left((1 - \tau_l) \mathbf{I}^{-1} \mathbf{X}_l^\top \mathbf{X}_l + \tau_l \mathbf{I}_{J_l} \right)}_{\text{Regularized version of the sample covariance matrix}} \mathbf{w}_l = 1.$$

Regularized version of the sample covariance matrix

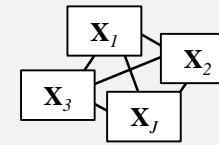


ALL BLOCKS ARE INTERCONNECTED	
SUMCOR (Horst, 1961)	$\max_{\mathbf{w}_j} \sum_{j,k} \text{cor}(\mathbf{X}_j \mathbf{w}_j, \mathbf{X}_k \mathbf{w}_k)$
SSQCOR (Kettenring, 1961)	$\max_{\mathbf{w}_j} \sum_{j,k} \text{cor}^2(\mathbf{X}_j \mathbf{w}_j, \mathbf{X}_k \mathbf{w}_k)$
SABSCOR (Wold, 1982)	$\max_{\mathbf{w}_j} \sum_{j,k} \text{cor}(\mathbf{X}_j \mathbf{w}_j, \mathbf{X}_k \mathbf{w}_k) $





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SUMCOV (Van de Geer, 1984)	$\max_{\ \mathbf{w}_j\ =1} \sum_{j,k} \text{cov}(\mathbf{X}_j \mathbf{w}_j, \mathbf{X}_k \mathbf{w}_k)$
SSQCOV (Hanafi & Kiers, 2006)	$\max_{\ \mathbf{w}_j\ =1} \sum_{j,k} \text{cov}^2(\mathbf{X}_j \mathbf{w}_j, \mathbf{X}_k \mathbf{w}_k)$
SABSCOV (Krämer, 2007)	$\max_{\ \mathbf{w}_j\ =1} \sum_{j,k} \text{cov}(\mathbf{X}_j \mathbf{w}_j, \mathbf{X}_k \mathbf{w}_k) $





BLOCKS ARE PARTIALLY CONNECTED $c_{jk} = 1$ if $\mathbf{X}_j \leftrightarrow \mathbf{X}_k$, 0 otherwise	
SUMCOR	$\max_{\mathbf{w}_j} \sum_{j,k} c_{jk} \text{cor}(\mathbf{X}_j \mathbf{w}_j, \mathbf{X}_k \mathbf{w}_k)$
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Overview of the Multi-Block litterature

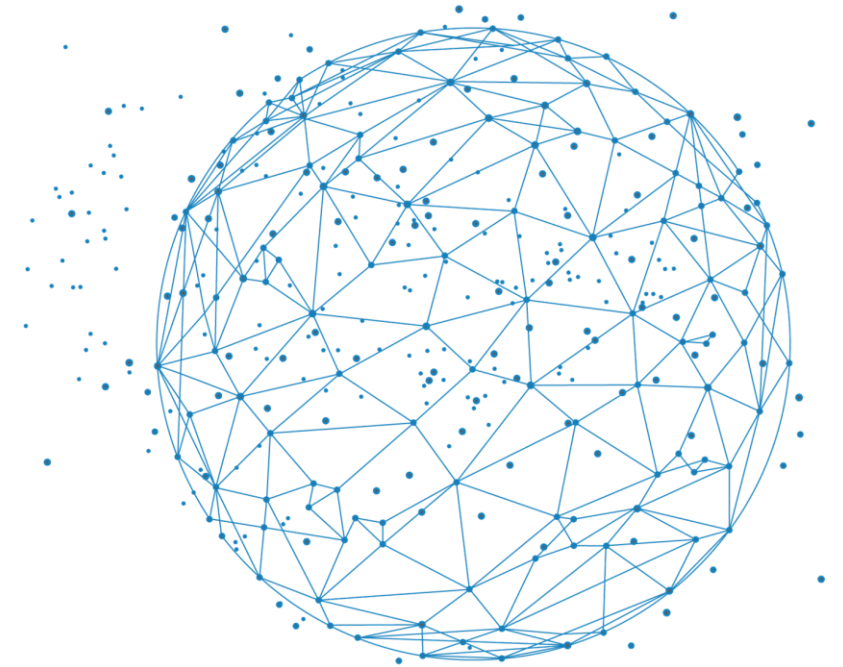


BLOCKS ARE PARTIALLY CONNECTED $c_{jk} = 1$ if $\mathbf{X}_j \leftrightarrow \mathbf{X}_k$, 0 otherwise	
SUMCOR	$\max_{\text{var}(\mathbf{X}_j \mathbf{w}_j)=1} \sum_{j,k} c_{jk} \text{cov}(\mathbf{X}_j \mathbf{w}_j, \mathbf{X}_k \mathbf{w}_k)$
SSQCOR	$\max_{\text{var}(\mathbf{X}_j \mathbf{w}_j)=1} \sum_{j,k} c_{jk} \text{cov}^2(\mathbf{X}_j \mathbf{w}_j, \mathbf{X}_k \mathbf{w}_k)$
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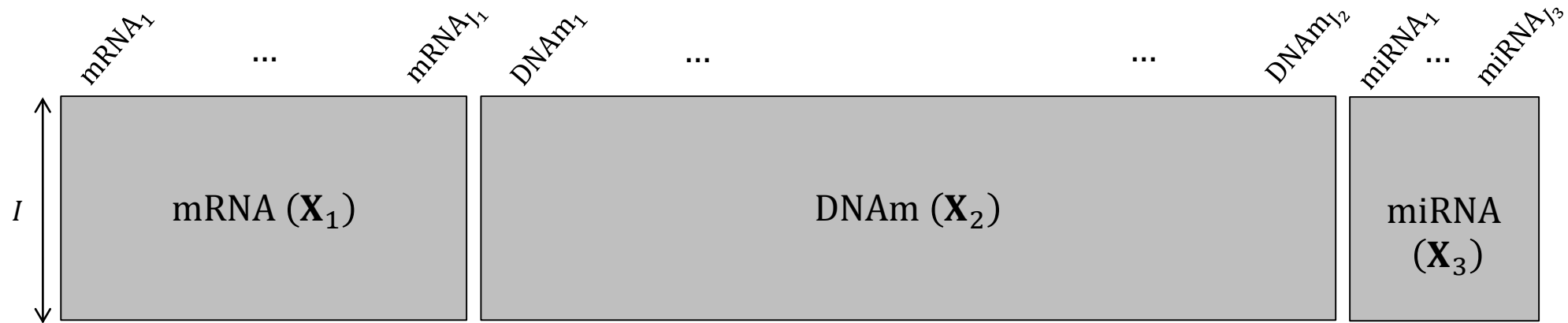
Courtesy to Arthur Tenenhaus.

Let us see how RGCCA performs on the MDD case study

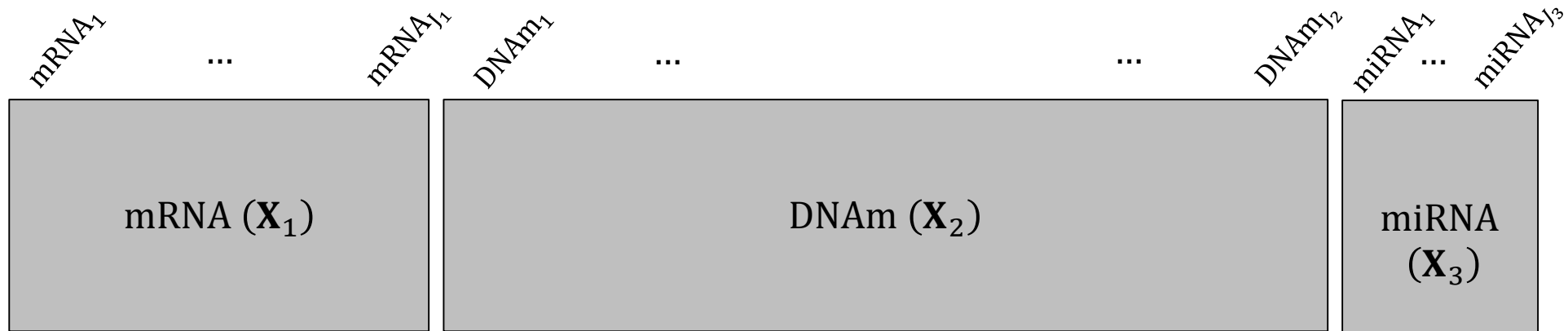
→ See section 3.2 on the Rmarkdown ``MDD_case_study_RGCCA``



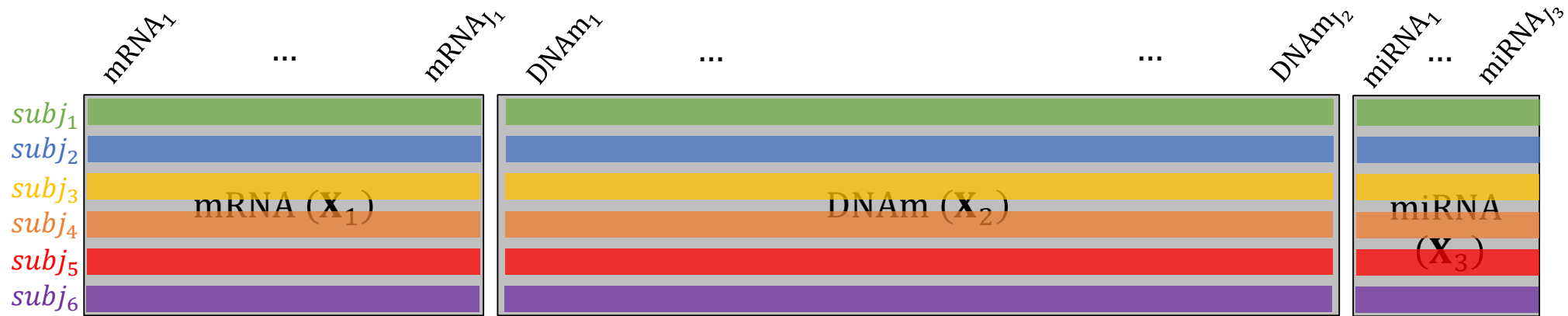
Tune parameters in an unsupervised setting



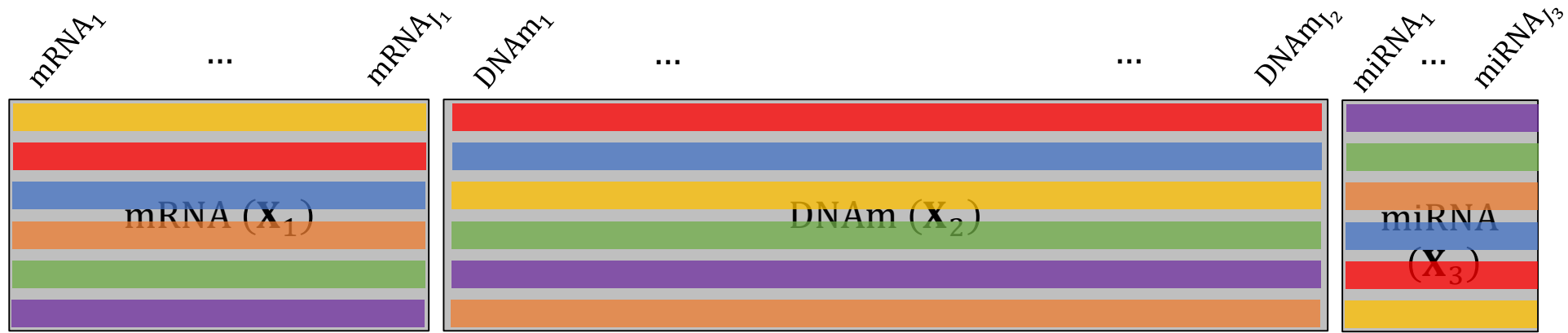
Tune parameters in an unsupervised setting



Tune parameters in an unsupervised setting

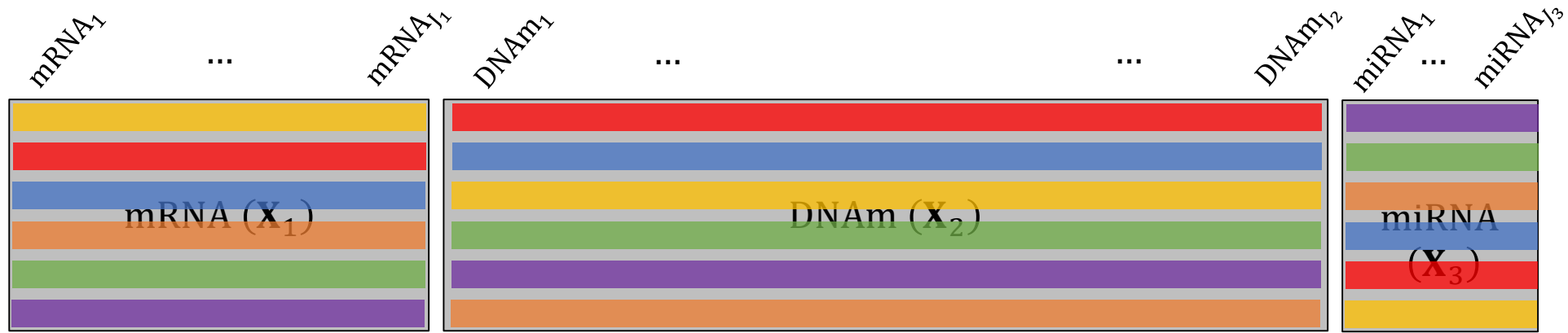


Tune parameters in an unsupervised setting



Permutation n°1

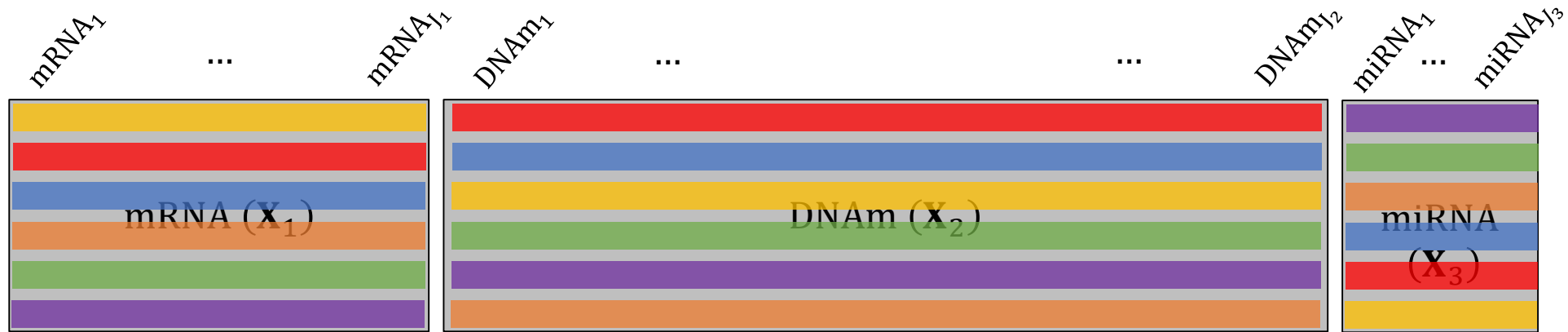
Tune parameters in an unsupervised setting



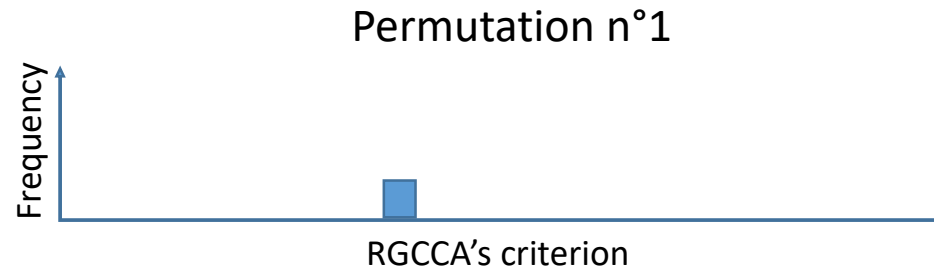
Permutation n°1

Parameter set n°1

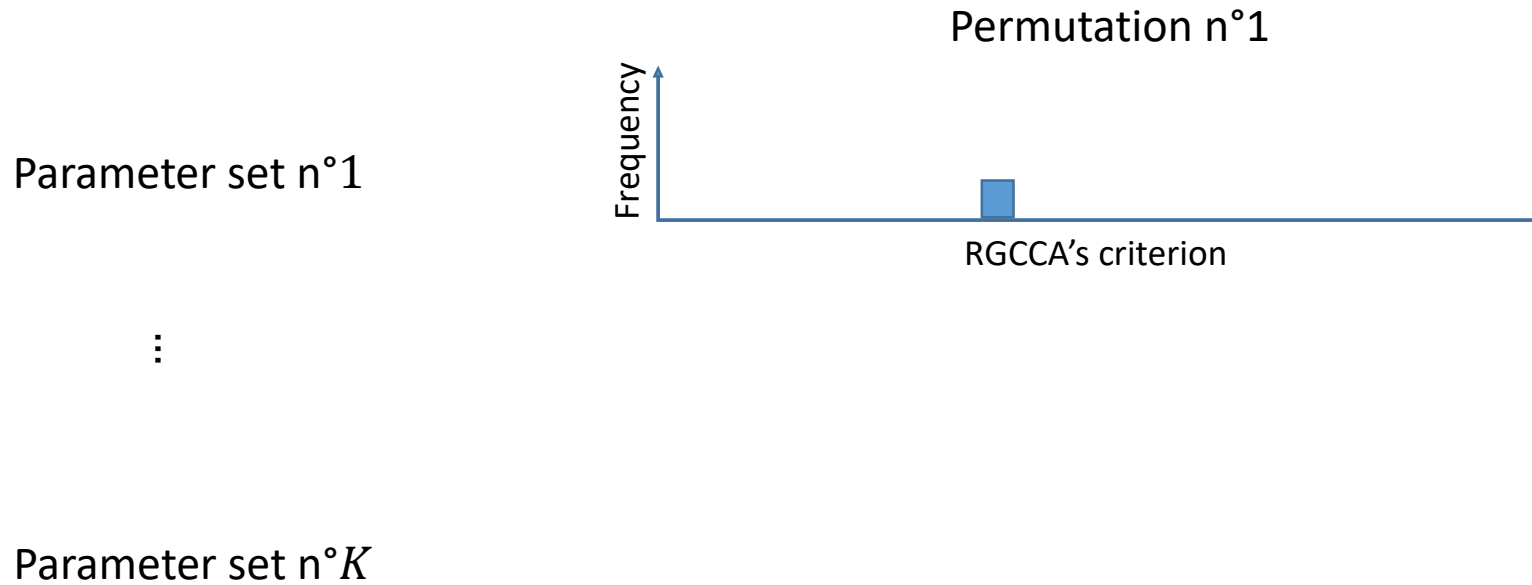
Tune parameters in an unsupervised setting



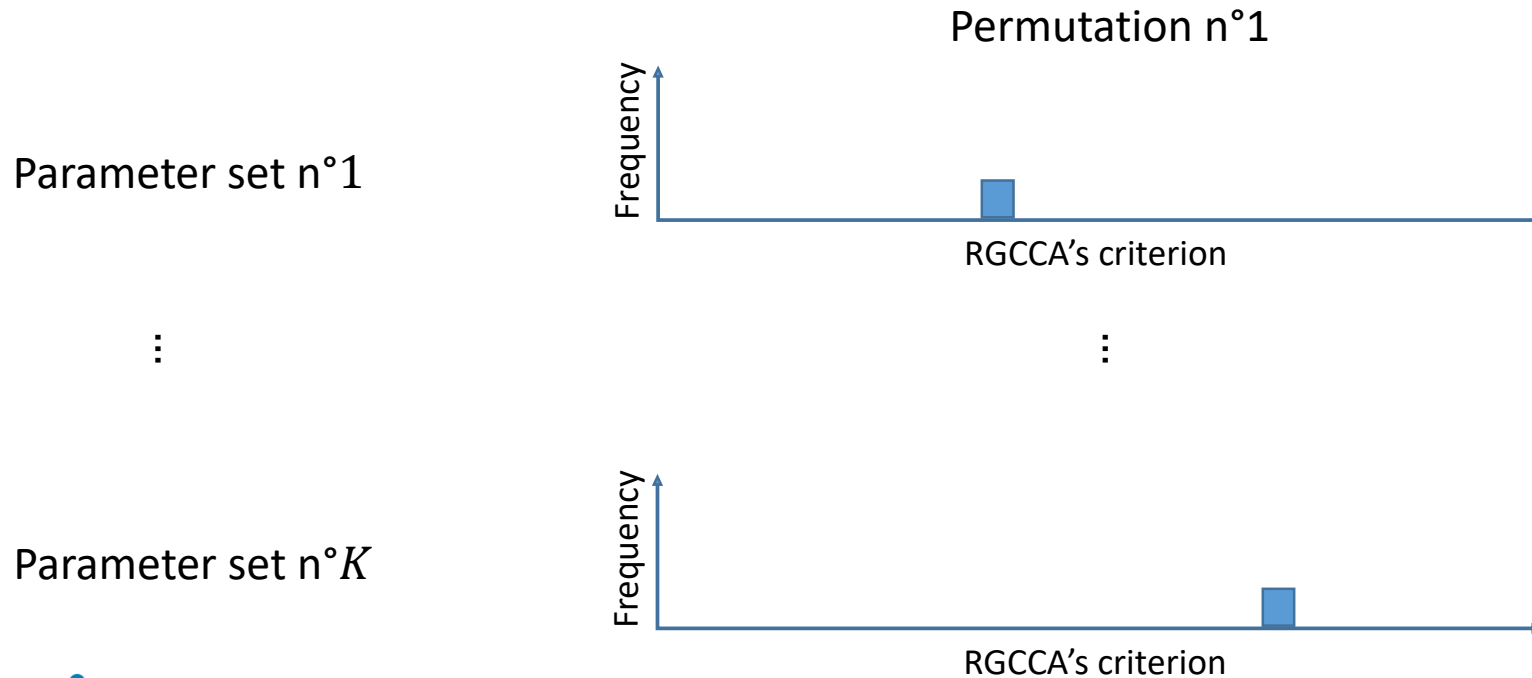
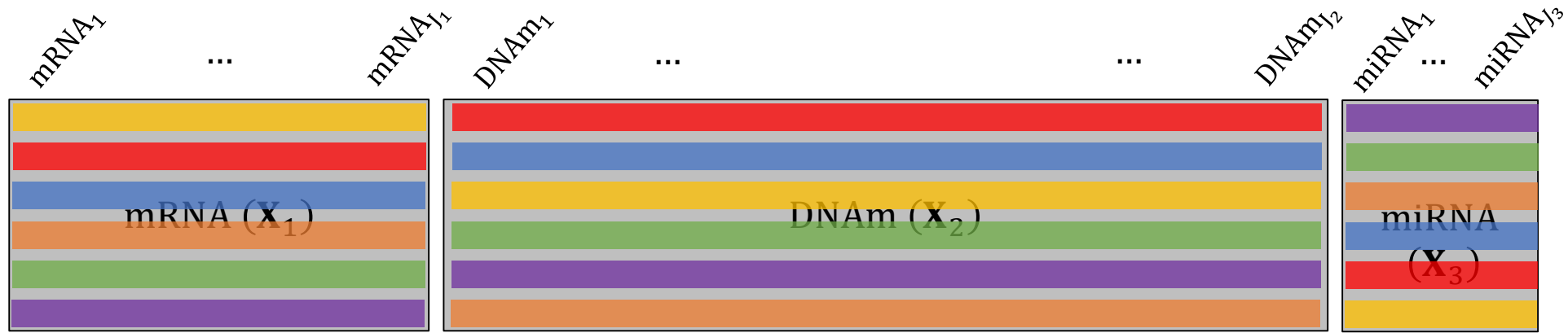
Parameter set n°1



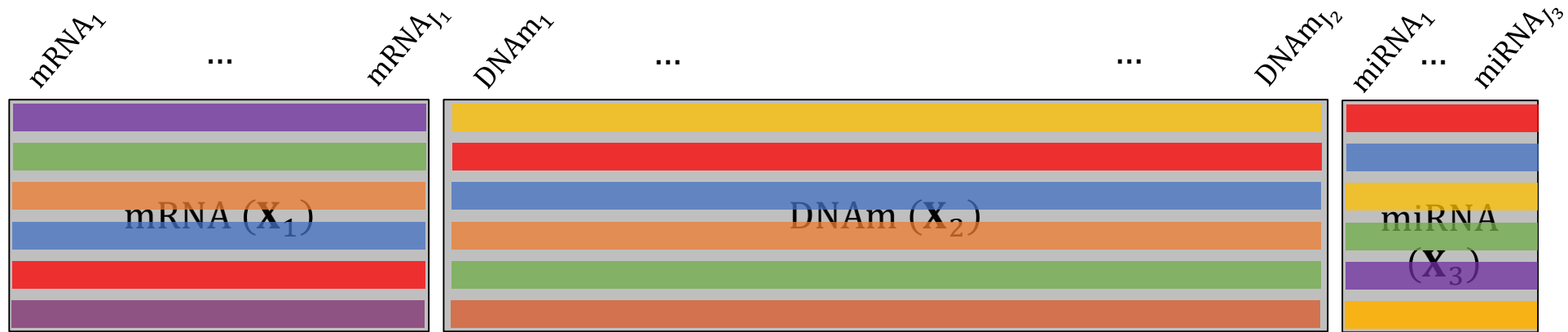
Tune parameters in an unsupervised setting



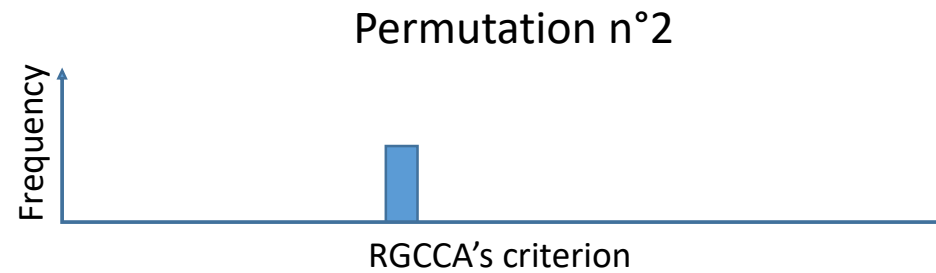
Tune parameters in an unsupervised setting



Tune parameters in an unsupervised setting



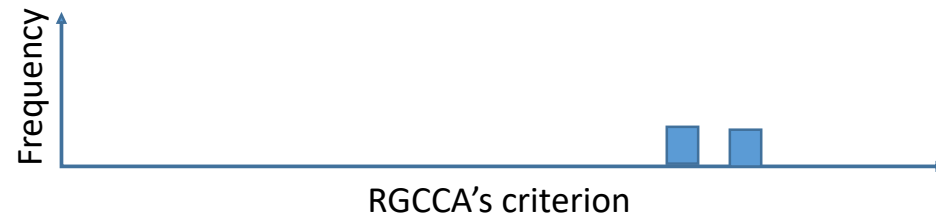
Parameter set n°1



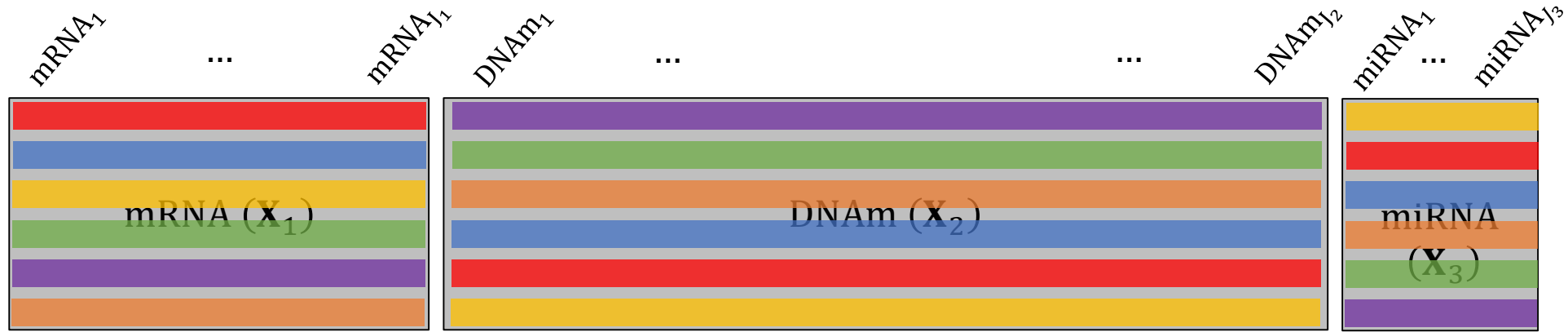
⋮

⋮

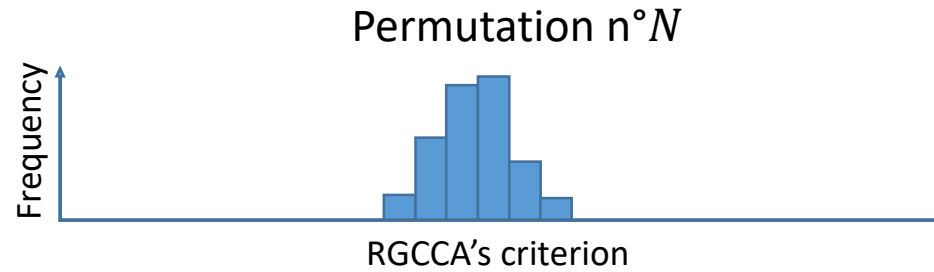
Parameter set n°K



Tune parameters in an unsupervised setting



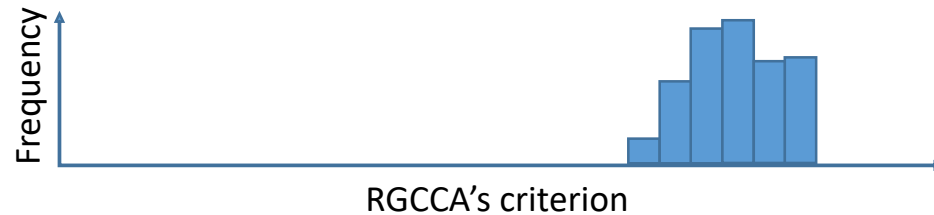
Parameter set n°1



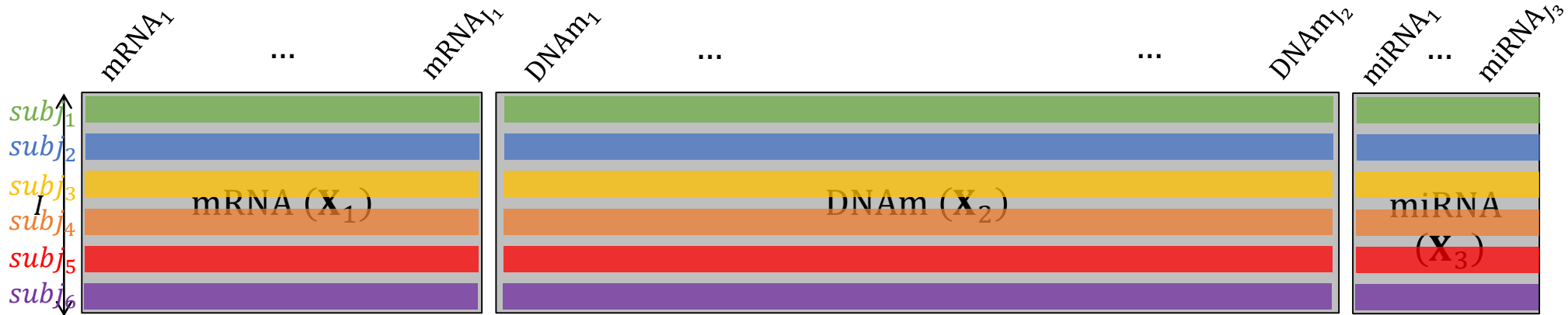
⋮

⋮

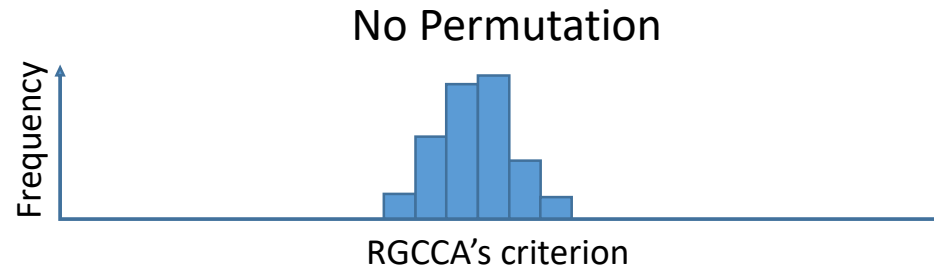
Parameter set n°K



Tune parameters in an unsupervised setting



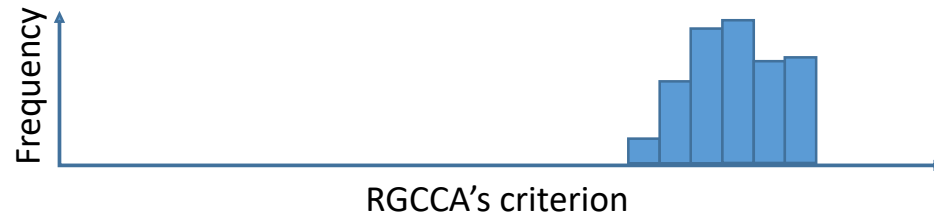
Parameter set n°1



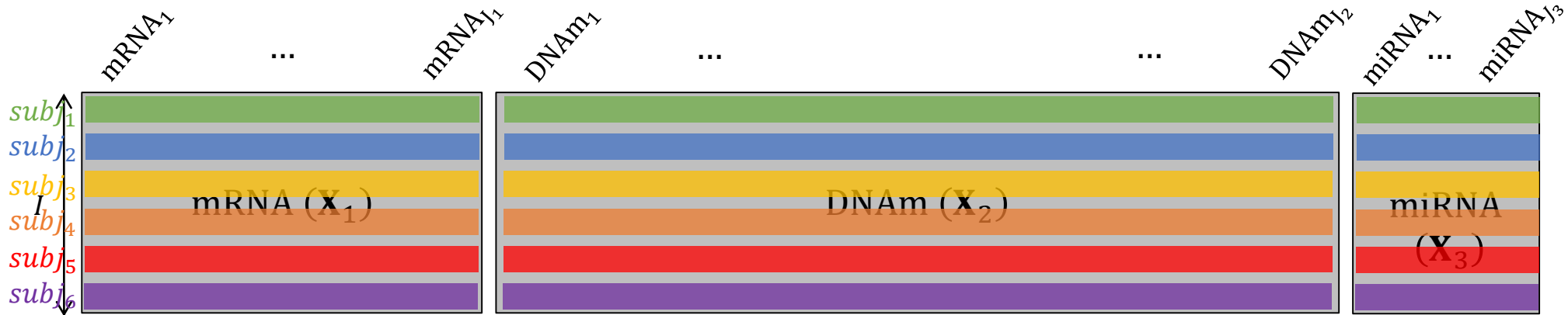
⋮

⋮

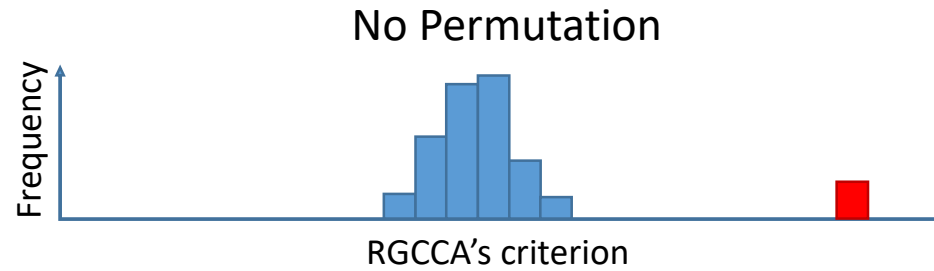
Parameter set n°K



Tune parameters in an unsupervised setting



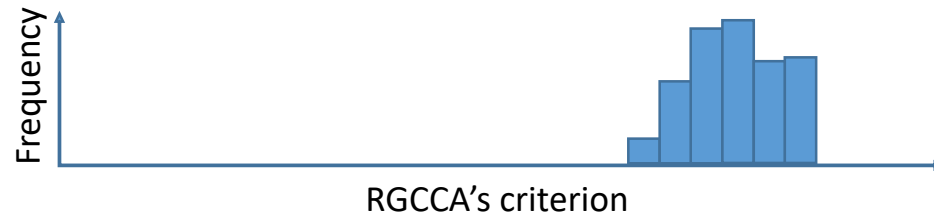
Parameter set n°1



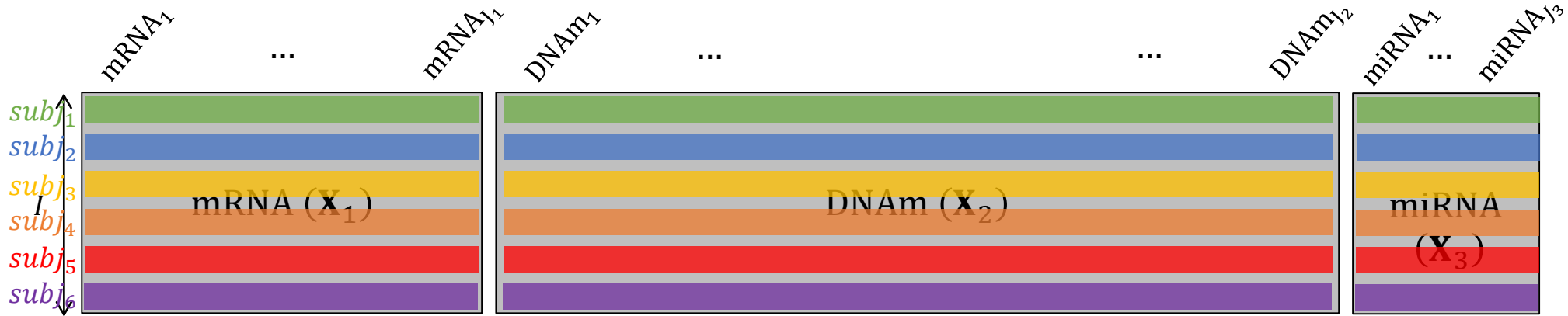
⋮

⋮

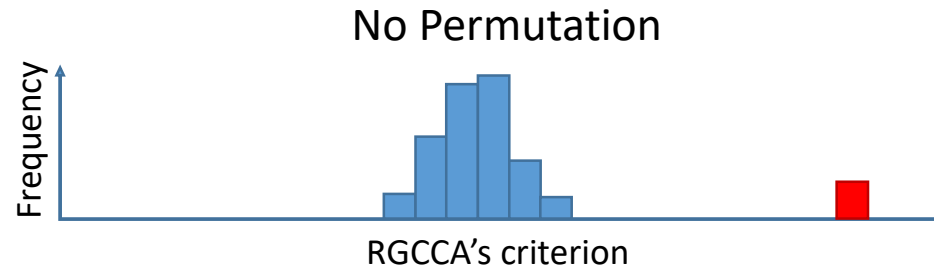
Parameter set n°K



Tune parameters in an unsupervised setting



Parameter set n°1

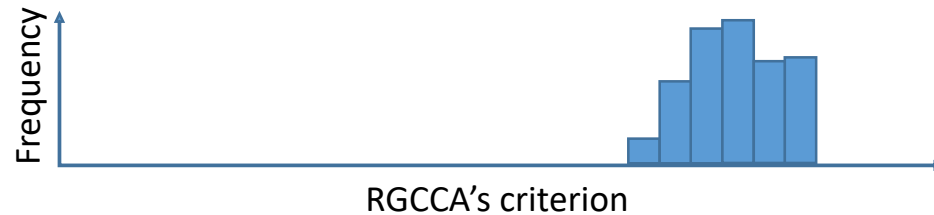


→ The set of parameters is likely to be selected.

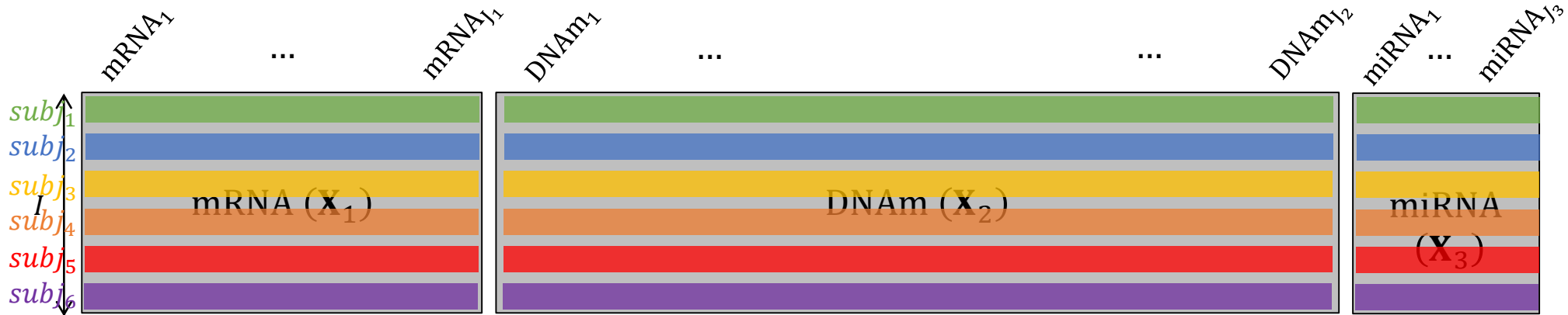
⋮

⋮

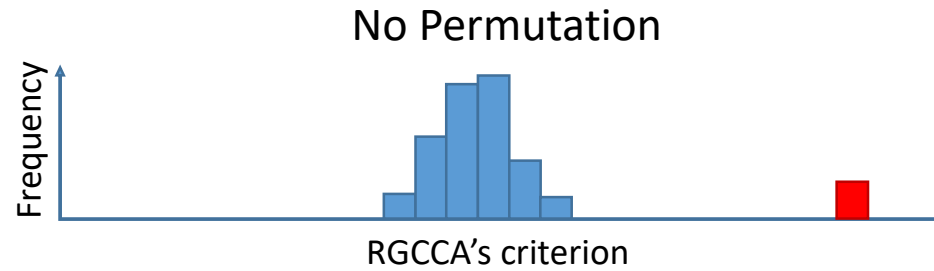
Parameter set n°K



Tune parameters in an unsupervised setting



Parameter set n°1

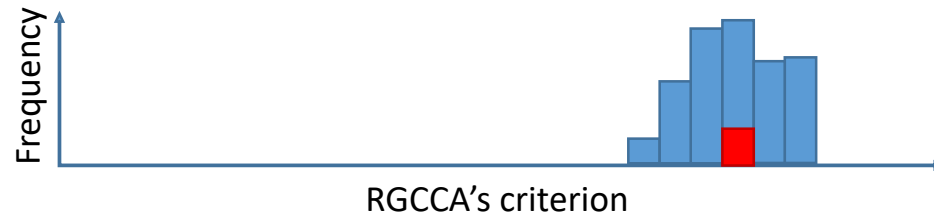


→ The set of parameters is likely to be selected.

⋮

⋮

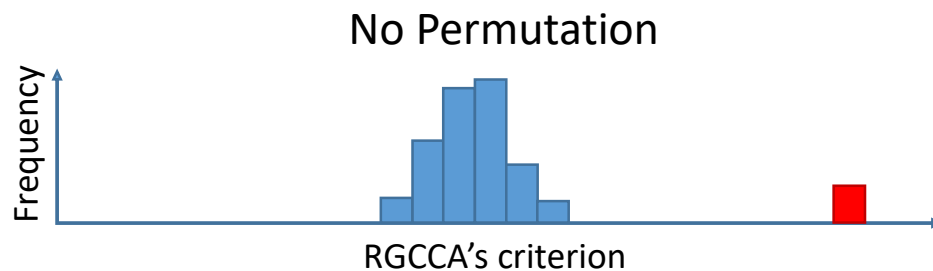
Parameter set n°K



Tune parameters in an unsupervised setting



Parameter set n°1

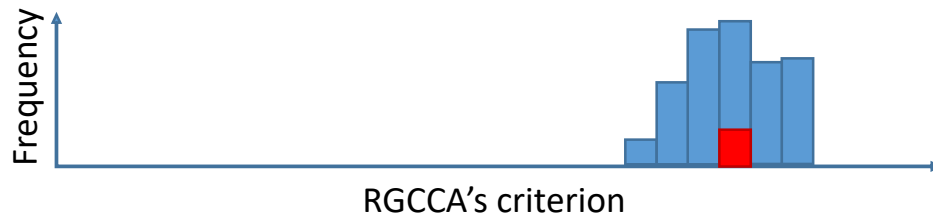


→ The set of parameters is likely to be selected.

⋮

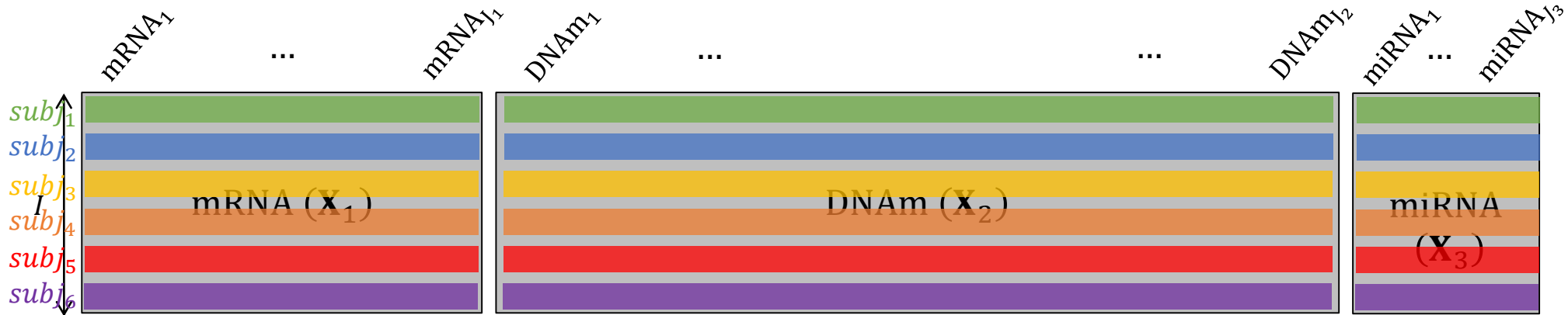
⋮

Parameter set n°K

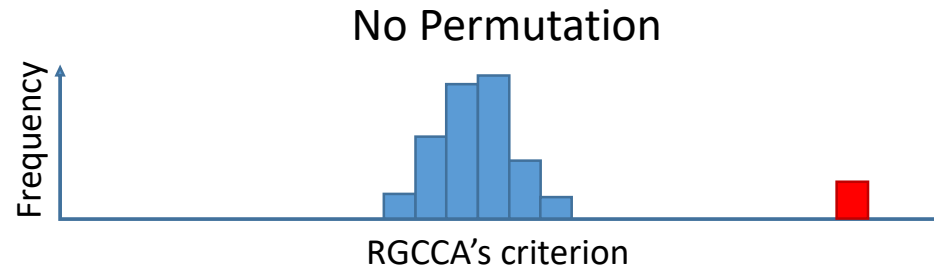


→ The set of parameters is unlikely to be selected.

Tune parameters in an unsupervised setting



Parameter set n°1

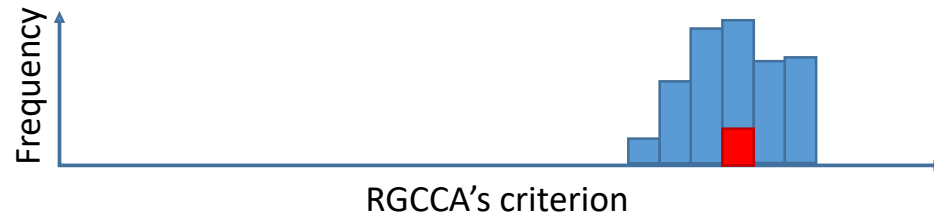


→ The set of parameters is likely to be selected.

⋮

RGCCA choose the best set of parameters as the one with the highest value of $Z_k = \frac{(crit_{unperm} - \mu_{crit}^{perm})}{\sigma_{crit}^{perm}}$

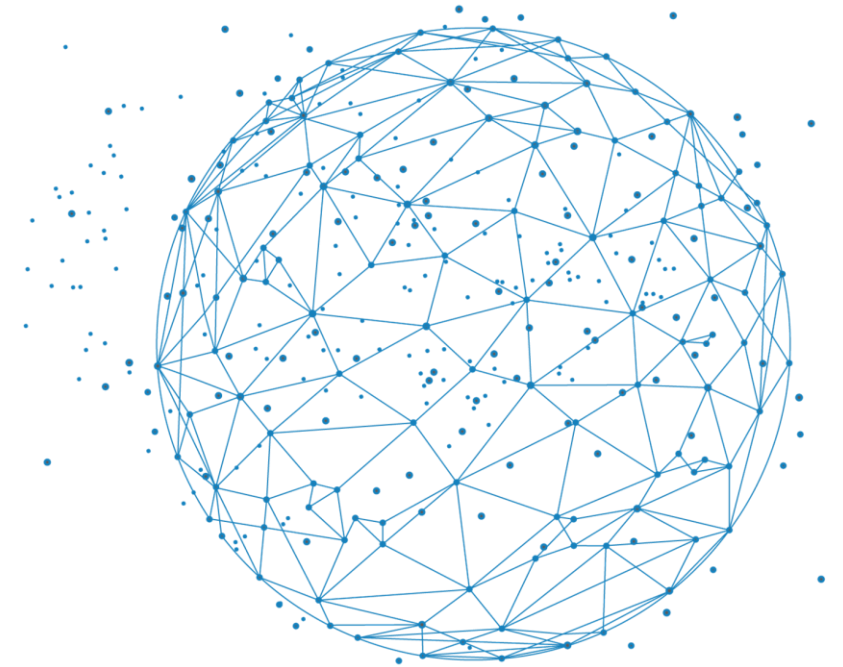
Parameter set n°K



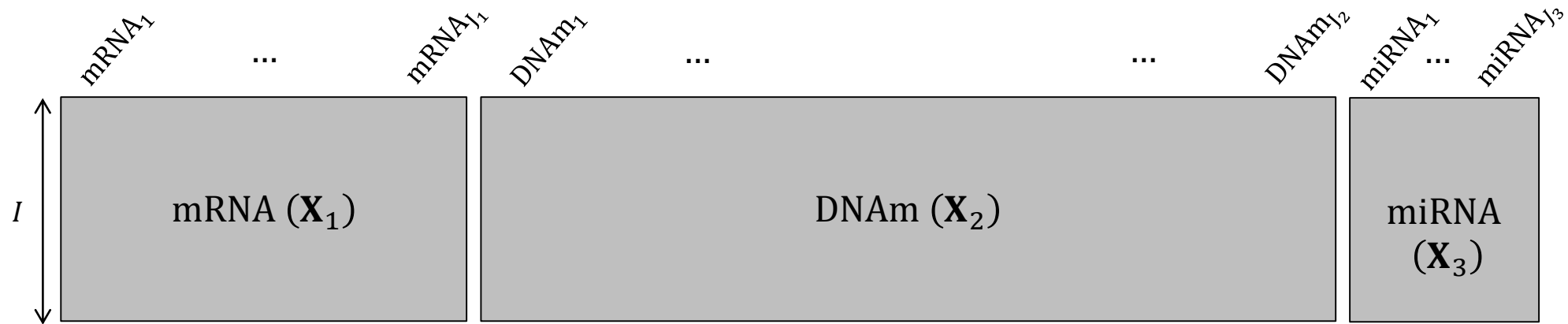
→ The set of parameters is unlikely to be selected.

Let us apply this permutation procedure on the MDD case study

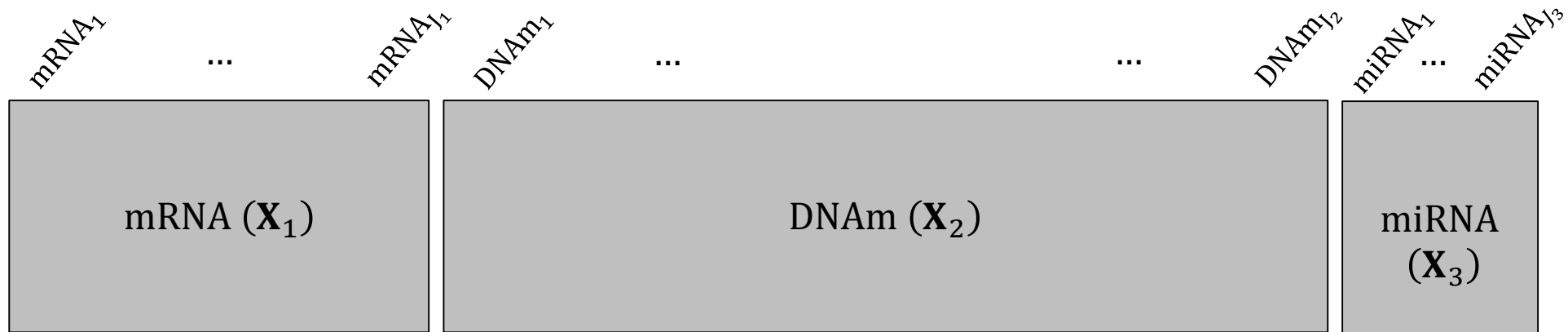
→ See section 3.3 on the Rmarkdown `MDD_case_study_RGCCA`



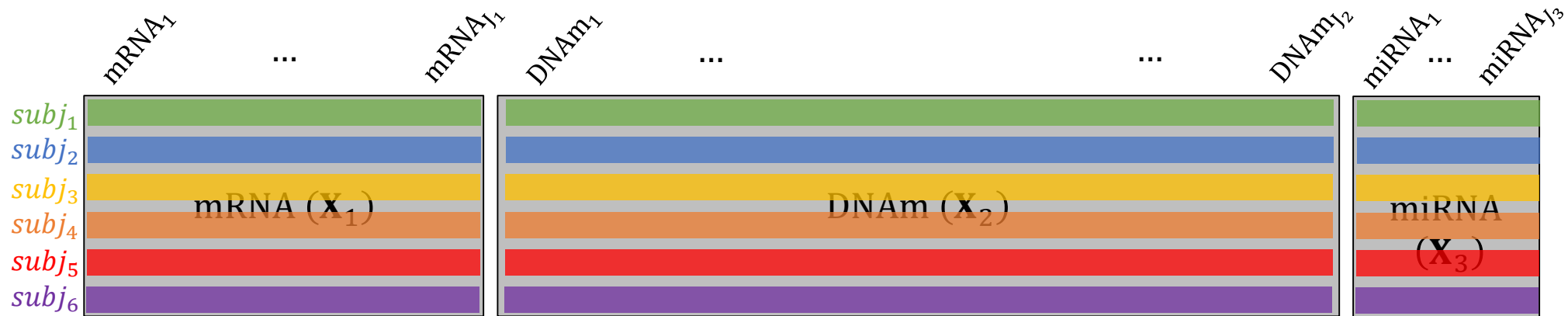
Evaluate the robustness of the model by bootstrapping.



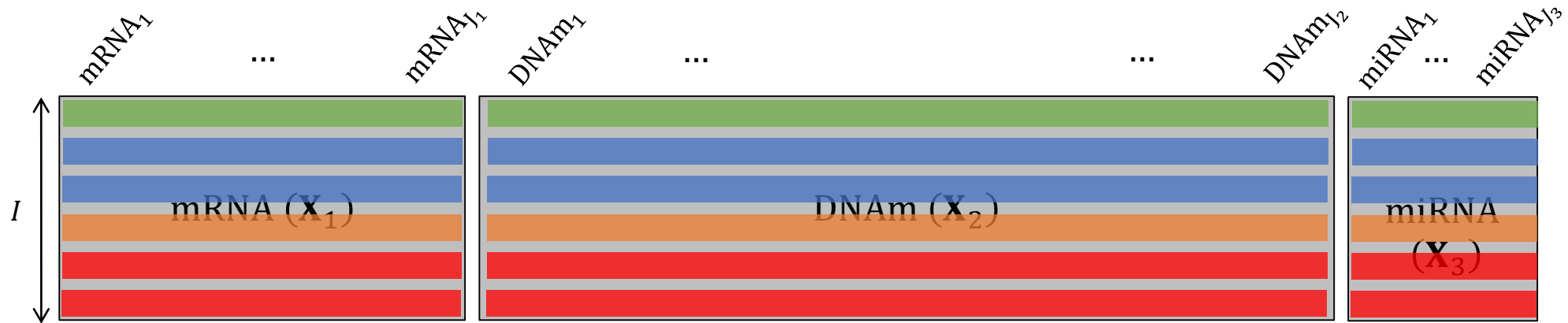
Evaluate the robustness of the model by bootstrapping.



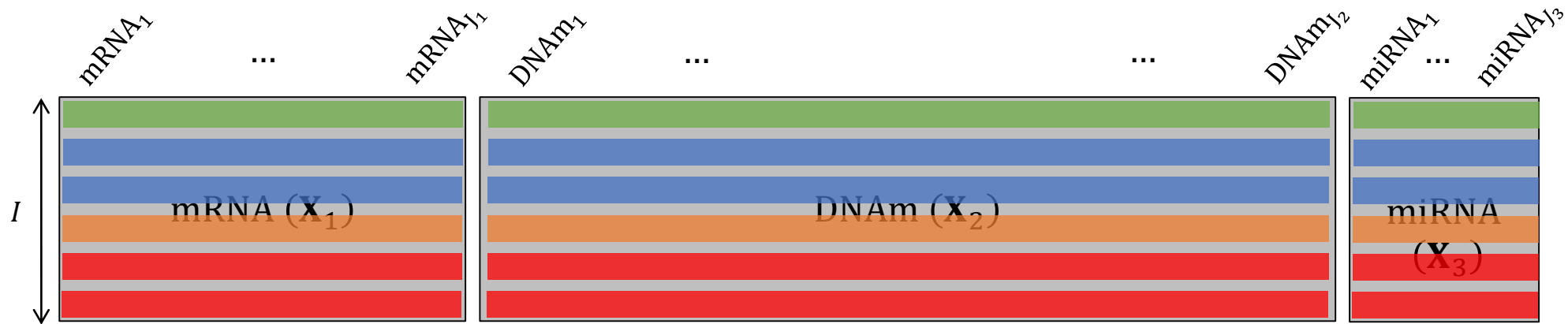
Evaluate the robustness of the model by bootstrapping.



Evaluate the robustness of the model by bootstrapping.

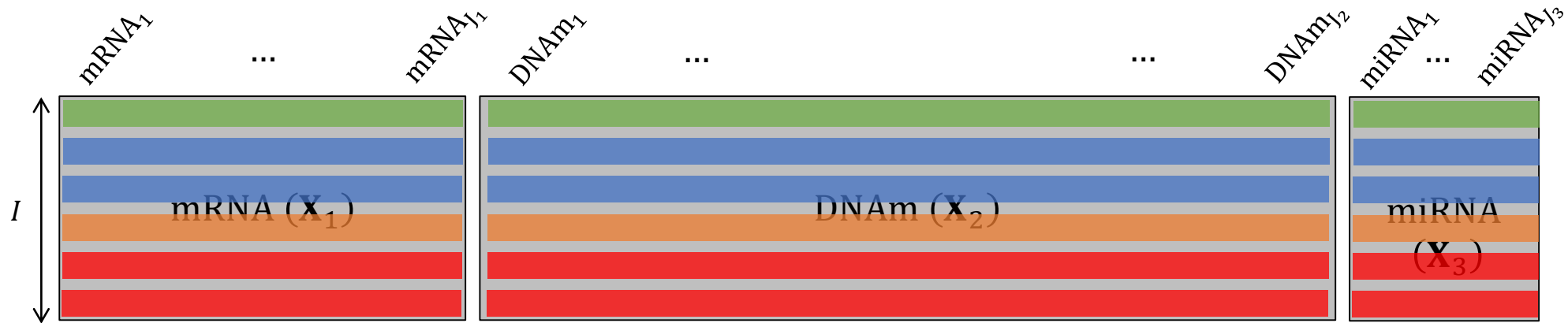


Evaluate the robustness of the model by bootstrapping.



Bootstrap sample n°1

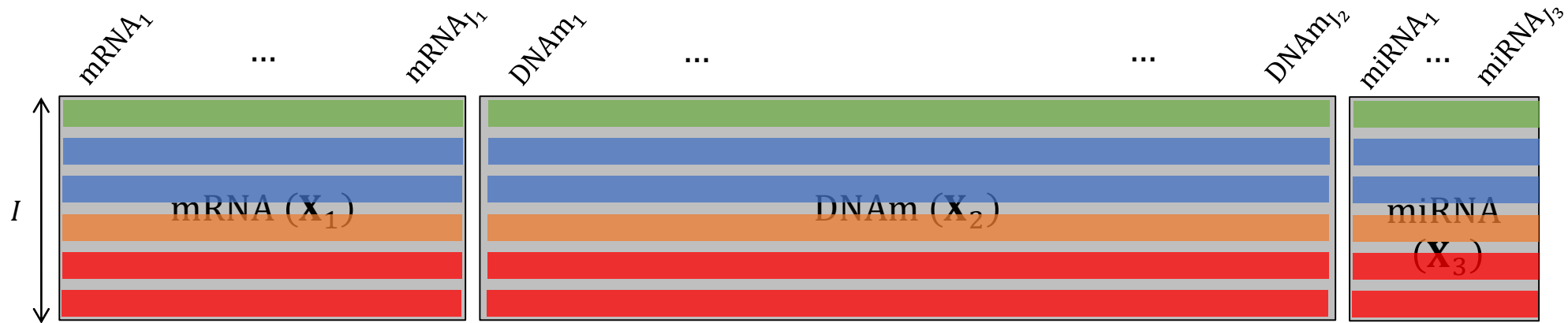
Evaluate the robustness of the model by bootstrapping.



Bootstrap sample n°1

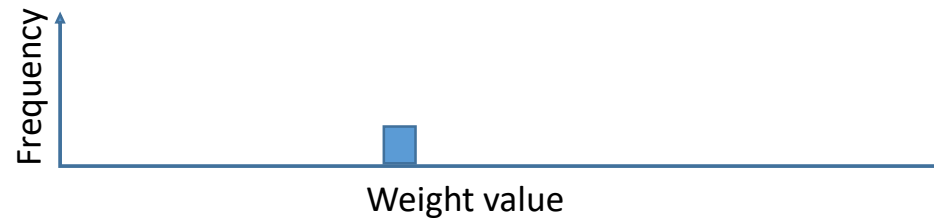
Weight for mRNA₁

Evaluate the robustness of the model by bootstrapping.

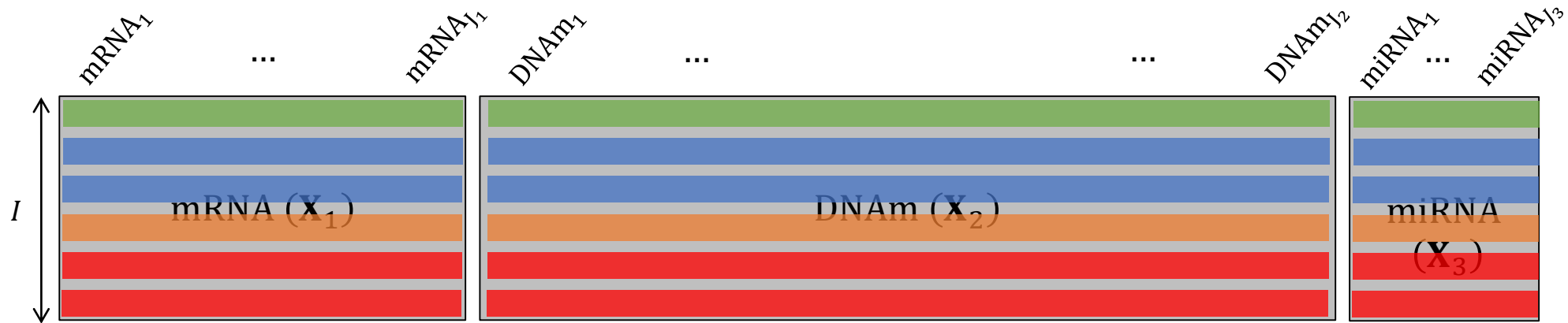


Bootstrap sample n°1

Weight for $mRNA_1$

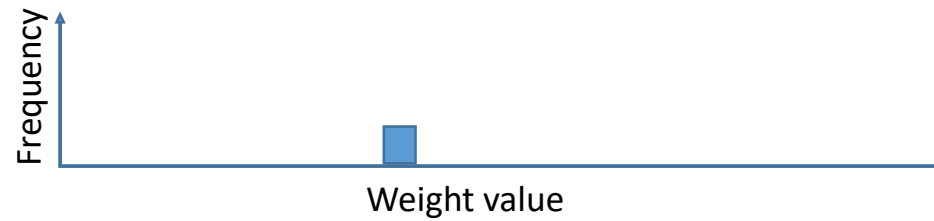


Evaluate the robustness of the model by bootstrapping.



Bootstrap sample n°1

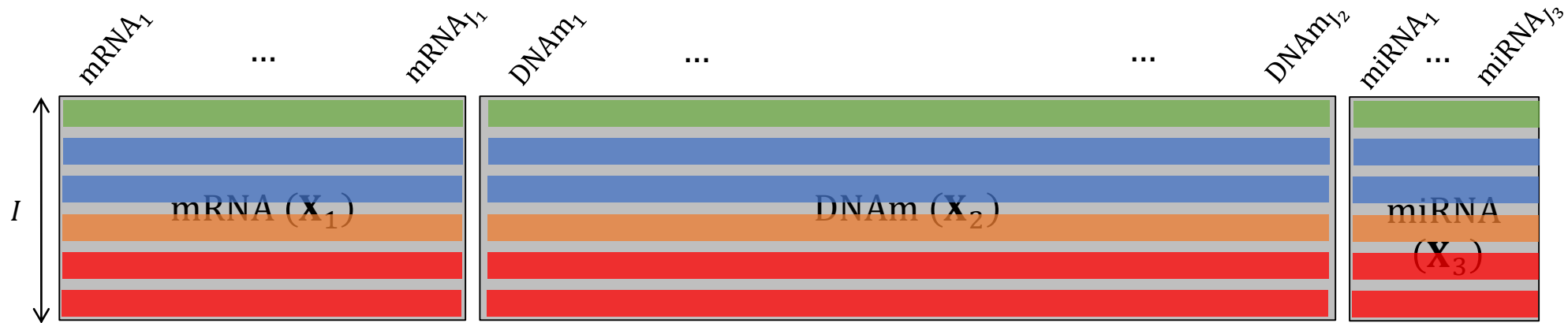
Weight for $mRNA_1$



⋮

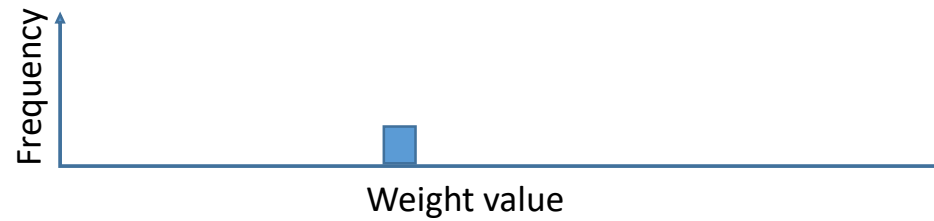
Weight for $miRNA_{j_3}$

Evaluate the robustness of the model by bootstrapping.



Bootstrap sample n°1

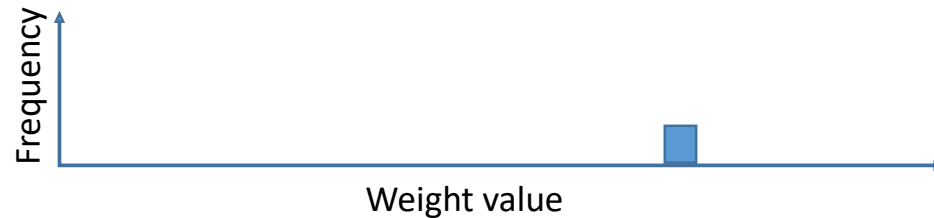
Weight for mRNA₁



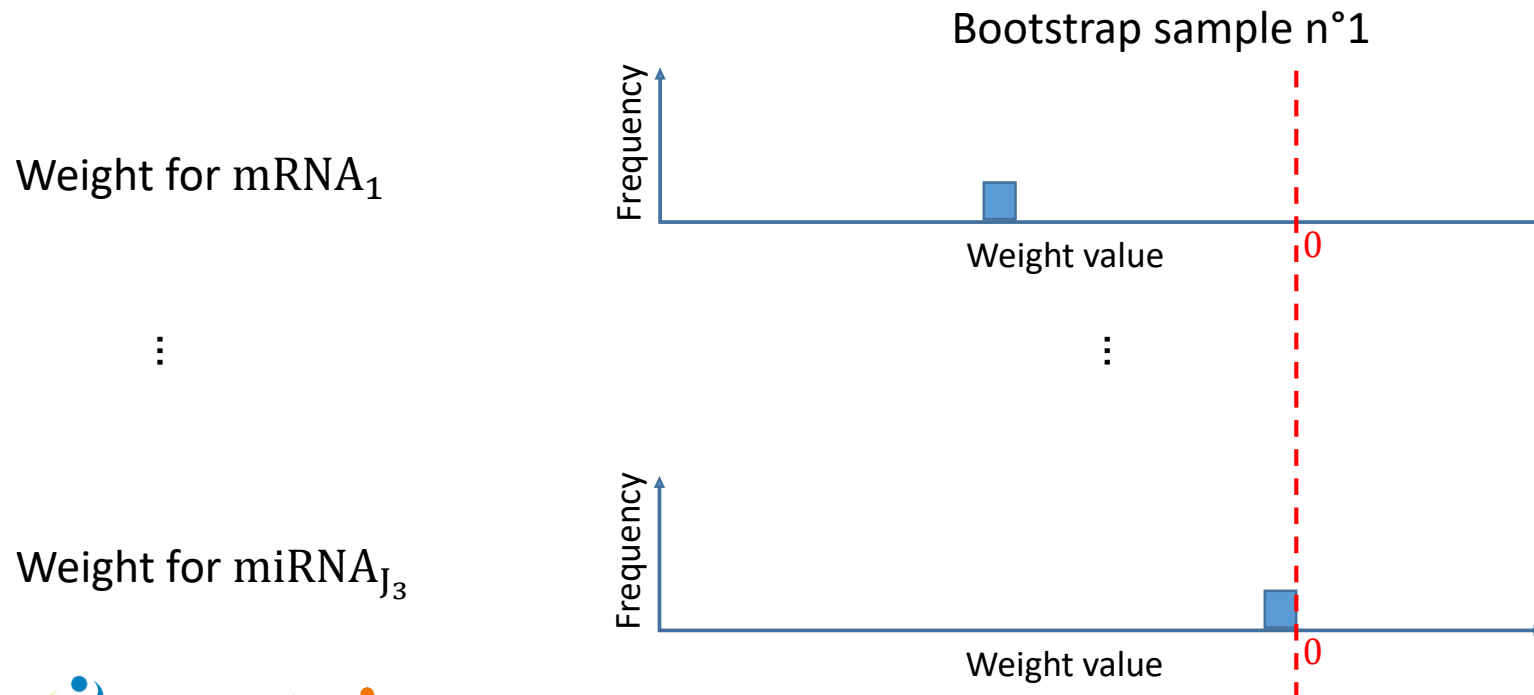
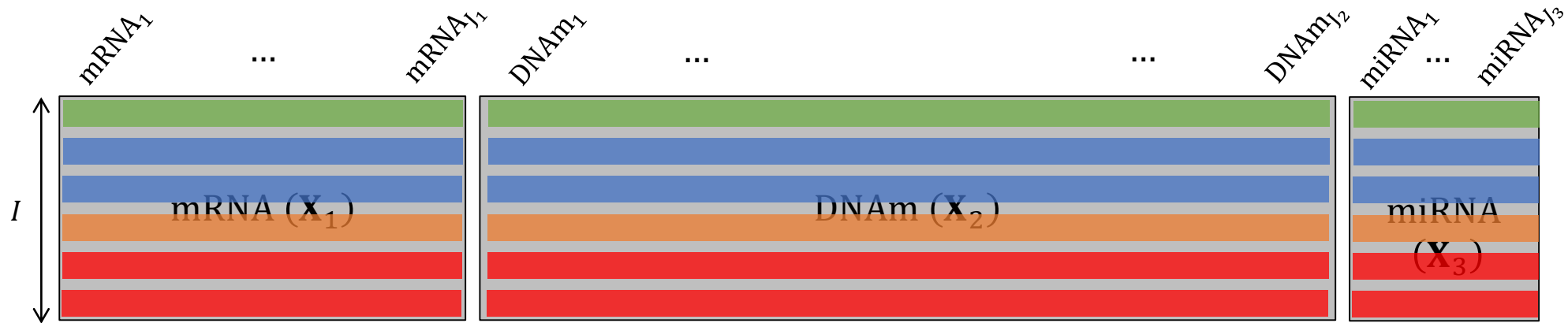
⋮

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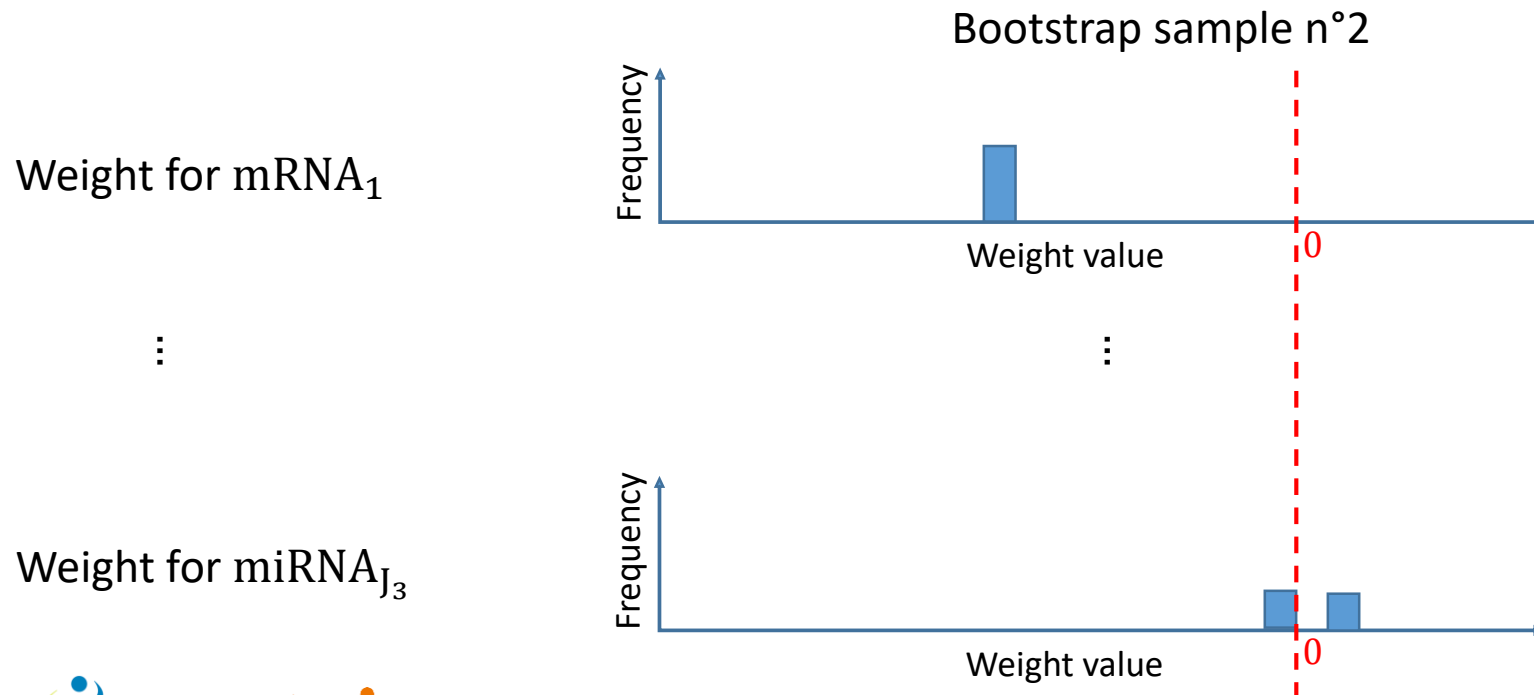
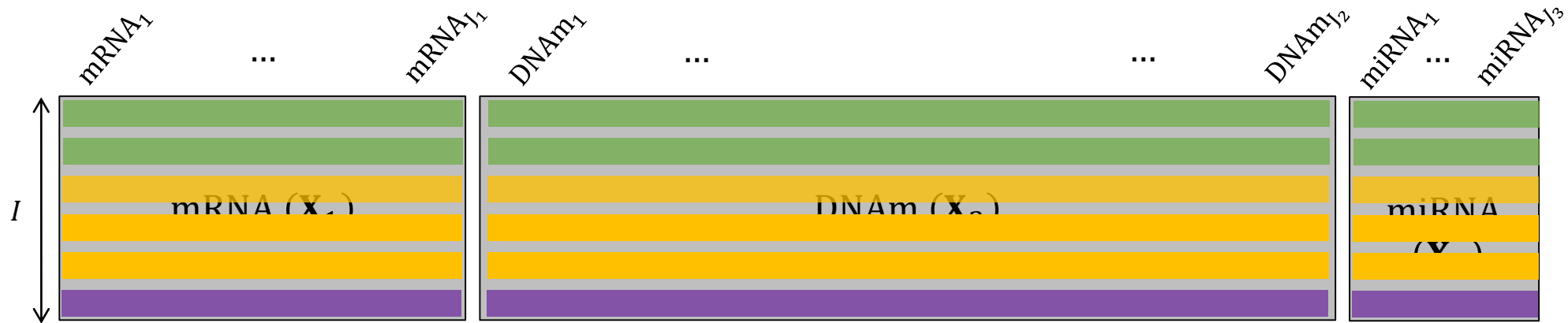
Weight for miRNA_{j₃}



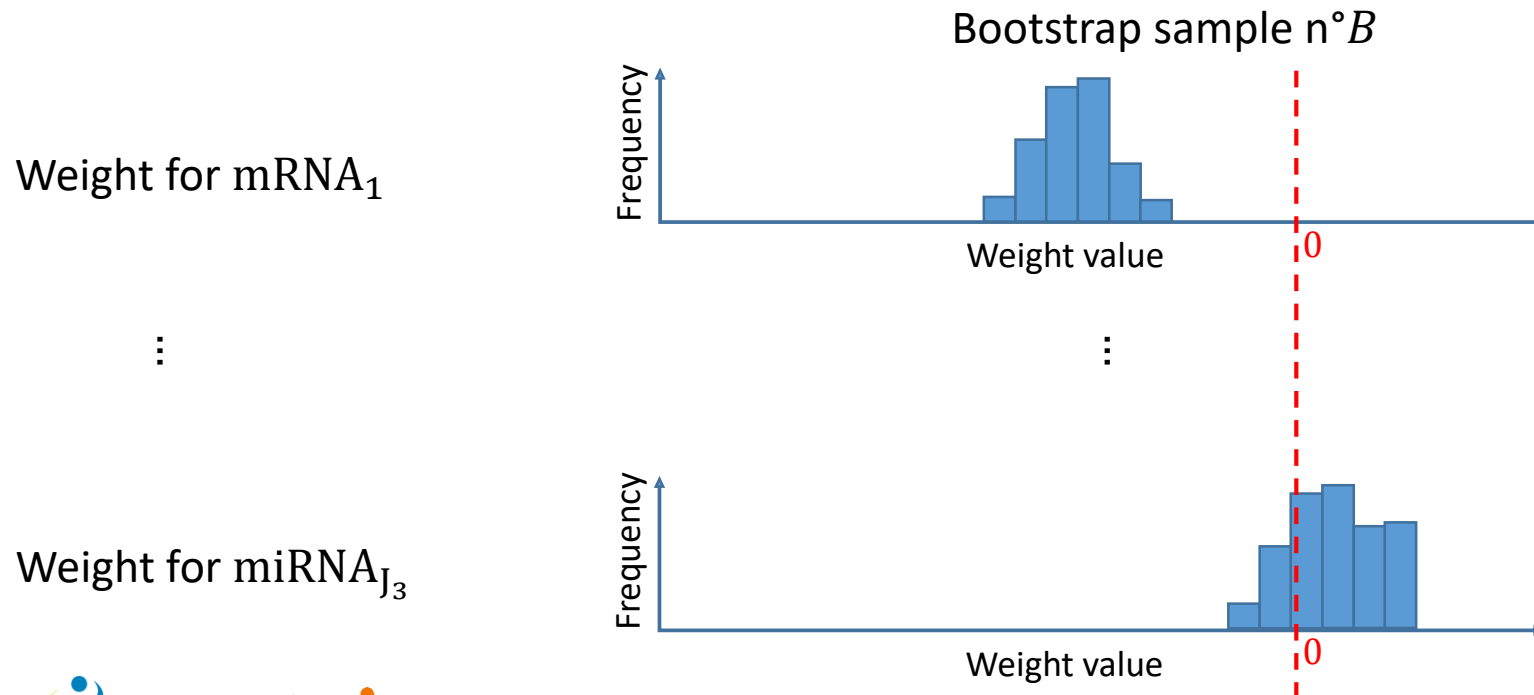
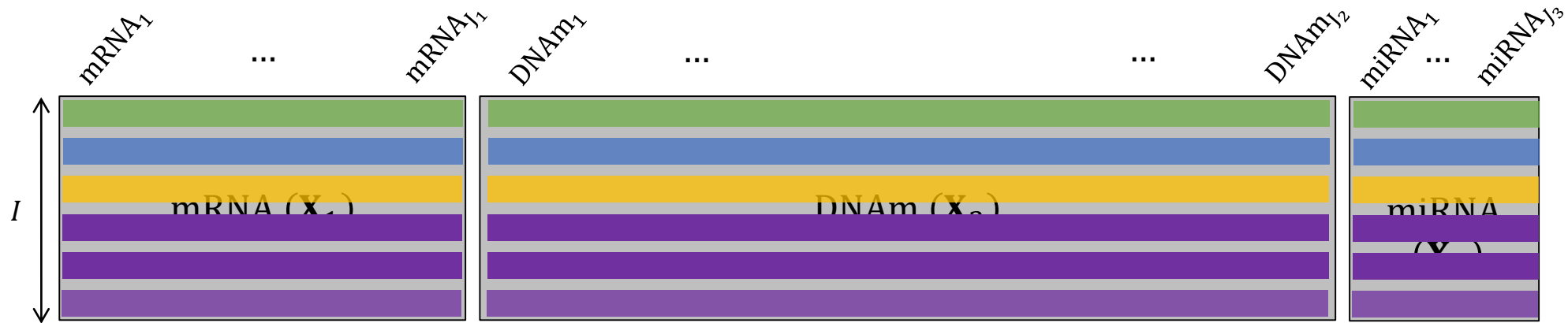
Evaluate the robustness of the model by bootstrapping.



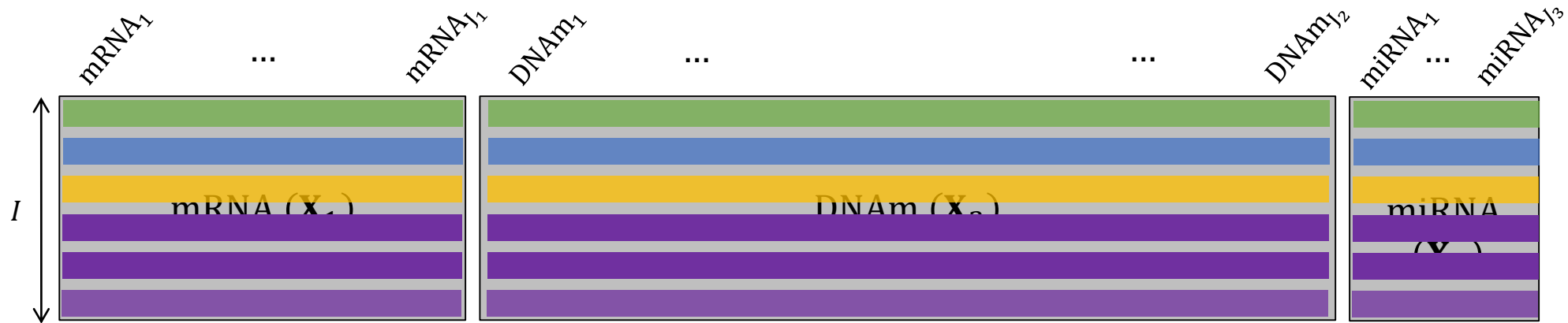
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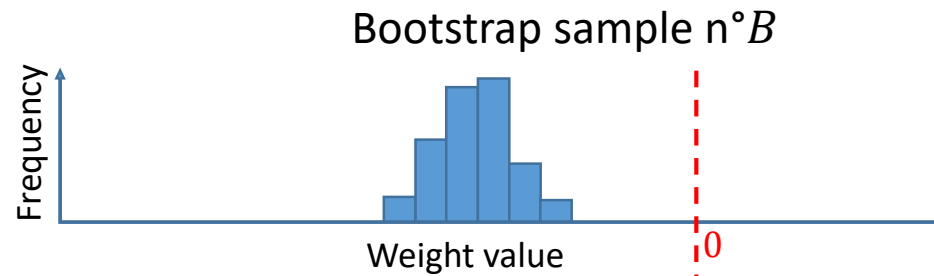
Evaluate the robustness of the model by bootstrapping.



Evaluate the robustness of the model by bootstrapping.



Weight for mRNA₁

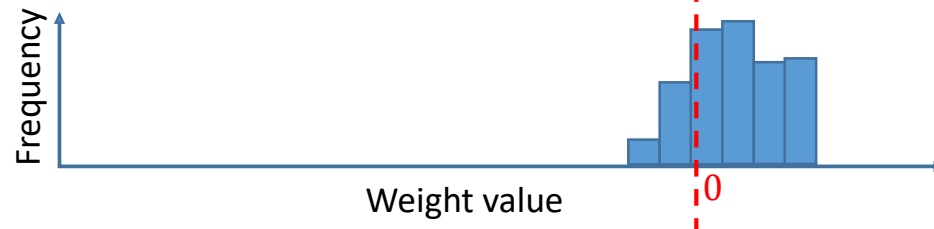


→ The weight is likely to be considered as it is significantly different from 0.

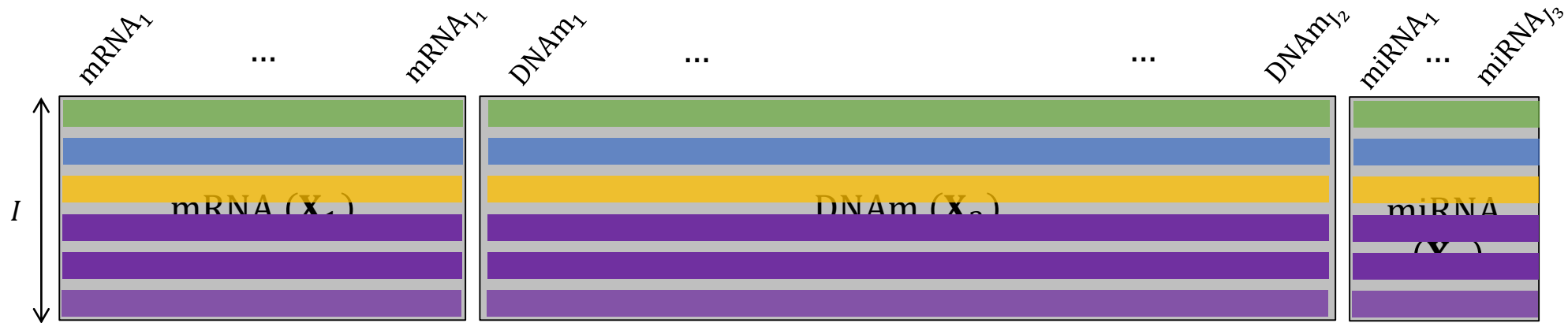
⋮

⋮

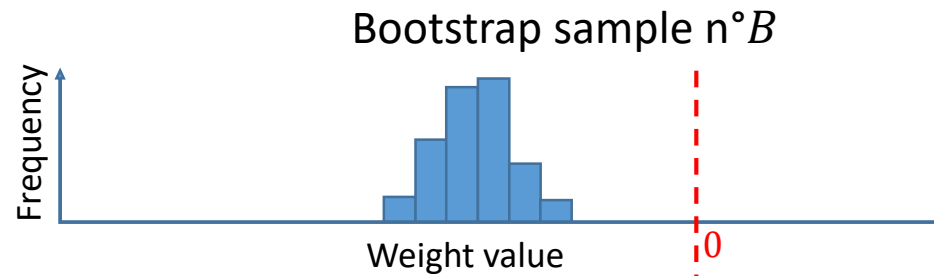
Weight for miRNA_{j₃}



Evaluate the robustness of the model by bootstrapping.



Weight for $mRNA_1$

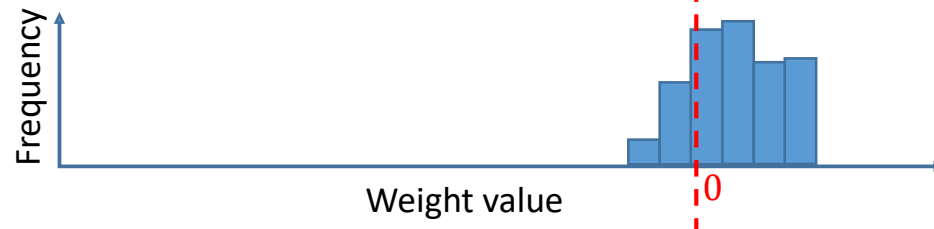


→ The weight is likely to be considered as It is significantly different from 0.

⋮

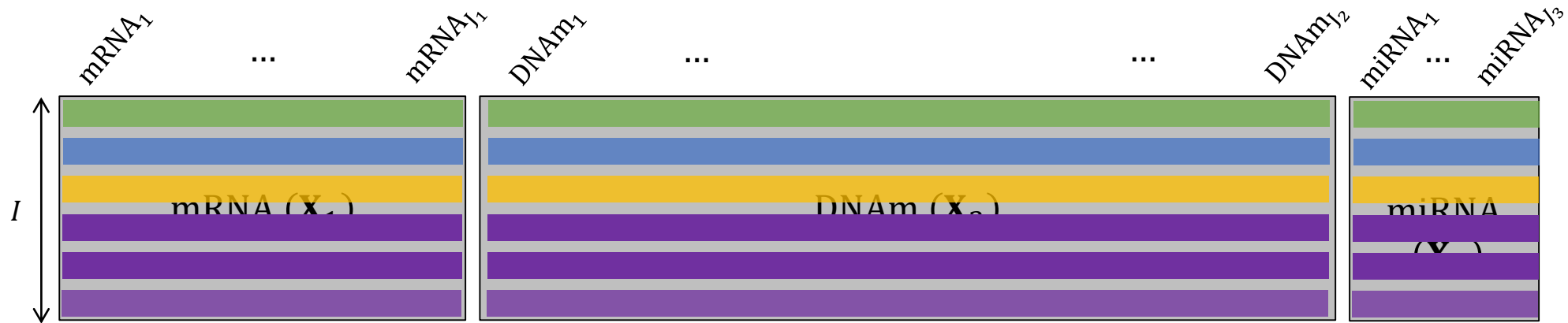
⋮

Weight for $miRNA_{j_3}$

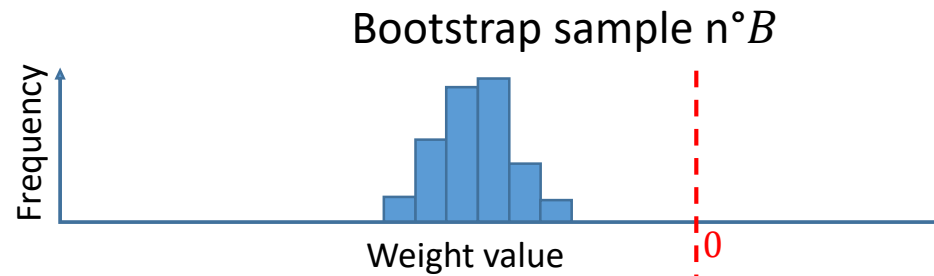


→ The weight is unlikely to be considered as It is not significantly different from 0.

Evaluate the robustness of the model by bootstrapping.



Weight for mRNA₁

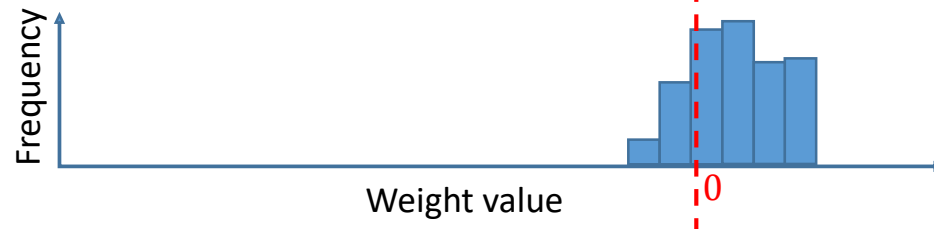


→ The weight is likely to be considered as It is significantly different from 0.

⋮

Out of these distributions, RGCCA non-parametrically estimates confidence intervals ($[q_{0.025}, q_{0.975}]$) and p-values ($\min(Nb_{\geq 0}, Nb_{\leq 0}) / \max(Nb_{\geq 0}, Nb_{\leq 0})$).

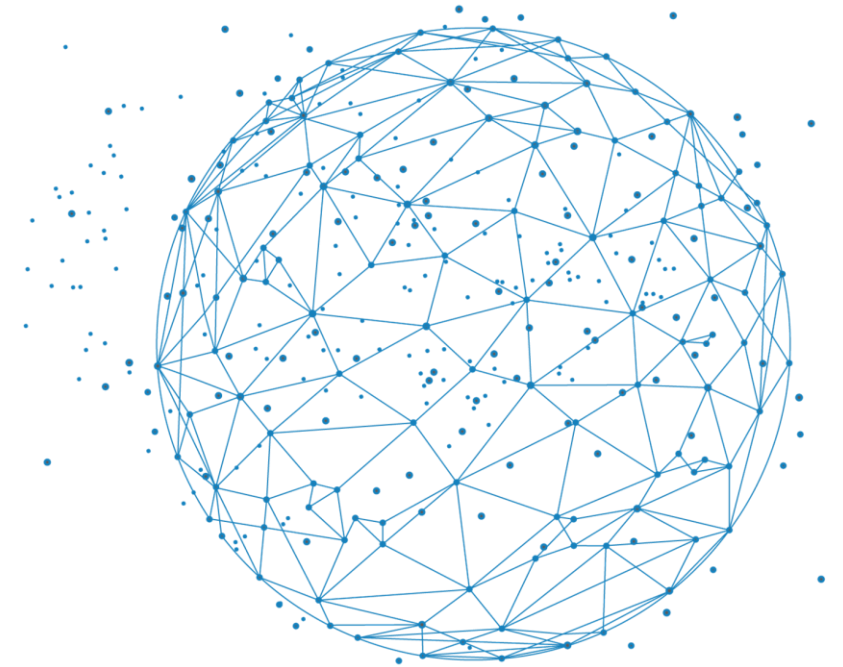
Weight for miRNA_{j₃}



→ The weight is unlikely to be considered as It is not significantly different from 0.

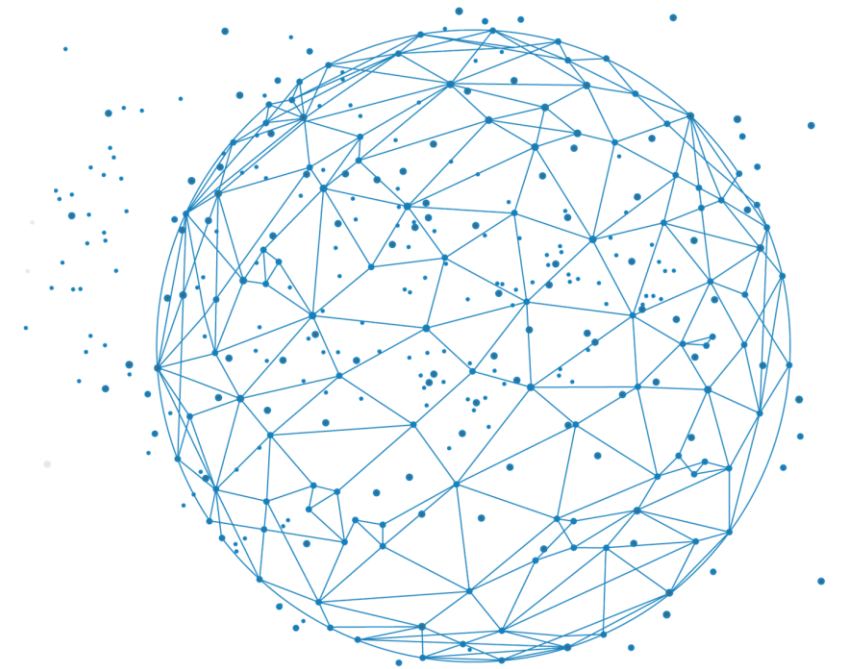
Let us apply this permutation procedure on the MDD case study

→ See section 3.4 on the Rmarkdown ``MDD_case_study_RGCCA``

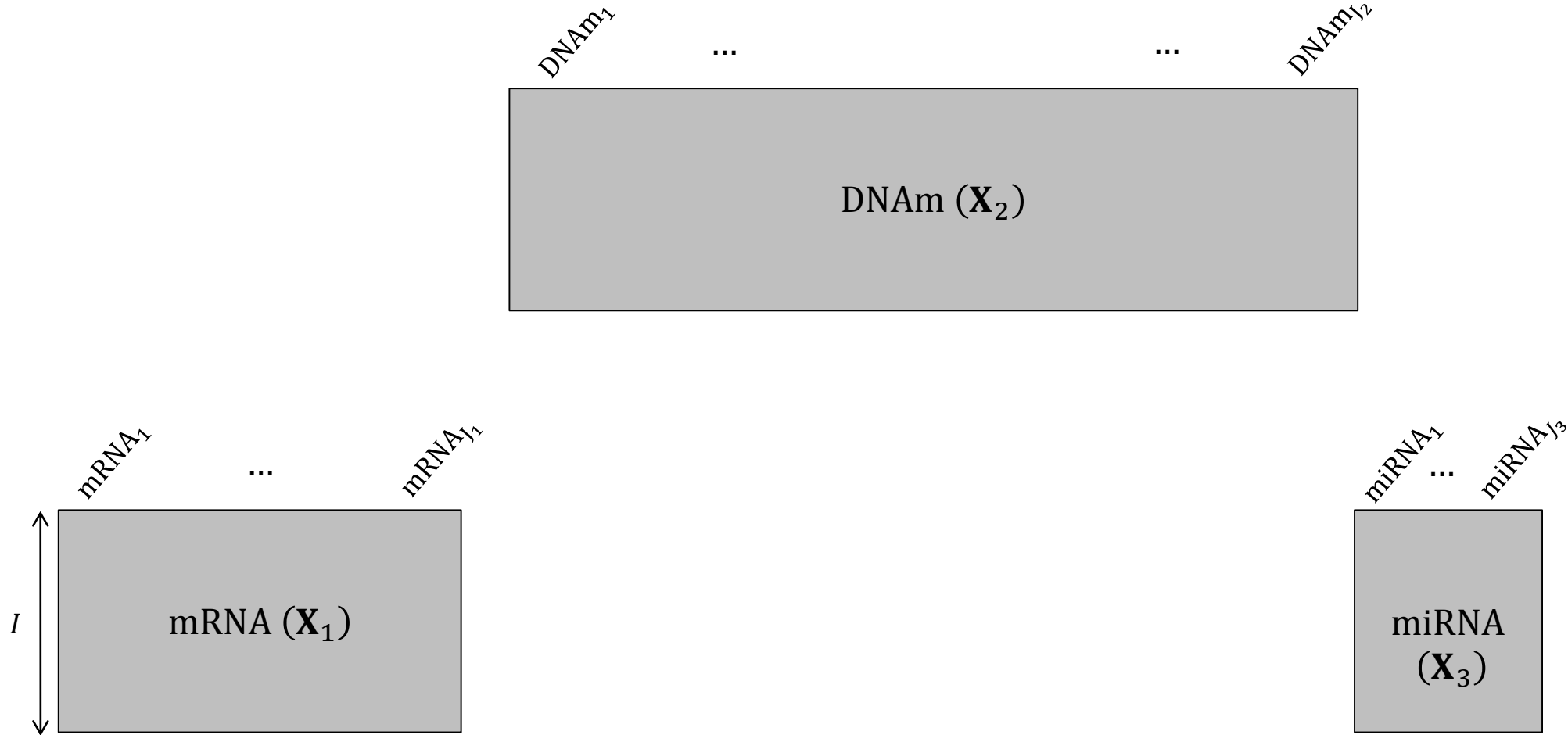


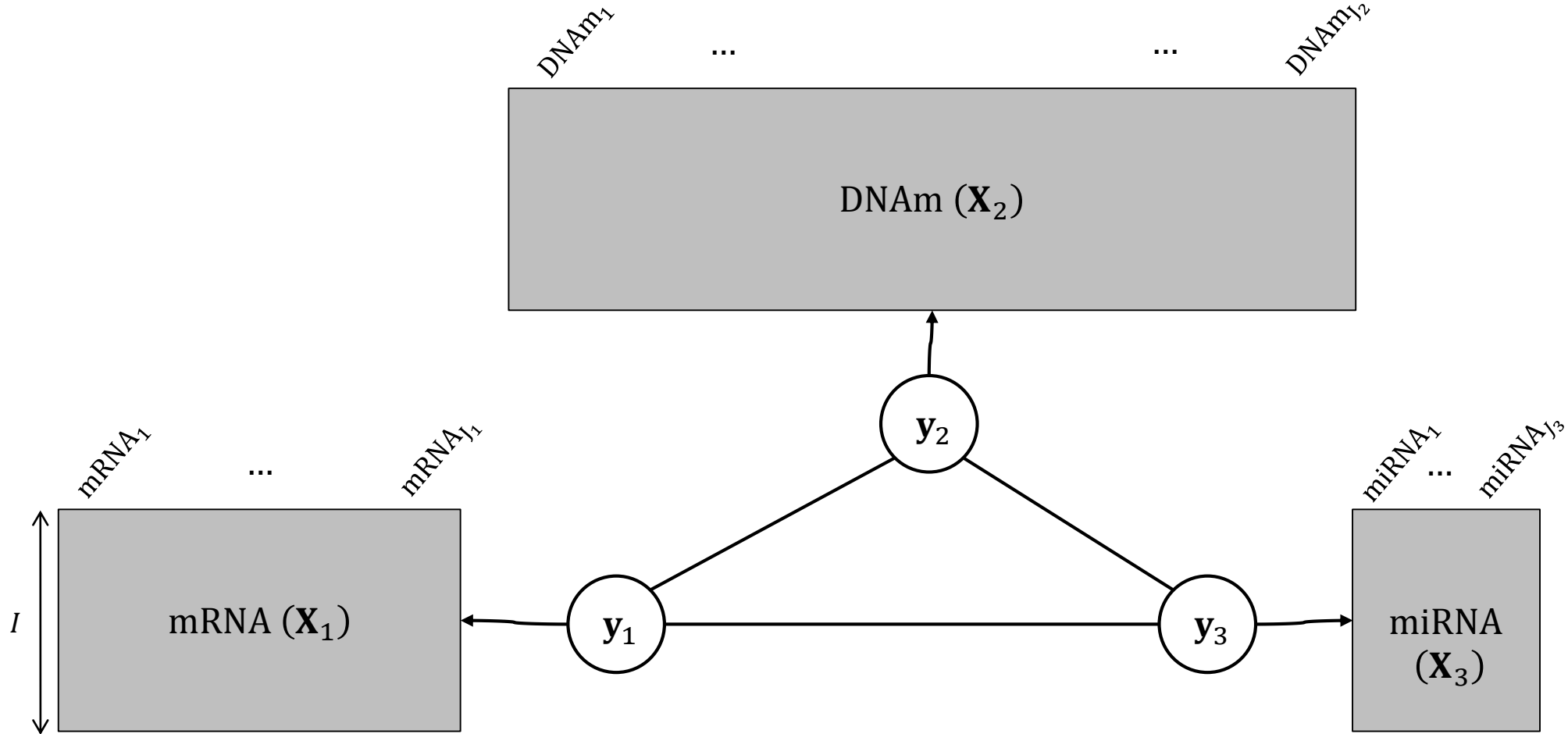
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3. Unsupervised analysis with two-blocks:
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5. **Supervised analysis with RGCCA**
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Sparse Generalized Canonical Correlation Analysis (SGCCA)
7. The flexible Optimization Framework of RGCCA

- ❖ The general principal
- ❖ Extension to multi-way analysis
- ❖ From Sequential to Global

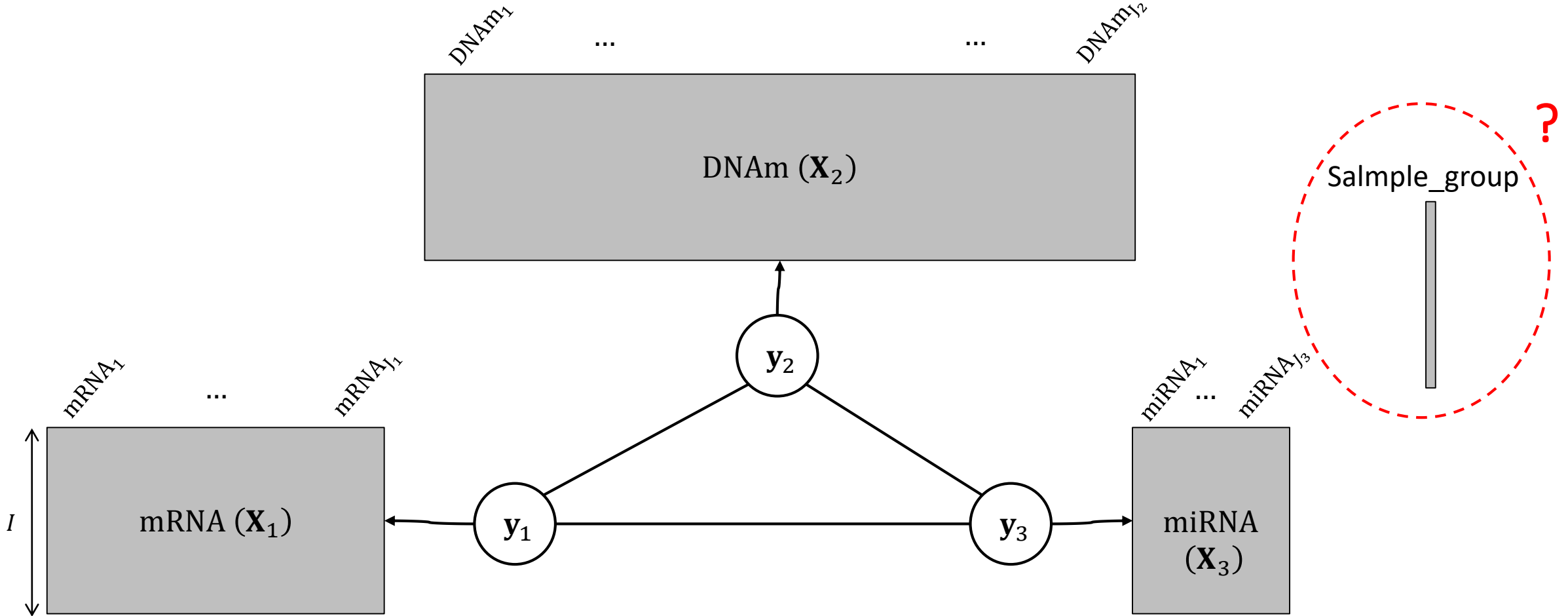


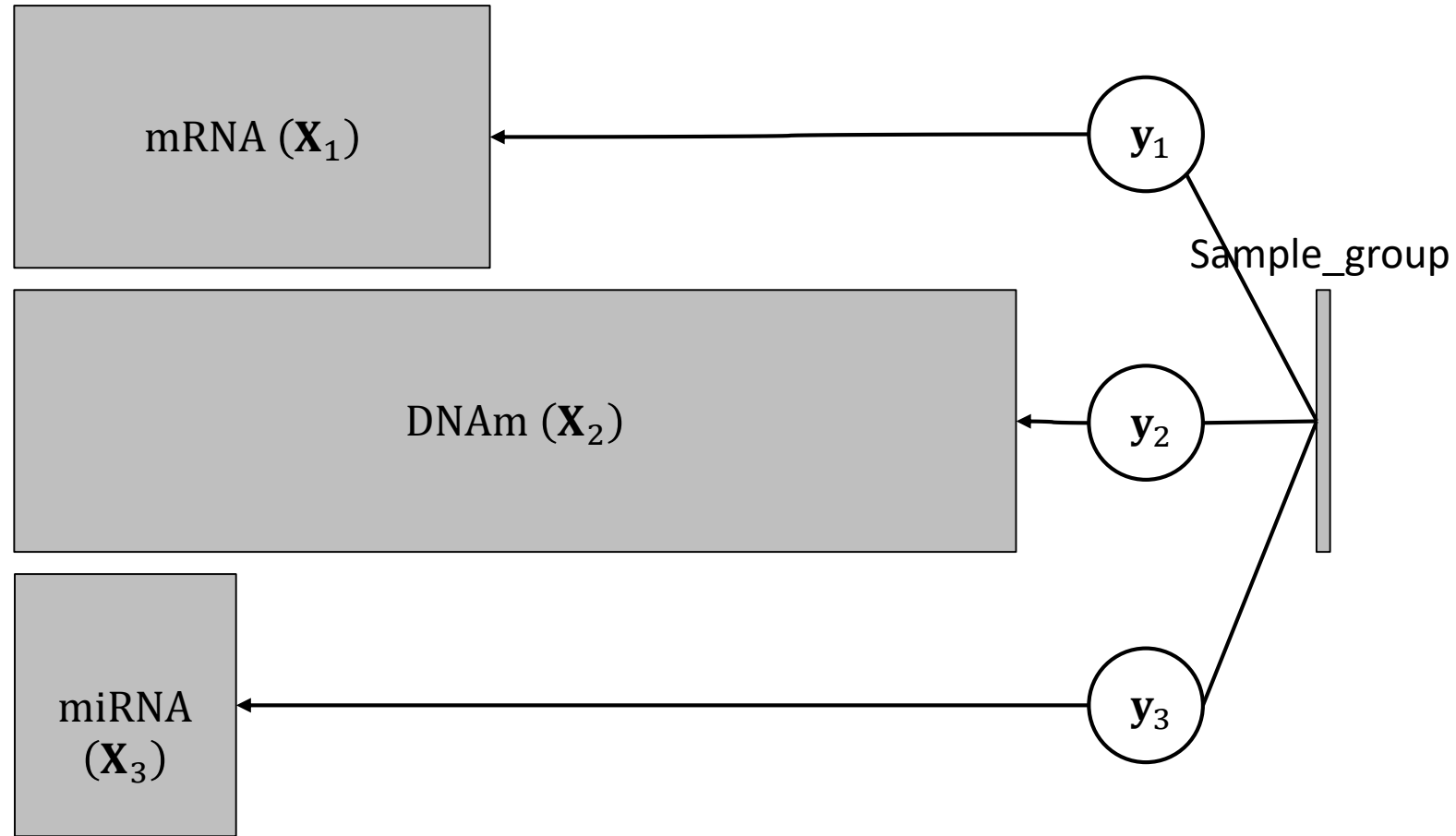
Supervising with RGCCA



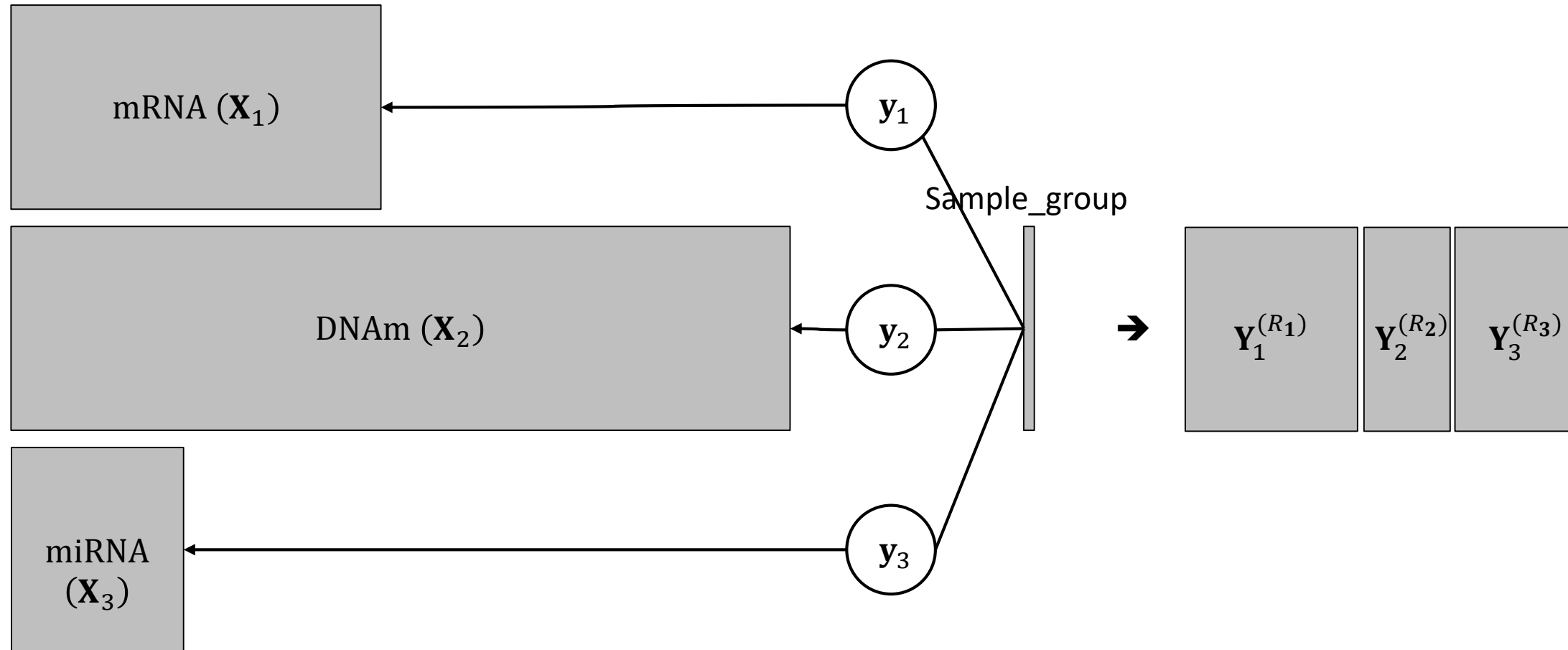


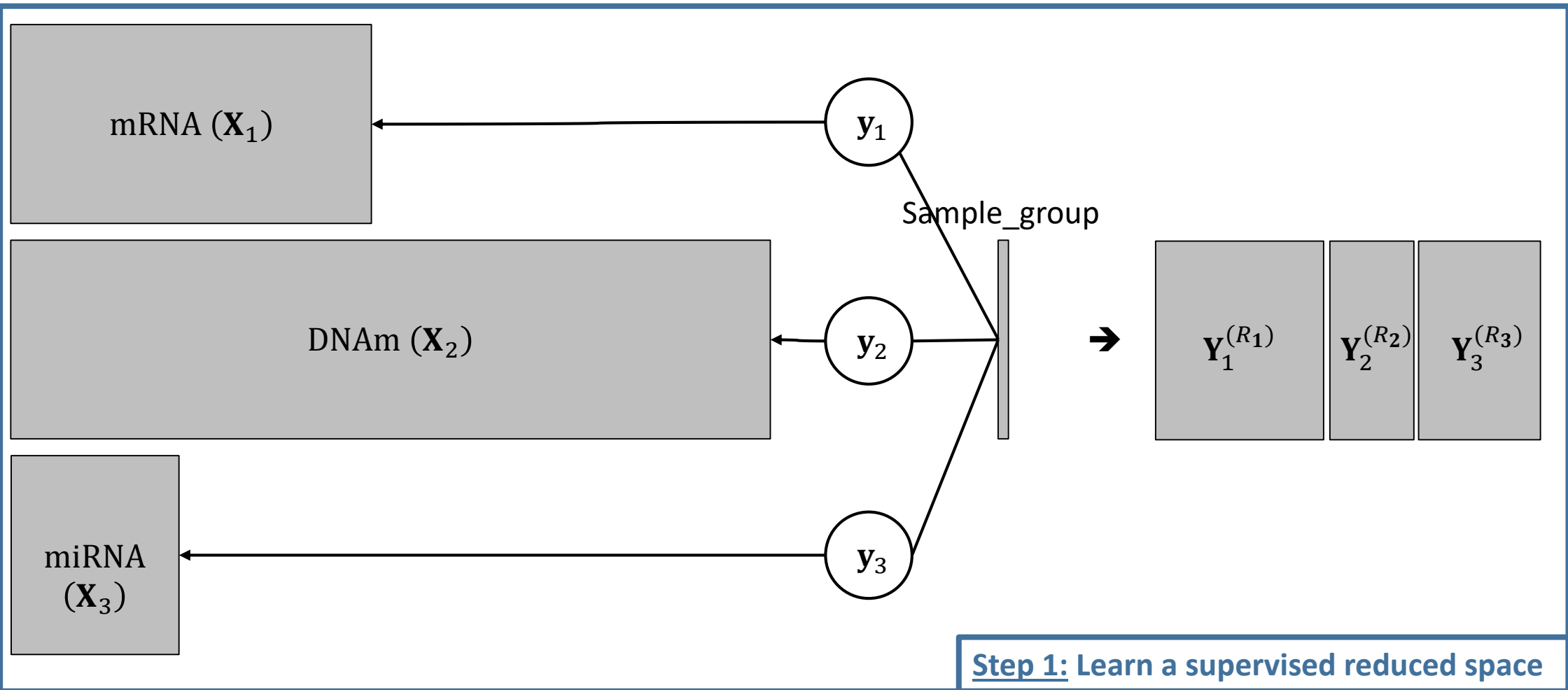
Supervising with RGCCA



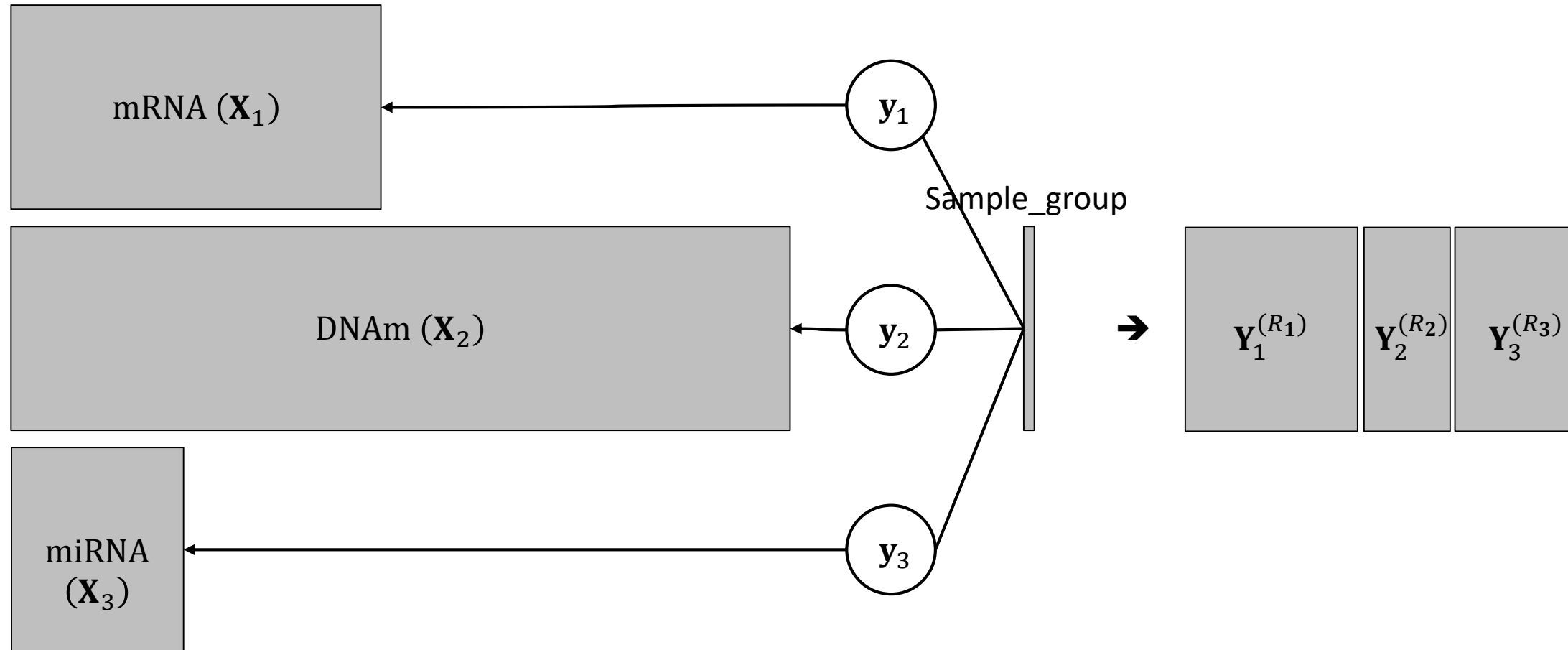


Supervising with RGCCA

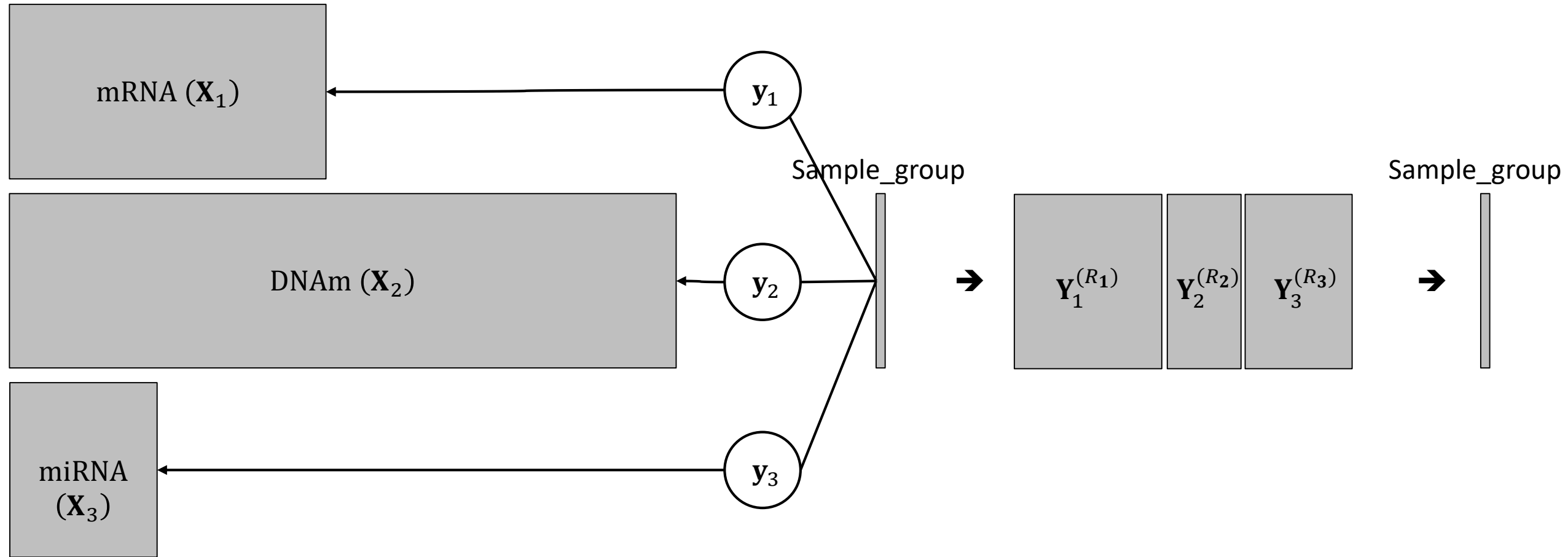




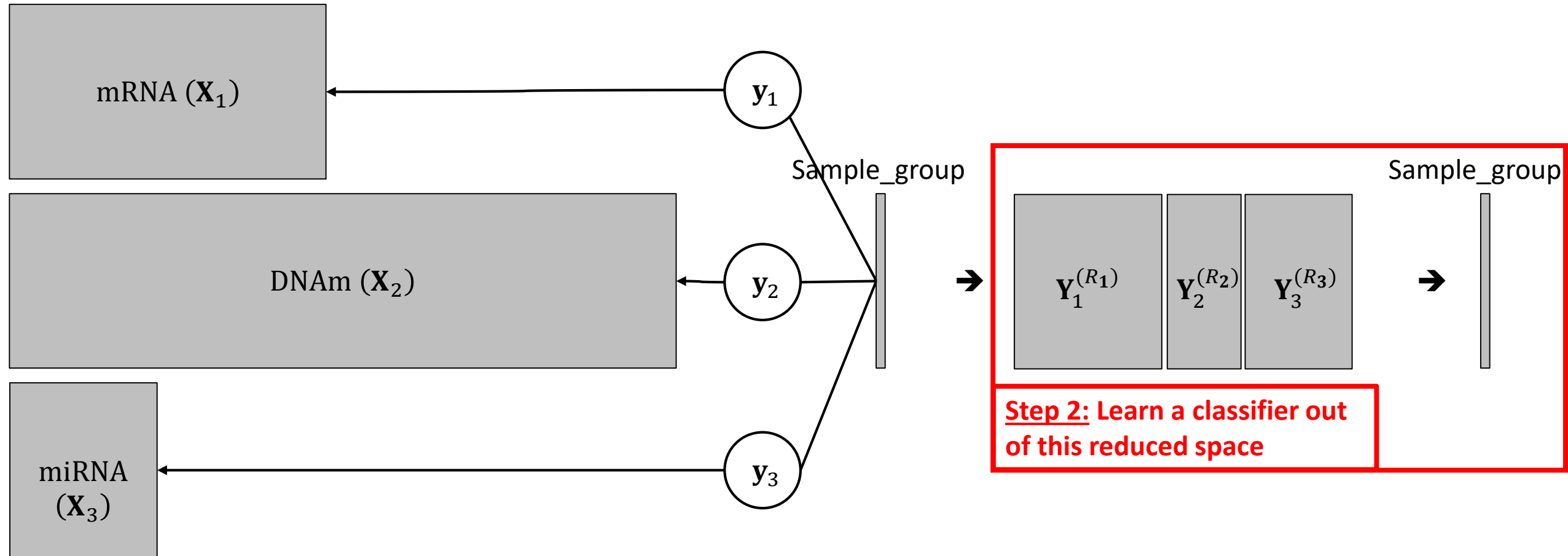
Supervising with RGCCA



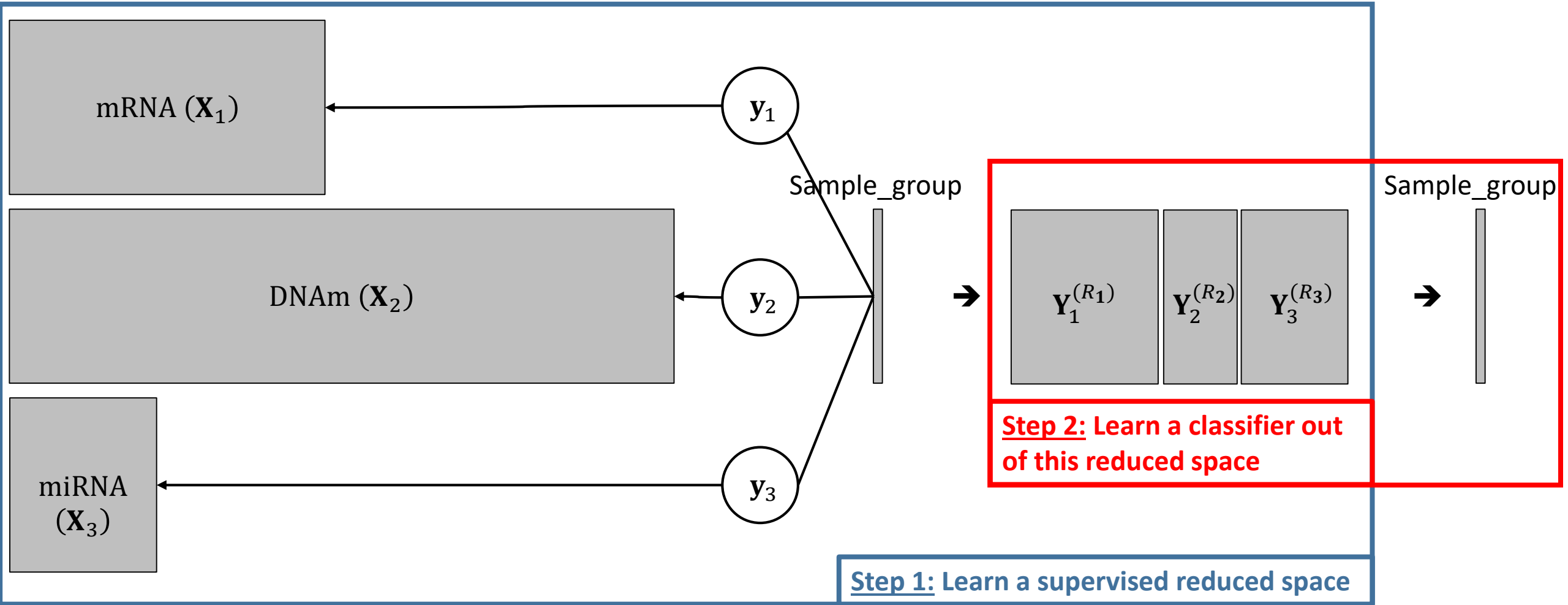
Supervising with RGCCA

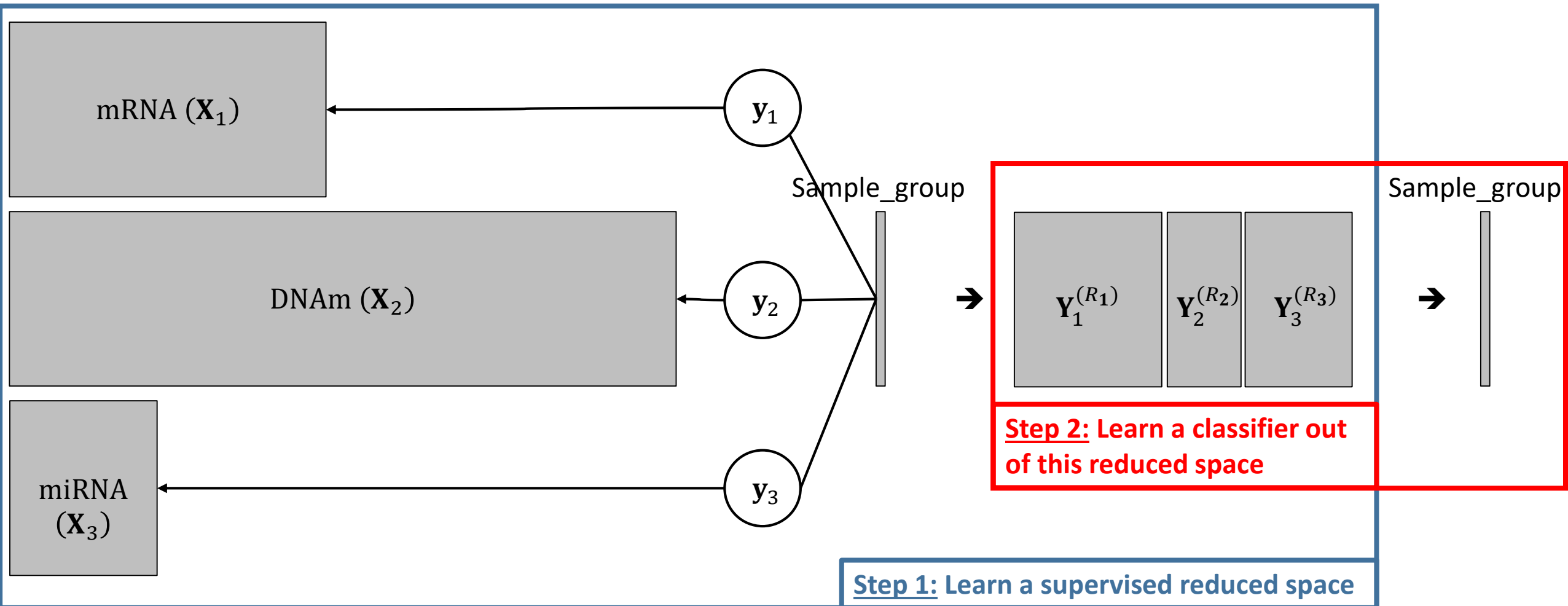


Supervising with RGCCA



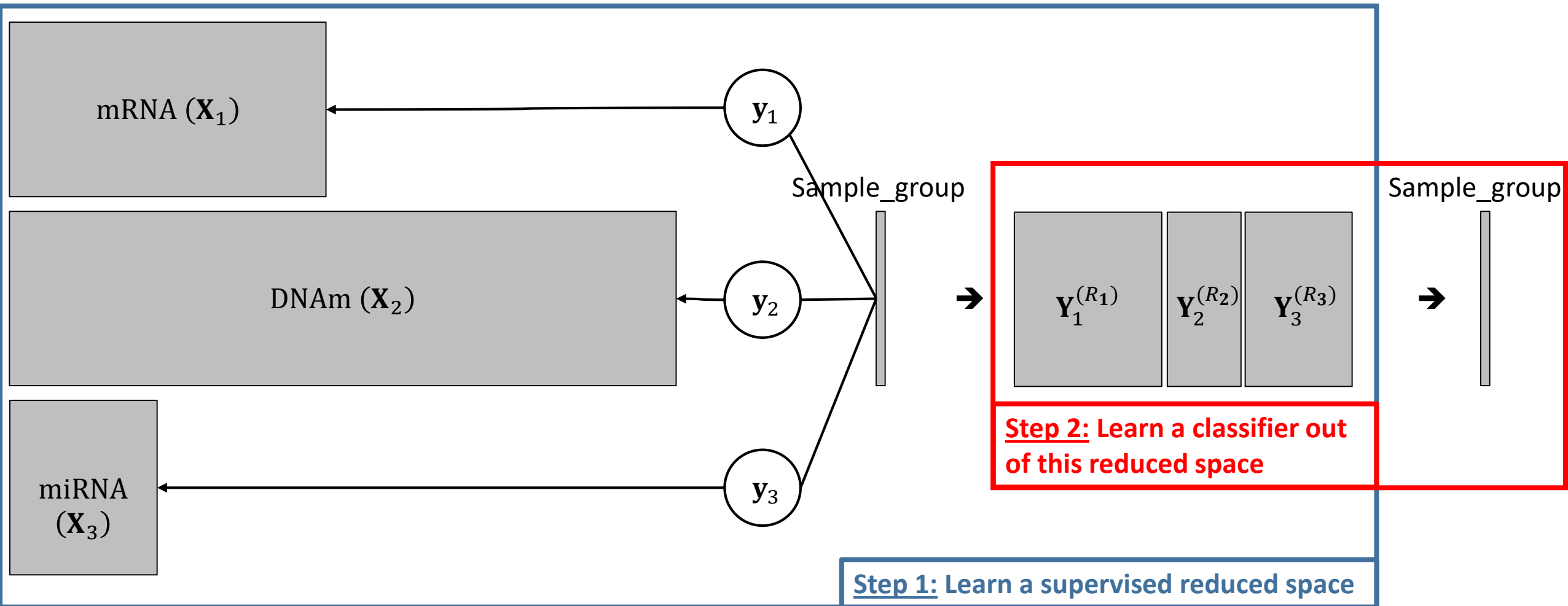
Supervising with RGCCA





➡ The model sequentially learn block-weight vectors to compute components and a classifier.

Supervising with RGCCA



➡ The model sequentially learn block-weight vectors to compute components and a classifier. ➡ Standard Cross-Validation can be performed.





Confusion Matrix:

		True labels	
		Positive	Negative
Predicted labels	Positive	True Positive (TP)	False Positive (FP)
	Negative	False Negative (FN)	True Negative (TN)



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$$precision = \frac{TP}{TP + FP}$$

→ How many positive predicted labels are true ?



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$$recall = \frac{TP}{TP + FN}$$

→ How many true positive labels are retrieved ?



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		True labels	
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→ How many positive predicted labels are true ?

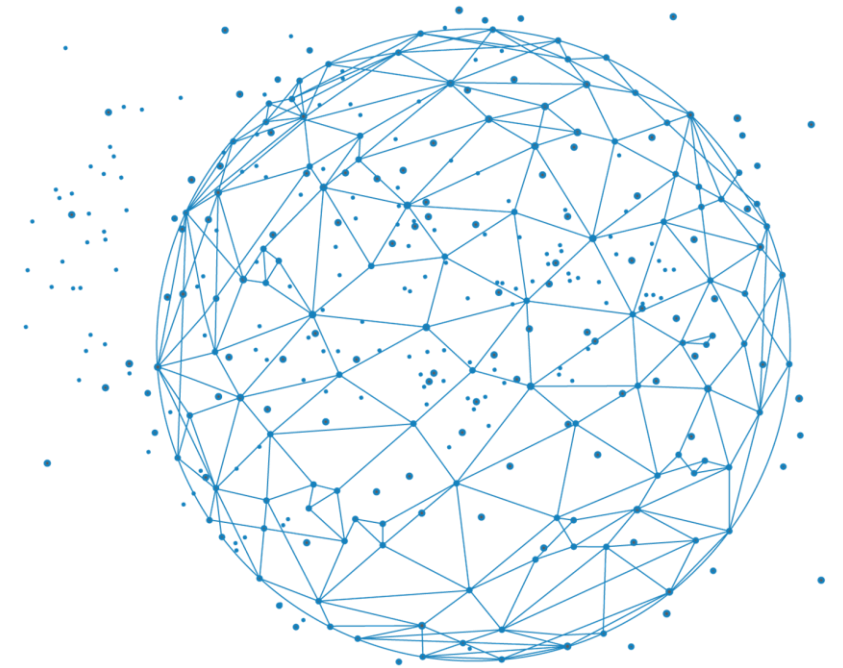
$$recall = \frac{TP}{TP + FN}$$

→ How many true positive labels are retrieved ?

$$F = \frac{2}{\frac{1}{recall} + \frac{1}{precision}} = \frac{2precision \cdot recall}{recall + precision}$$

Let us apply a supervised version of RGCCA on the MDD case study

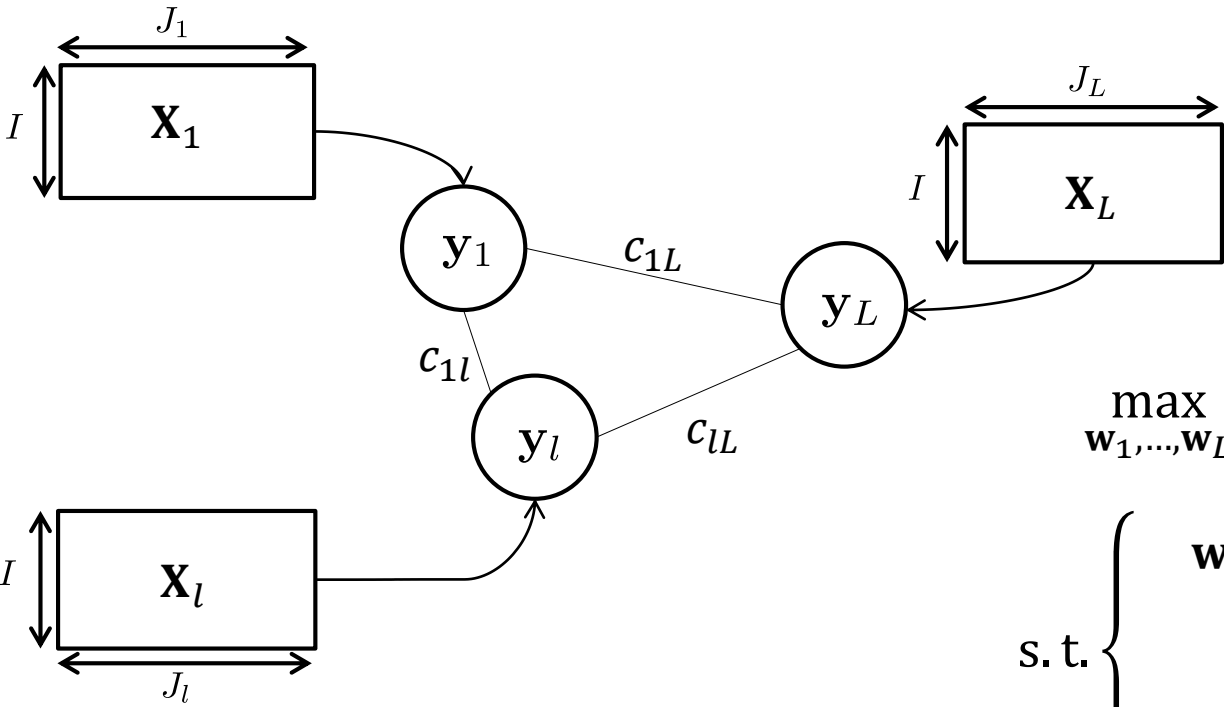
→ See section 4 on the Rmarkdown `MDD_case_study_RGCCA`



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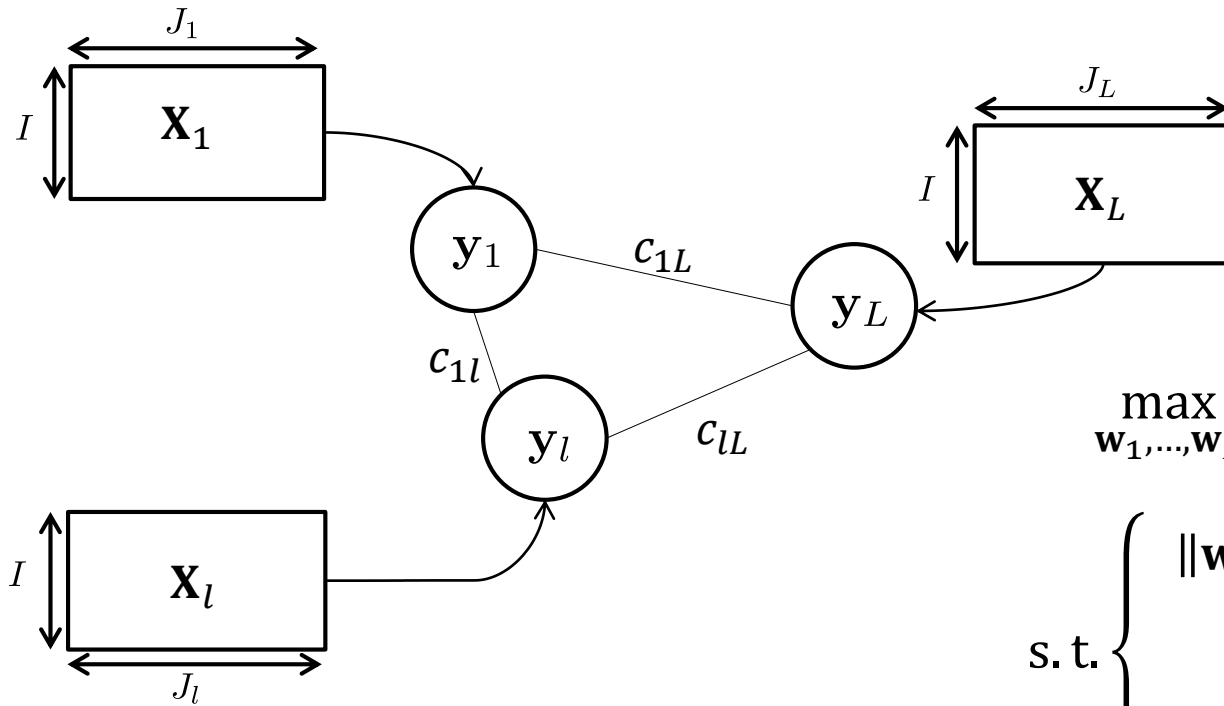
Sparse Generalized Canonical Correlation Analysis (SGCCA)



$$\max_{\mathbf{w}_1, \dots, \mathbf{w}_L} \sum_{k,l=1}^L c_{kl} g(\text{Cov}(\mathbf{X}_k \mathbf{w}_k, \mathbf{X}_l \mathbf{w}_l))$$

$$\text{s. t. } \left\{ \begin{array}{l} \mathbf{w}_l^T \mathbf{M}_l \mathbf{w}_l = 1 \\ , l = 1, \dots, L. \end{array} \right.$$

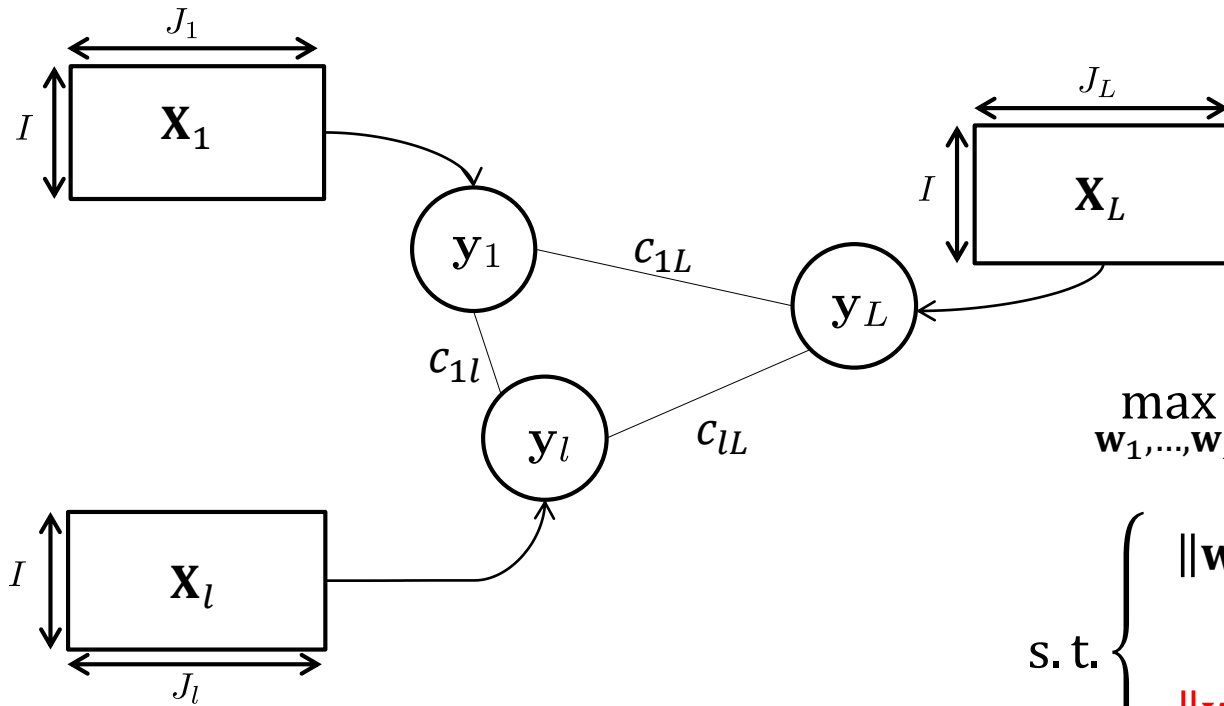
Sparse Generalized Canonical Correlation Analysis (SGCCA)



$$\max_{\mathbf{w}_1, \dots, \mathbf{w}_L} \sum_{k,l=1}^L c_{kl} g(\text{Cov}(\mathbf{X}_k \mathbf{w}_k, \mathbf{X}_l \mathbf{w}_l))$$

$$\text{s. t. } \left\{ \begin{array}{l} \|\mathbf{w}_l\|_2^2 = 1 \\ \phantom{\|\mathbf{w}_l\|_2^2 = 1}, l = 1, \dots, L. \end{array} \right.$$

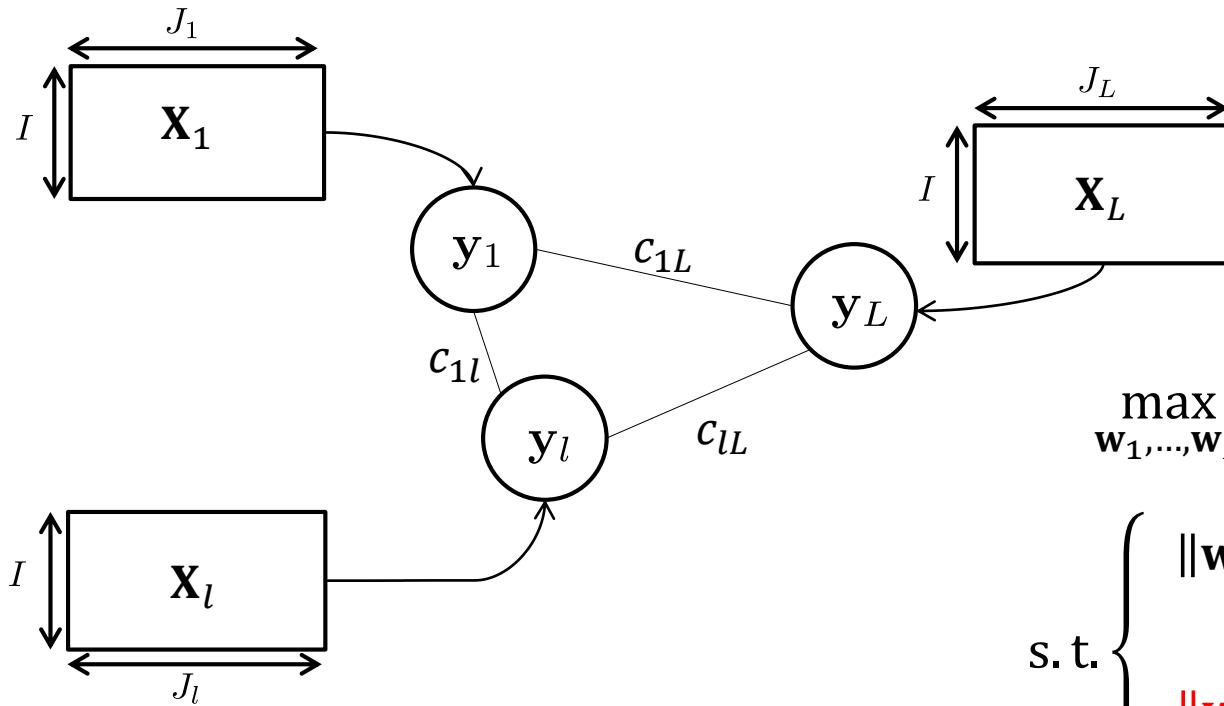
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Sparse Generalized Canonical Correlation Analysis (SGCCA)

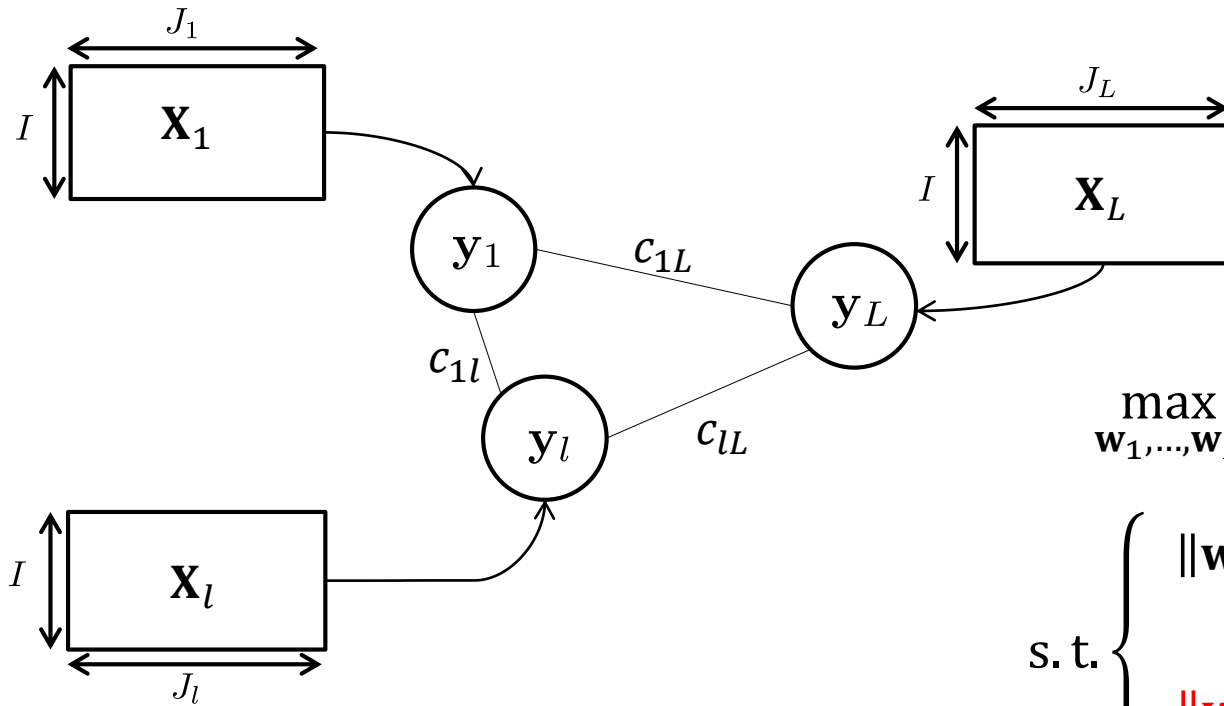


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➔ The LASSO regularization allows to perform variable selection.

Sparse Generalized Canonical Correlation Analysis (SGCCA)



$$\max_{\mathbf{w}_1, \dots, \mathbf{w}_L} \sum_{k,l=1}^L c_{kl} g(\text{Cov}(\mathbf{X}_k \mathbf{w}_k, \mathbf{X}_l \mathbf{w}_l))$$

$$\text{s. t. } \begin{cases} \|\mathbf{w}_l\|_2^2 = 1 \\ \|\mathbf{w}_l\|_1 = \sum_{j=1}^{J_l} |w_{lj}| \leq s_l, \quad l = 1, \dots, L. \end{cases}$$

Controls the level of sparsity (has to be tuned).

➔ The LASSO regularization allows to perform variable selection.

The Variable Importance in Projection (VIP) score



The Variable Importance in Projection (VIP) score



$$\text{VIP}(\mathbf{x}_{lj}) = \frac{1}{R} \sum_{r=1}^R \left(w_{lj}^{(r)2} \text{AVE}(\mathbf{X}_l^{(r)}) \right)$$

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The Variable Importance in Projection (VIP) score



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❖ R is the number of extracted components.



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Where:

- ❖ R is the number of extracted components.
- ❖ $\mathbf{X}_l = [\mathbf{x}_{l1}, \dots, \mathbf{x}_{lJ_l}]$ and $\mathbf{w}_l = [w_{l1}, \dots, w_{lJ_l}]^T$.



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- ❖ RGCCA uses a deflation procedure to extract the following components.
Thus, $\mathbf{X}_l^{(r)}$ correspond to the projection of $\mathbf{X}_l^{(r-1)}$ onto the space orthogonal to $\mathbf{y}_l^{(r)}$:



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Where:

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- ❖ RGCCA uses a deflation procedure to extract the following components.

Thus, $\mathbf{X}_l^{(r)}$ correspond to the projection of $\mathbf{X}_l^{(r-1)}$ onto the space orthogonal to $\mathbf{y}_l^{(r)}$:

$$\mathbf{X}_l^{(r)} = \left(\mathbf{I}_{J_l} - \frac{\mathbf{y}_l^{(r)} \mathbf{y}_l^{(r)\top}}{\|\mathbf{y}_l^{(r)}\|_2^2} \right) \mathbf{X}_l^{(r-1)}$$



$$\text{VIP}(\mathbf{x}_{lj}) = \frac{1}{R} \sum_{r=1}^R \left(w_{lj}^{(r)2} \text{AVE}(\mathbf{X}_l^{(r)}) \right)$$

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- ❖ Furthermore $\mathbf{X}_l^{(0)} = \mathbf{X}_l$



$$\text{VIP}(\mathbf{x}_{lj}) = \frac{1}{R} \sum_{r=1}^R \left(w_{lj}^{(r)2} \text{AVE}(\mathbf{X}_l^{(r)}) \right)$$

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- ❖ Furthermore $\mathbf{X}_l^{(0)} = \mathbf{X}_l$
- ❖ The Average Variance Explained (AVE) associated with $\mathbf{y}_l^{(r)}$ is:



$$\text{VIP}(\mathbf{x}_{lj}) = \frac{1}{R} \sum_{r=1}^R \left(w_{lj}^{(r)2} \text{AVE}(\mathbf{X}_l^{(r)}) \right)$$

Where:

- ❖ R is the number of extracted components.
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- ❖ The Average Variance Explained (AVE) associated with $\mathbf{y}_l^{(r)}$ is:

$$\text{AVE}(\mathbf{X}_l^{(r)}) = \frac{1}{\|\mathbf{X}_l^{(r)}\|_F^2} \sum_{j=1}^{J_l} \left(\text{var}(\mathbf{x}_{lj}^{(r)}) \times \text{cor}^2(\mathbf{x}_{lj}^{(r)}, \mathbf{y}_l^{(r+1)}) \right)$$

Let us apply both an unsupervised/supervised version of SGCCA on the MDD case study

→ See section 5 & 6 on the Rmarkdown `MDD_case_study_RGCCA`

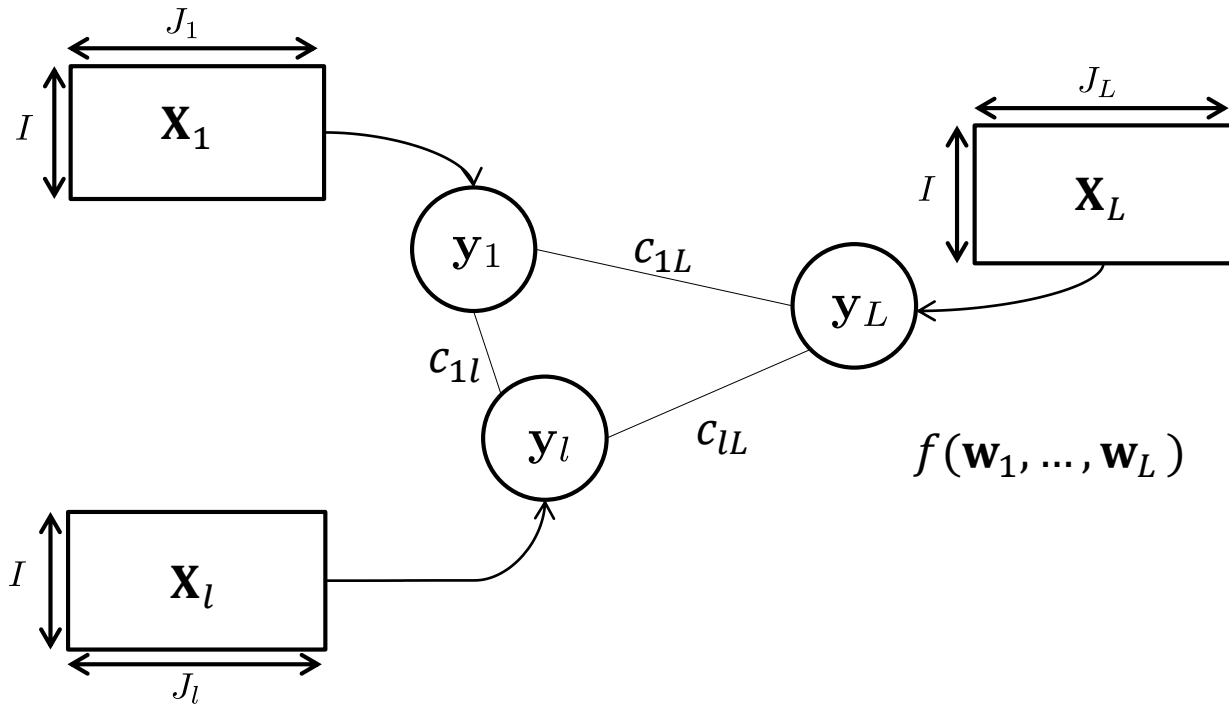


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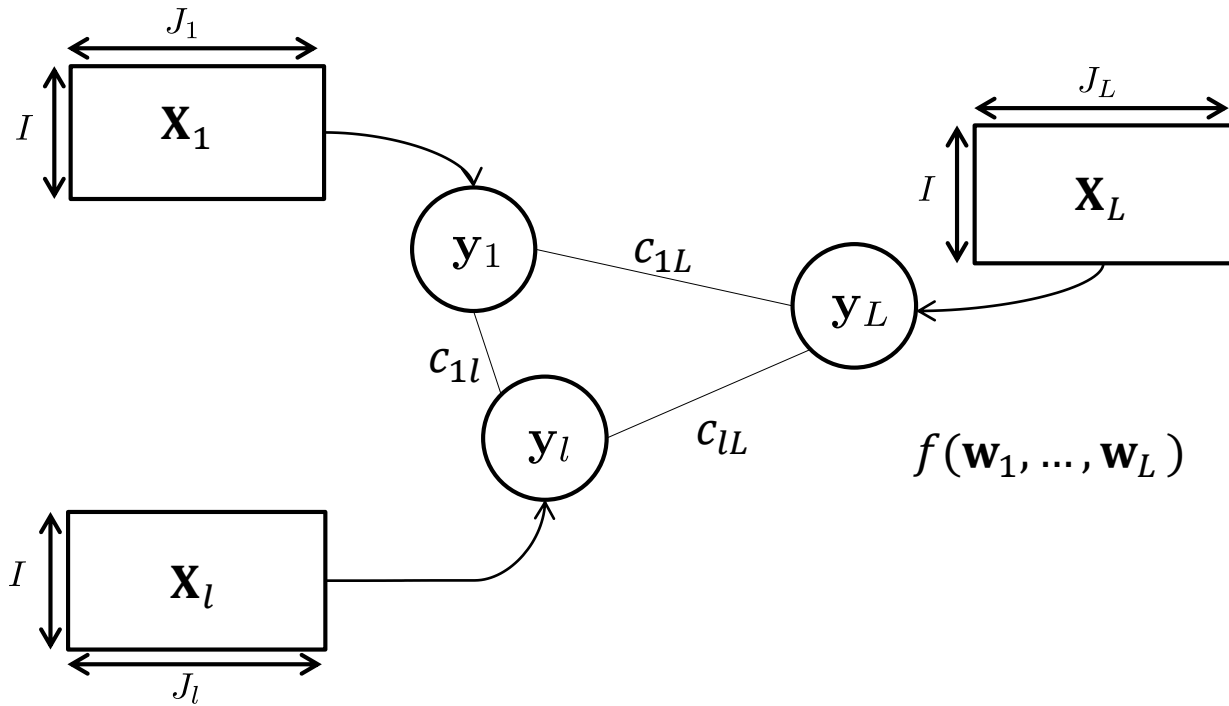
Principle of the RGCCA Optimization Algorithm



$$\max_{\mathbf{w}_1, \dots, \mathbf{w}_L} \sum_{k,l=1}^L c_{kl} g(\text{Cov}(\mathbf{X}_k \mathbf{w}_k, \mathbf{X}_l \mathbf{w}_l))$$

$$\text{s. t. } \begin{cases} \mathbf{w}_l^\top \mathbf{M}_l \mathbf{w}_l = 1 \\ , l = 1, \dots, L. \end{cases}$$

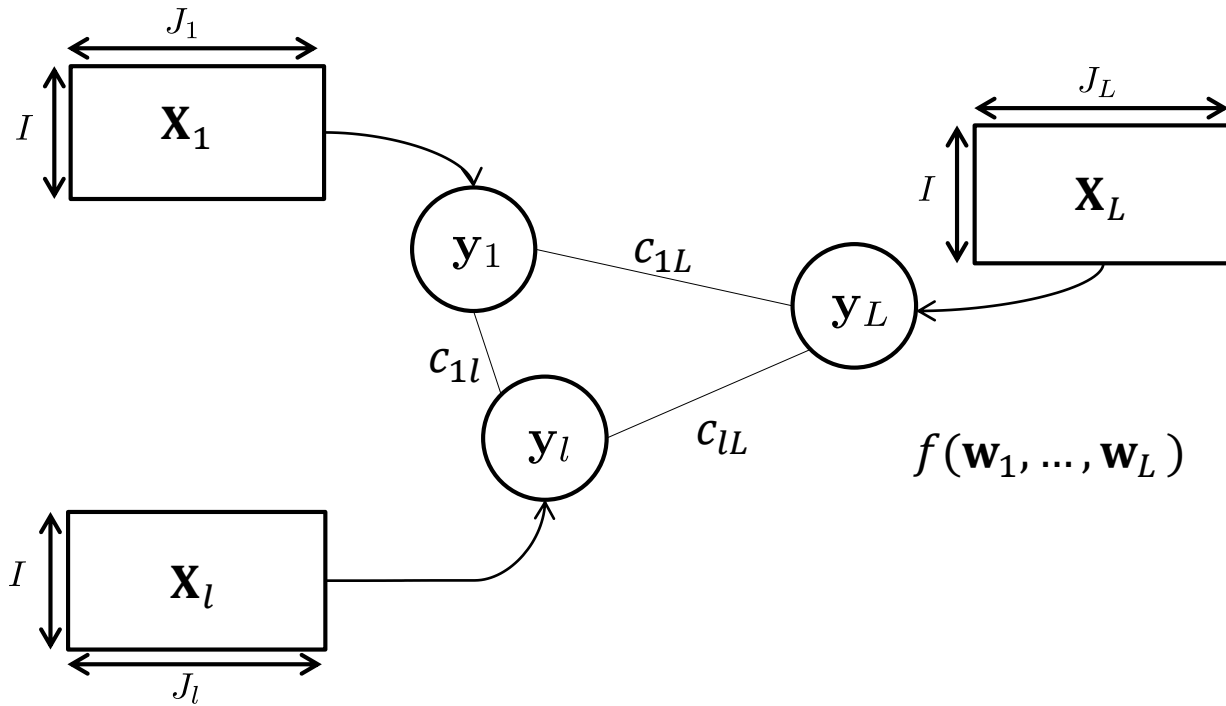
Principle of the RGCCA Optimization Algorithm



$$\max_{\mathbf{w}_1, \dots, \mathbf{w}_L} \sum_{k,l=1}^L c_{kl} g(\text{Cov}(\mathbf{X}_k \mathbf{w}_k, \mathbf{X}_l \mathbf{w}_l))$$

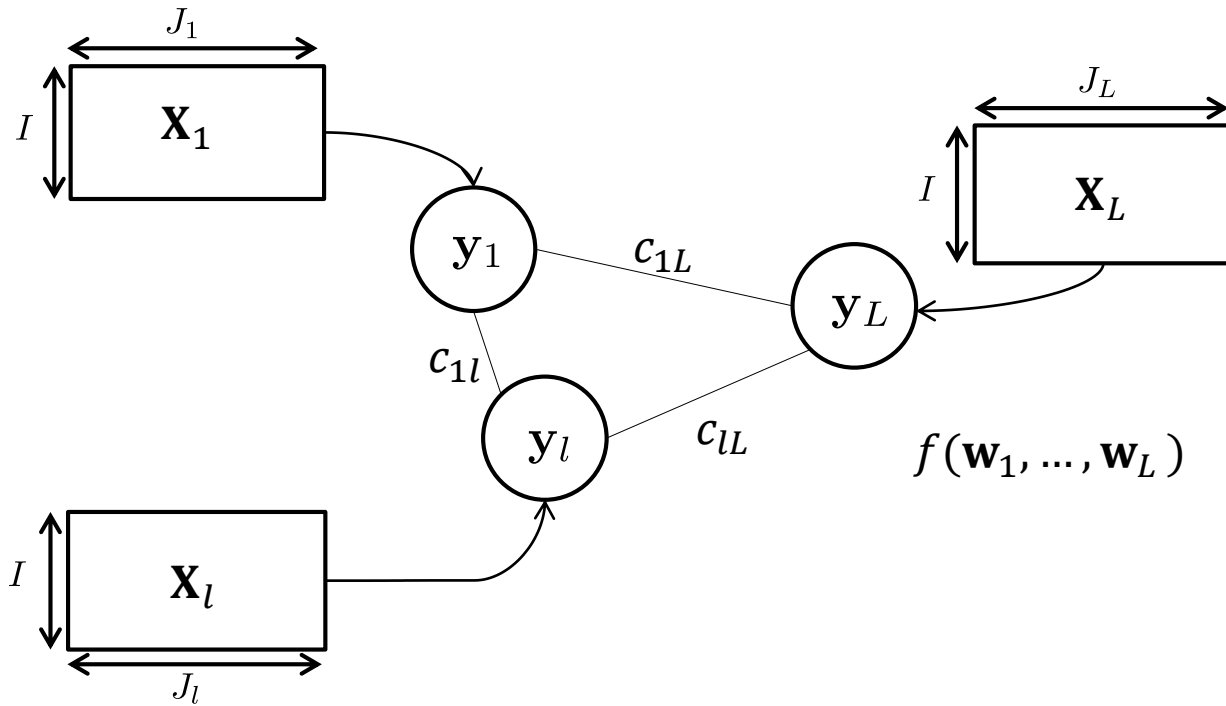
$$\text{s. t. } \begin{cases} \mathbf{w}_l^\top \mathbf{M}_l \mathbf{w}_l = 1 \\ , l = 1, \dots, L. \end{cases}$$

Principle of the RGCCA Optimization Algorithm



$$\begin{aligned} & f(\mathbf{w}_1, \dots, \mathbf{w}_L) \\ \max_{\mathbf{w}_1, \dots, \mathbf{w}_L} & \sum_{k,l=1}^L c_{kl} g(\text{Cov}(\mathbf{X}_k \mathbf{w}_k, \mathbf{X}_l \mathbf{w}_l)) \\ \text{s. t.} & \left\{ \begin{array}{l} \mathbf{w}_l^T \mathbf{M}_l \mathbf{w}_l = 1 \\ \quad \quad \quad , l = 1, \dots, L. \end{array} \right. \end{aligned}$$

Principle of the RGCCA Optimization Algorithm



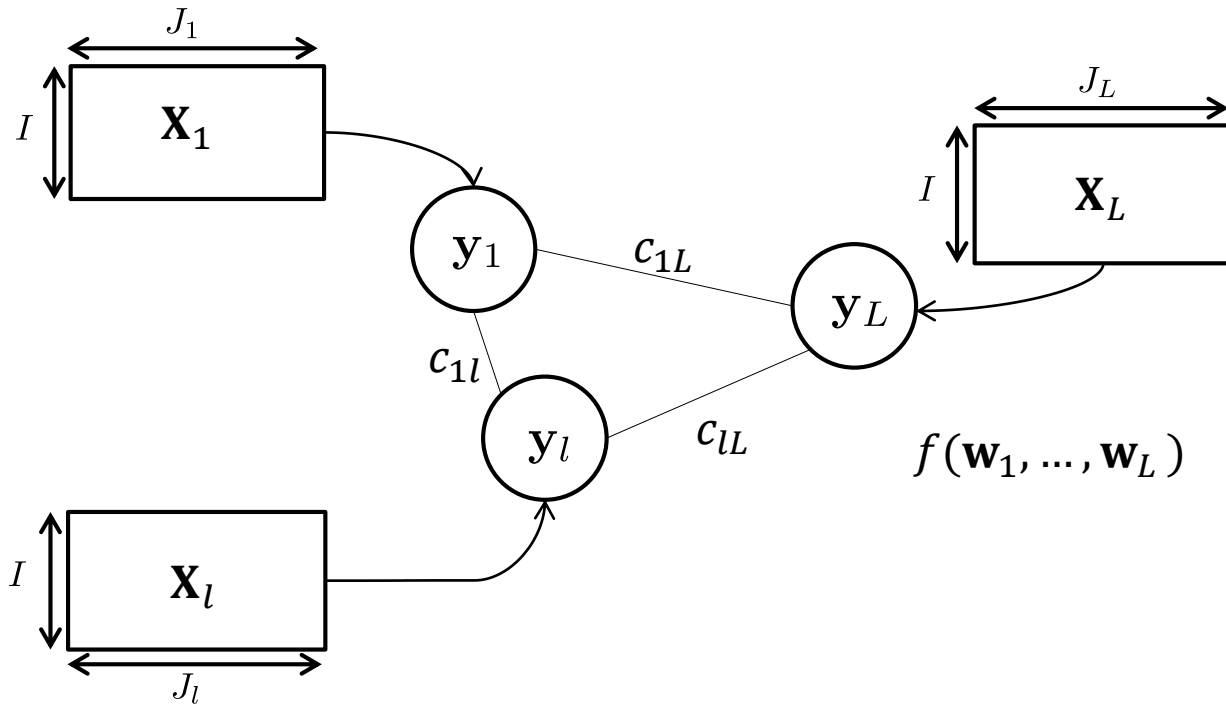
$$f(\mathbf{w}_1, \dots, \mathbf{w}_L)$$

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In order to maximize the multi-convex function $f(\mathbf{w}_1, \dots, \mathbf{w}_L)$, two key ingredients are used:

Principle of the RGCCA Optimization Algorithm



$$f(\mathbf{w}_1, \dots, \mathbf{w}_L)$$

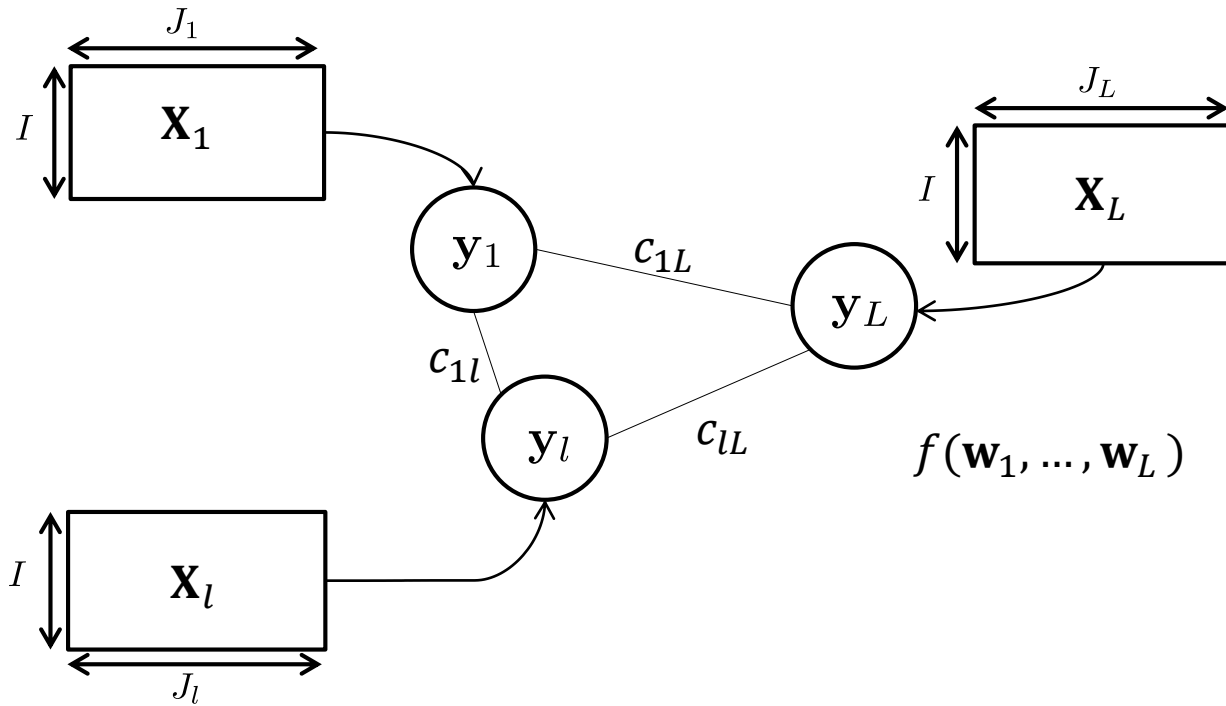
$$\max_{\mathbf{w}_1, \dots, \mathbf{w}_L} \sum_{k,l=1}^L c_{kl} g(\text{Cov}(\mathbf{X}_k \mathbf{w}_k, \mathbf{X}_l \mathbf{w}_l))$$

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In order to maximize the multi-convex function $f(\mathbf{w}_1, \dots, \mathbf{w}_L)$, two key ingredients are used:

➔ Block Coordinate Ascent (BCA).

Principle of the RGCCA Optimization Algorithm



$$f(\mathbf{w}_1, \dots, \mathbf{w}_L)$$

$$\max_{\mathbf{w}_1, \dots, \mathbf{w}_L} \sum_{k,l=1}^L c_{kl} g(\text{Cov}(\mathbf{X}_k \mathbf{w}_k, \mathbf{X}_l \mathbf{w}_l))$$

$$\text{s. t. } \begin{cases} \mathbf{w}_l^T \mathbf{M}_l \mathbf{w}_l = 1 \\ , l = 1, \dots, L. \end{cases}$$

In order to maximize the multi-convex function $f(\mathbf{w}_1, \dots, \mathbf{w}_L)$, two key ingredients are used:

- ➡ Block Coordinate Ascent (BCA).
- ➡ Minorize-Maximize (MM) principle.



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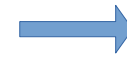
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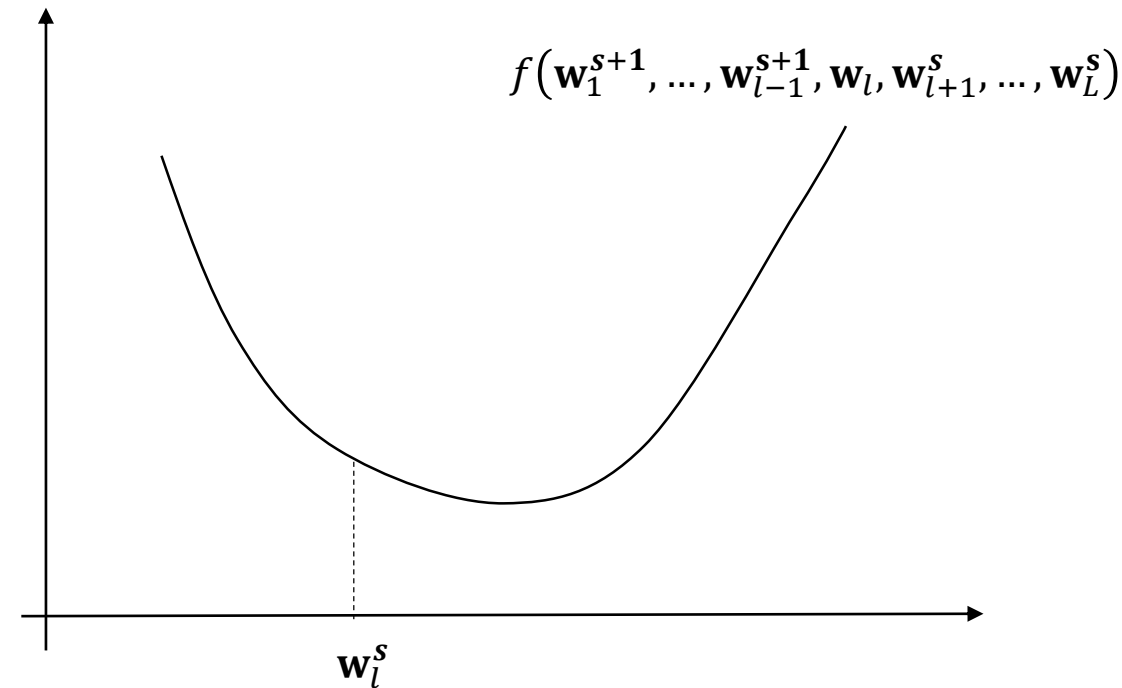
Minorize-Maximize (MM) principle

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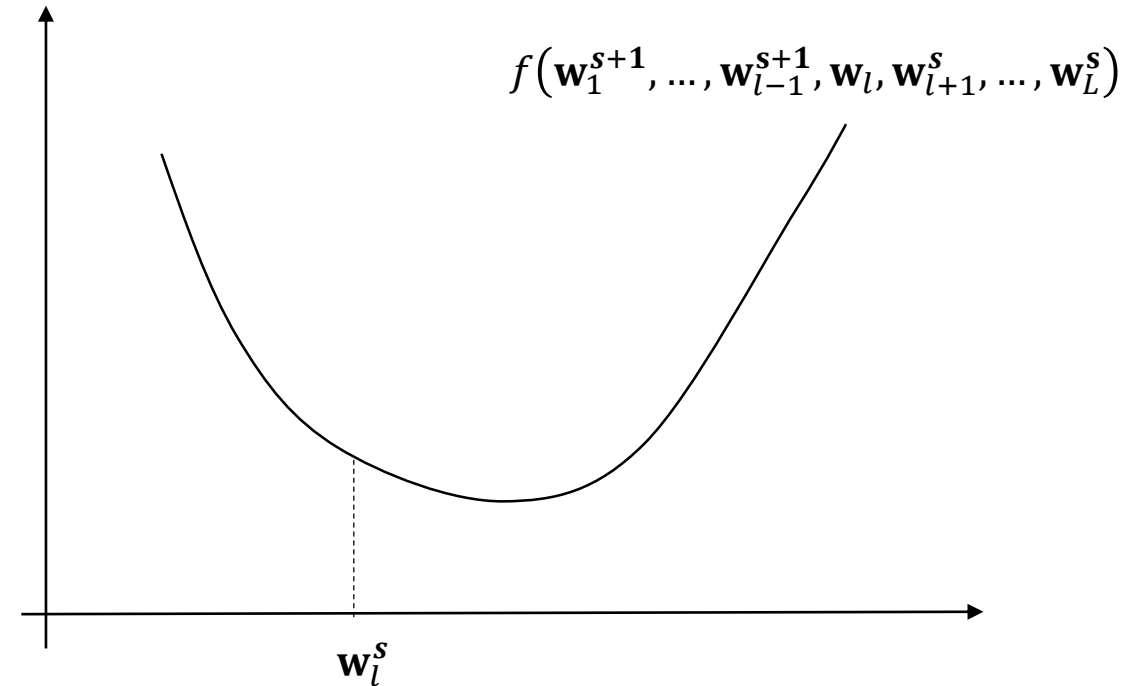


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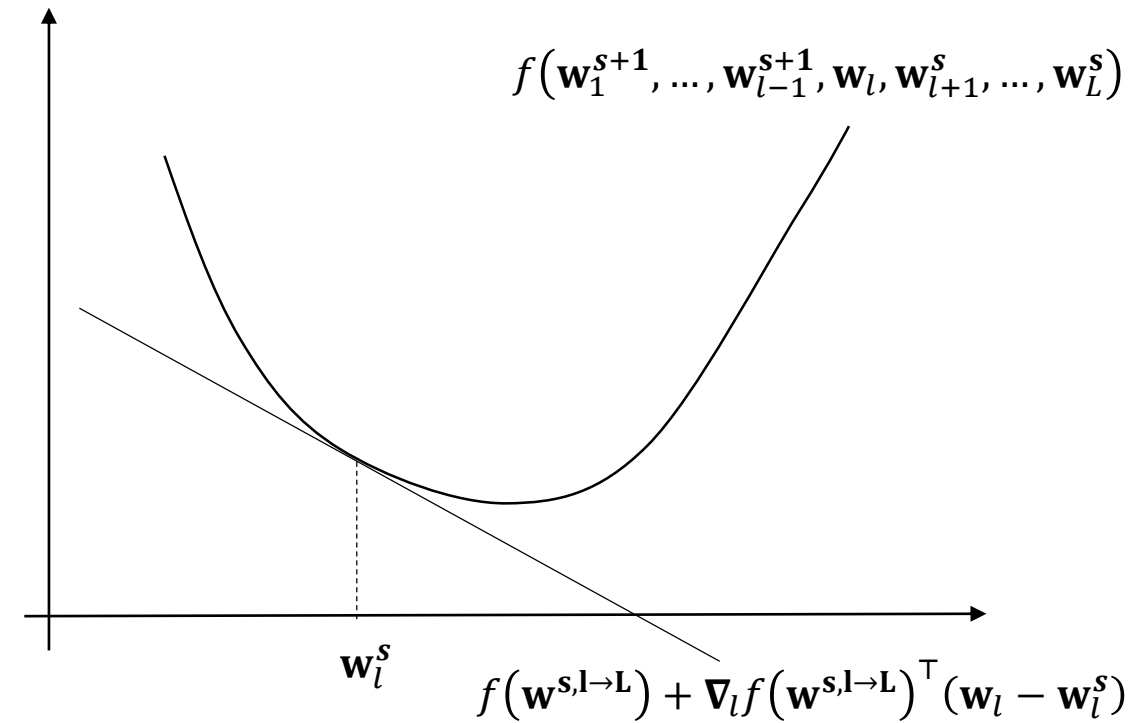


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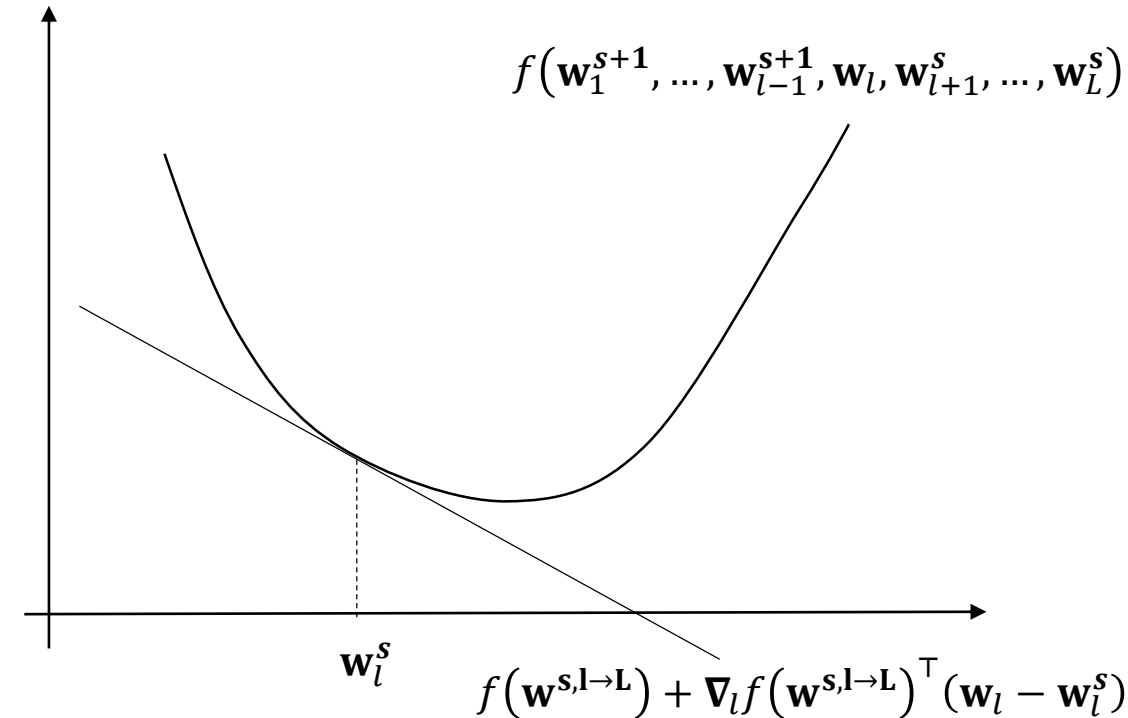
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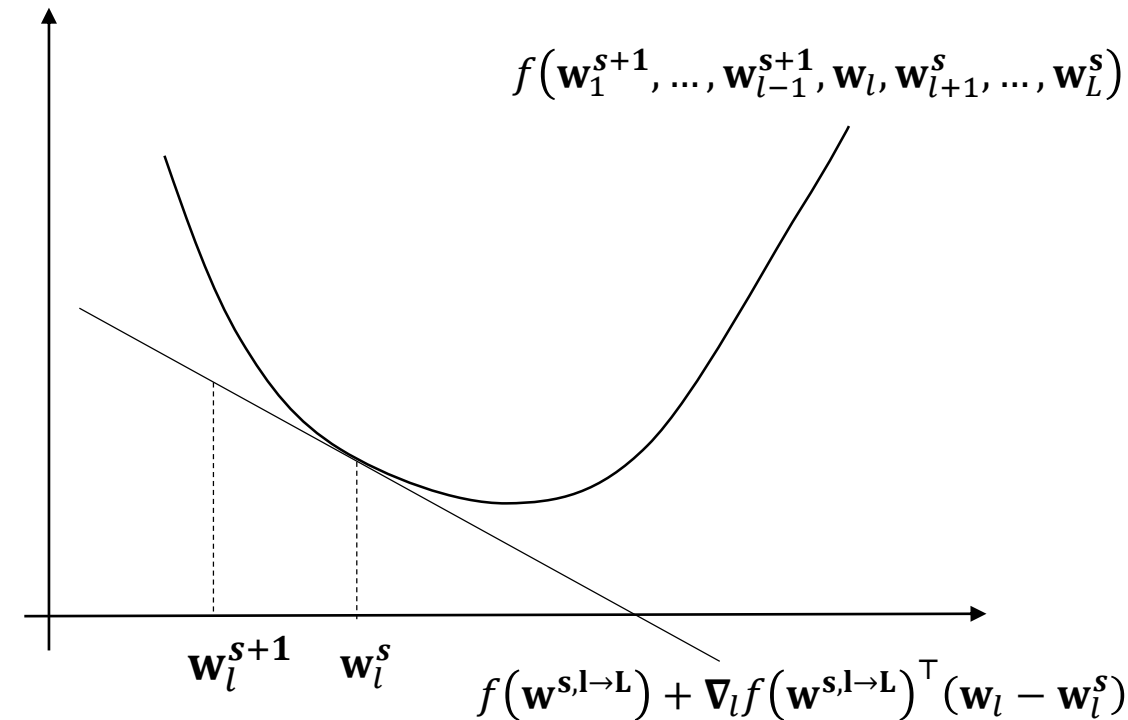
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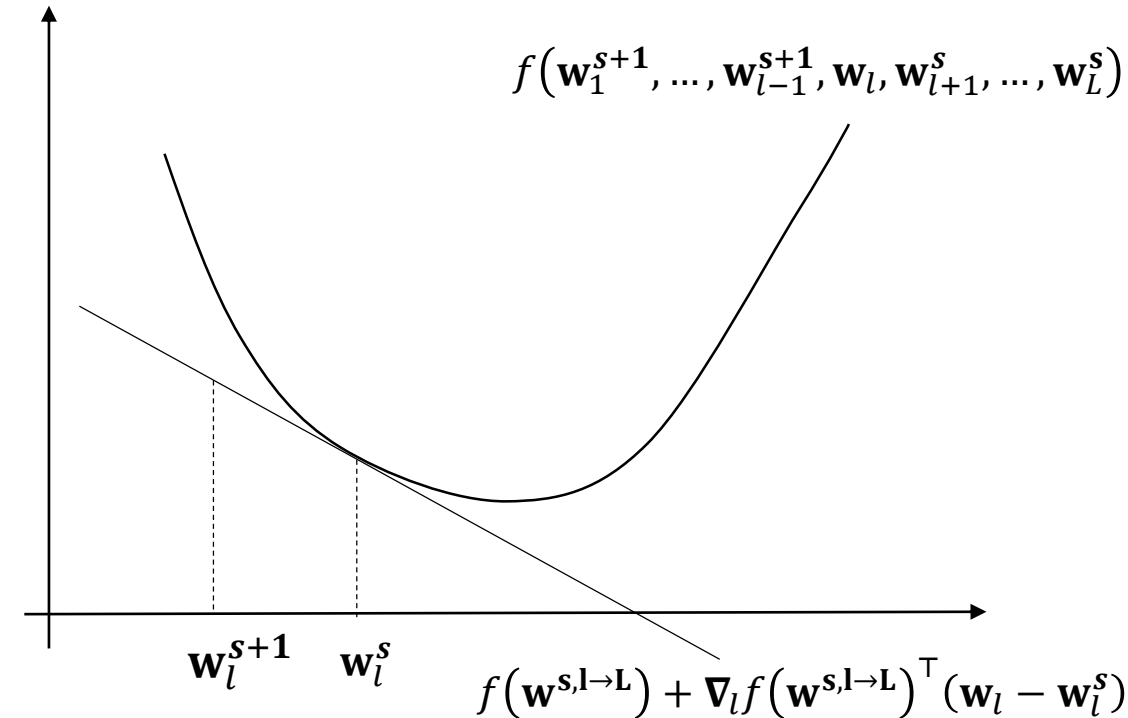


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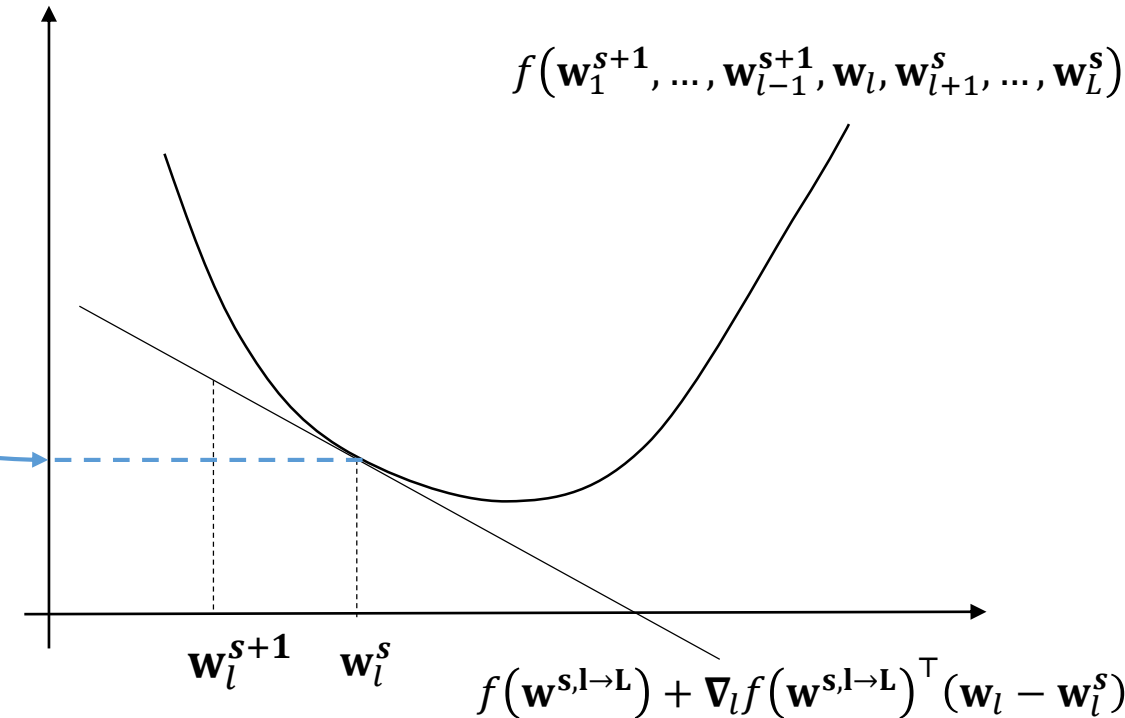


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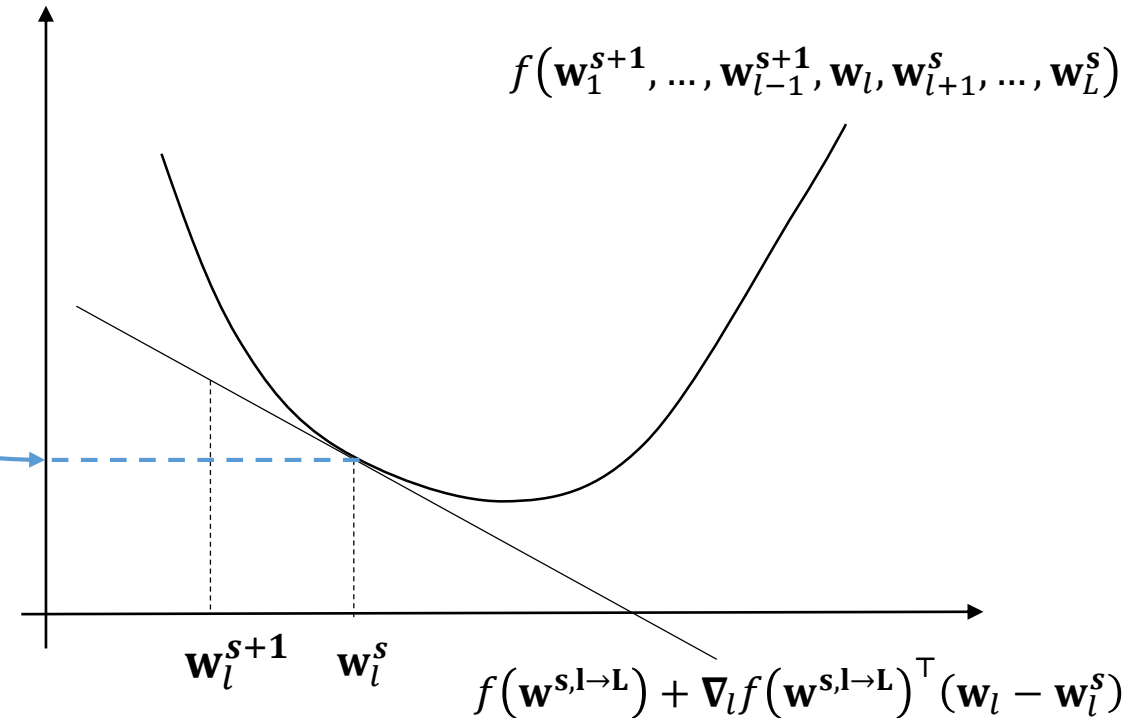


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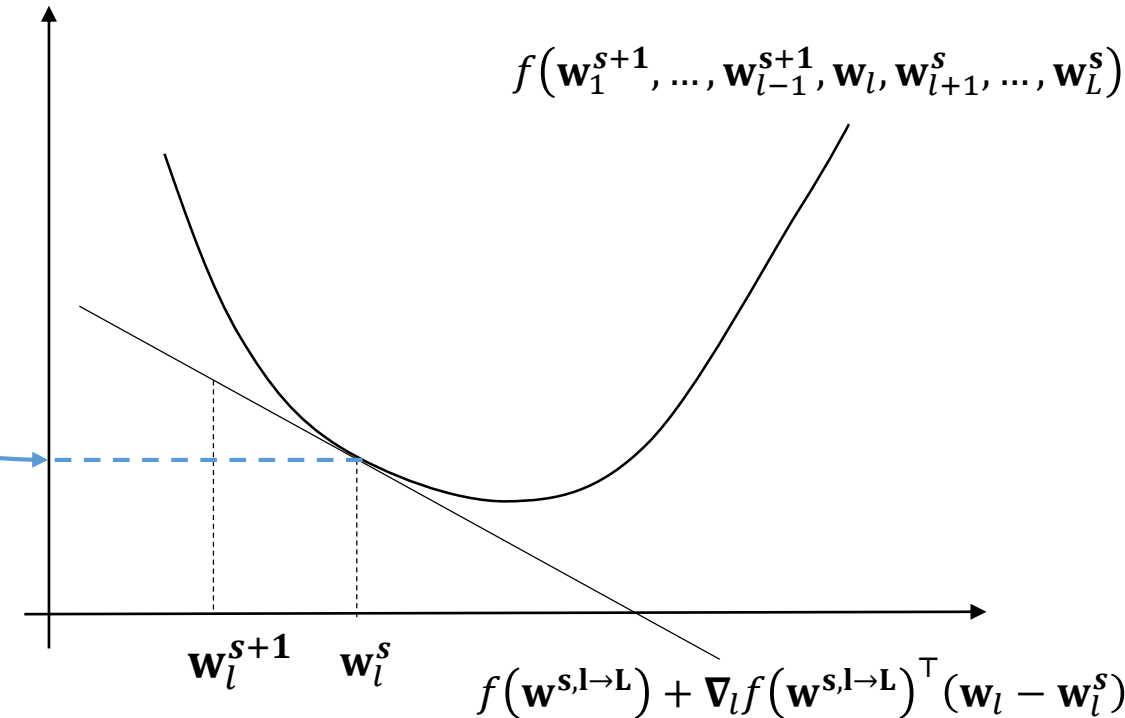


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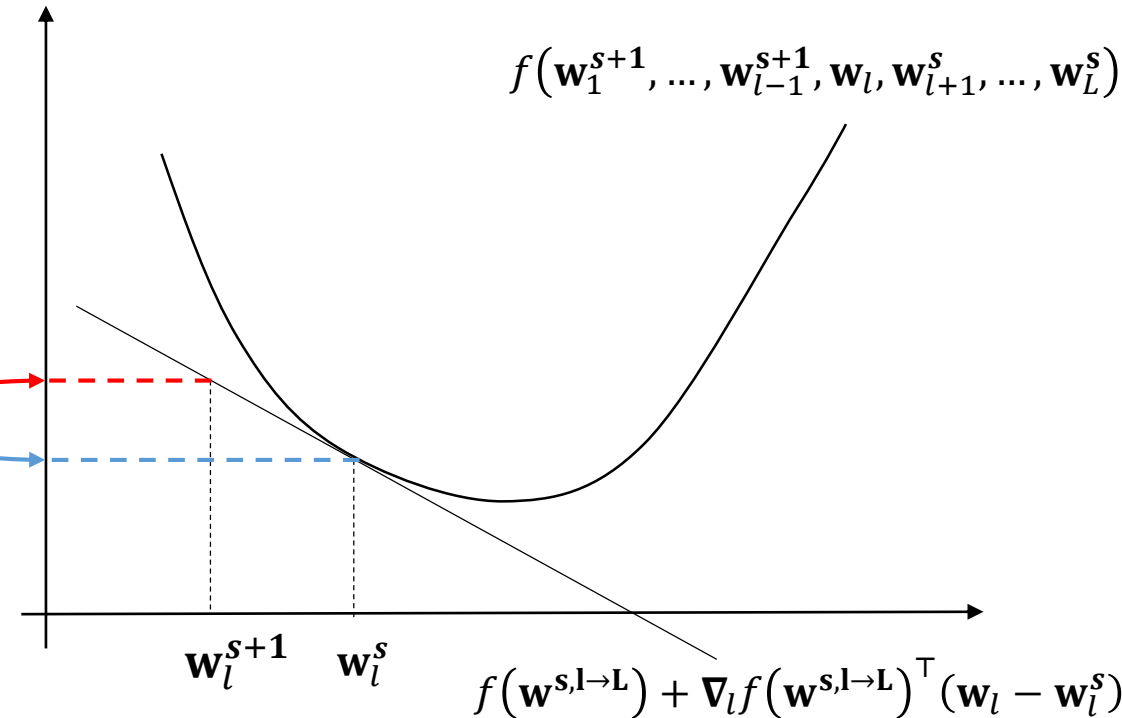


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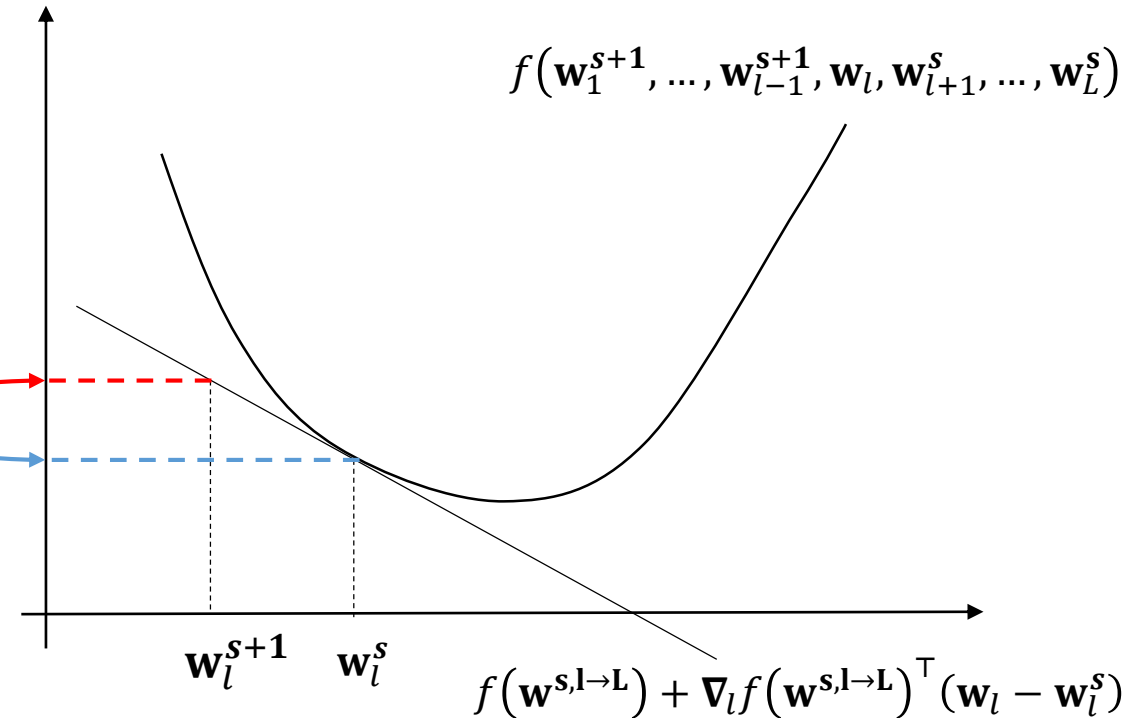


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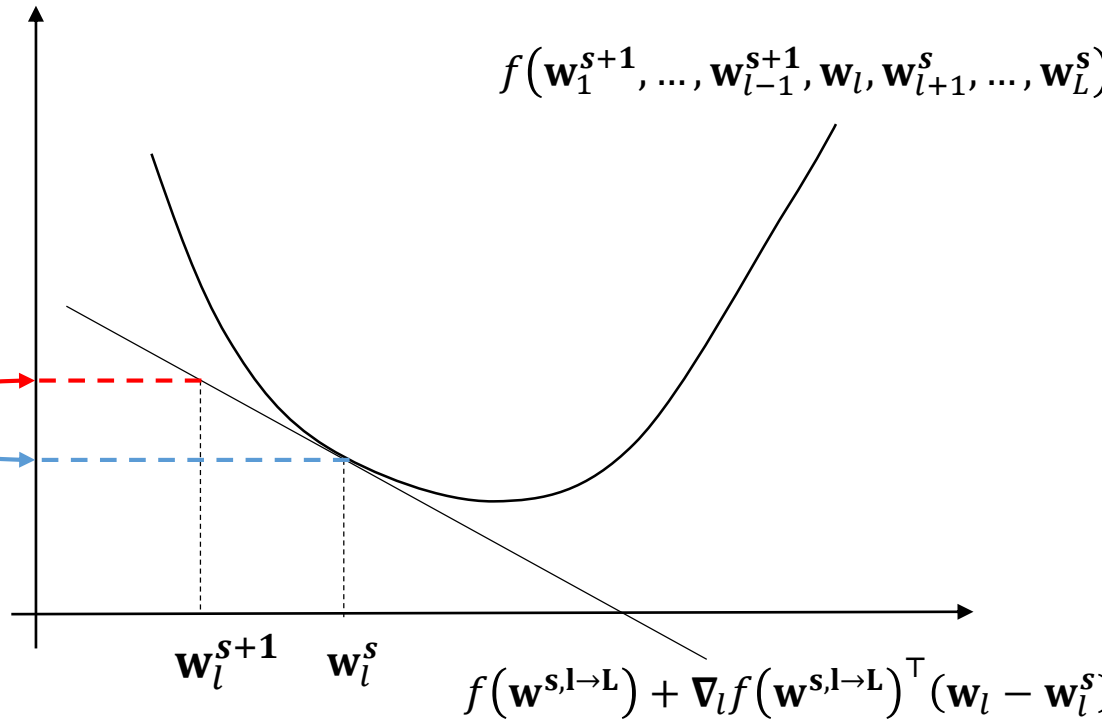
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Comes from the multi-convexity of f and so the convexity of $f(\mathbf{w}_1^{s+1}, \dots, \mathbf{w}_{l-1}^{s+1}, \mathbf{w}_l, \mathbf{w}_{l+1}^s, \dots, \mathbf{w}_L^s)$



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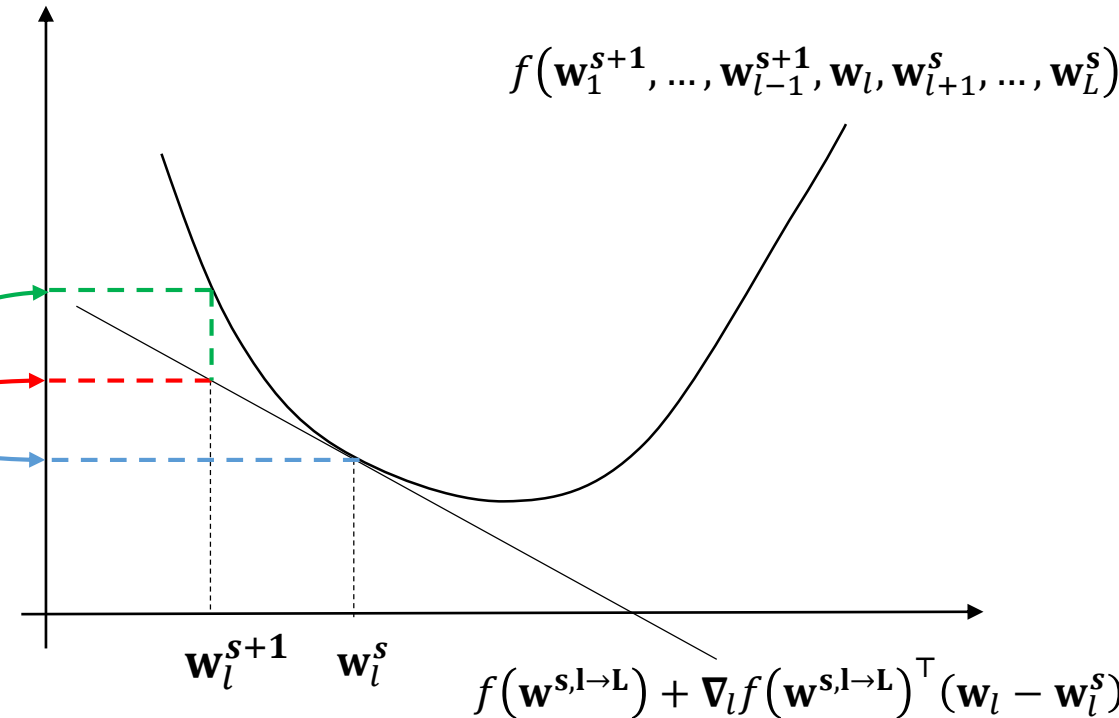
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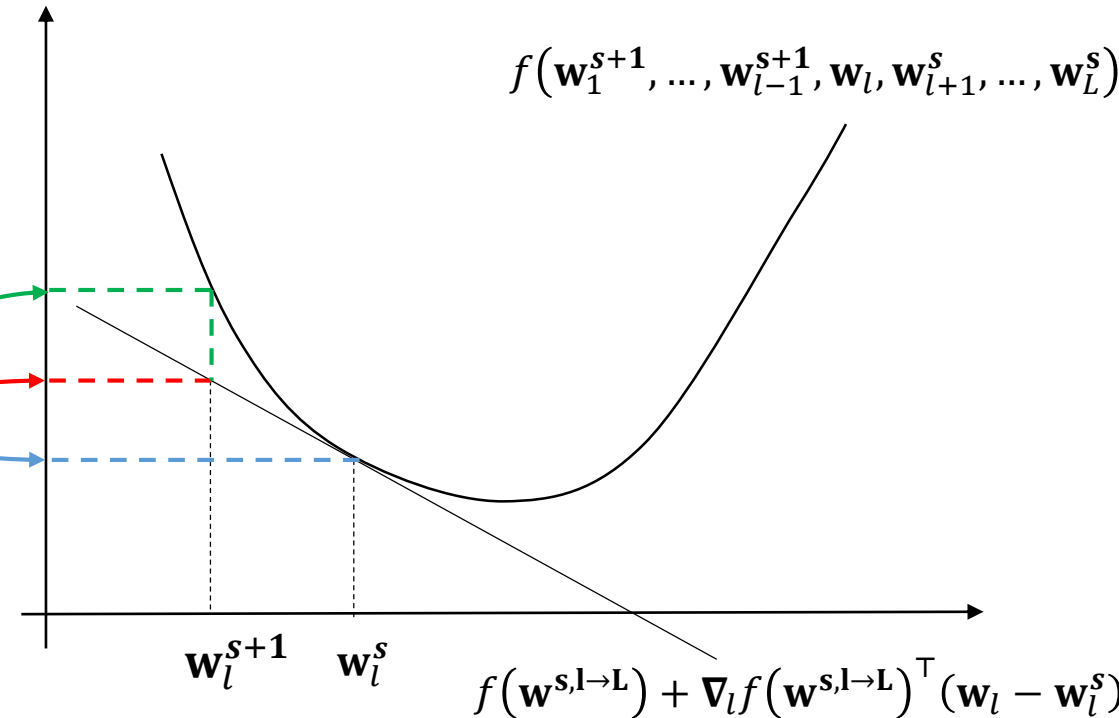
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$$\mathbf{w}_l^{s+1} = \operatorname{argmax}_{\mathbf{w}_l, \mathbf{w}_l^\top \mathbf{M}_l \mathbf{w}_l = 1} \nabla_l f(\mathbf{w}^{s,l \rightarrow L})^\top \mathbf{w}_l$$

$$\begin{aligned} f(\mathbf{w}^{s,l \rightarrow L}) &= f(\mathbf{w}^{s,l \rightarrow L}) + \nabla_l f(\mathbf{w}^{s,l \rightarrow L})^\top (\mathbf{w}_l^s - \mathbf{w}_l^s) \\ &\leq f(\mathbf{w}^{s,l \rightarrow L}) + \nabla_l f(\mathbf{w}^{s,l \rightarrow L})^\top (\mathbf{w}_l^{s+1} - \mathbf{w}_l^s) \\ &\leq f(\mathbf{w}_1^{s+1}, \dots, \mathbf{w}_{l-1}^{s+1}, \mathbf{w}_l^{s+1}, \mathbf{w}_{l+1}^s, \dots, \mathbf{w}_L^s) \end{aligned}$$

Comes from the multi-convexity of f and so the convexity of $f(\mathbf{w}_1^{s+1}, \dots, \mathbf{w}_{l-1}^{s+1}, \mathbf{w}_l, \mathbf{w}_{l+1}^s, \dots, \mathbf{w}_L^s)$



$$\text{In the end } f(\mathbf{w}_1^{s+1}, \dots, \mathbf{w}_{l-1}^{s+1}, \mathbf{w}_l^s, \mathbf{w}_{l+1}^s, \dots, \mathbf{w}_L^s) \leq f(\mathbf{w}_1^{s+1}, \dots, \mathbf{w}_{l-1}^{s+1}, \mathbf{w}_l^{s+1}, \mathbf{w}_{l+1}^s, \dots, \mathbf{w}_L^s)$$

Properties of this Master Algorithm





❖ Monotone convergence of the algorithm:

$$f(\mathbf{w}_1^s, \dots, \mathbf{w}_L^s) \leq f(\mathbf{w}_1^{s+1}, \dots, \mathbf{w}_L^{s+1})$$



❖ Monotone convergence of the algorithm:

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In addition, assuming uniqueness of the solution of the MM step, the following properties hold:



- ❖ Monotone convergence of the algorithm:

$$f(\mathbf{w}_1^s, \dots, \mathbf{w}_L^s) \leq f(\mathbf{w}_1^{s+1}, \dots, \mathbf{w}_L^{s+1})$$

In addition, assuming uniqueness of the solution of the MM step, the following properties hold:

- ❖ The sequence $\{\mathbf{w}^s\}$ is asymptotically regular:

$$\lim_{s \rightarrow +\infty} \|\mathbf{w}^{s+1} - \mathbf{w}^s\|_2 = 0$$



- ❖ Monotone convergence of the algorithm:

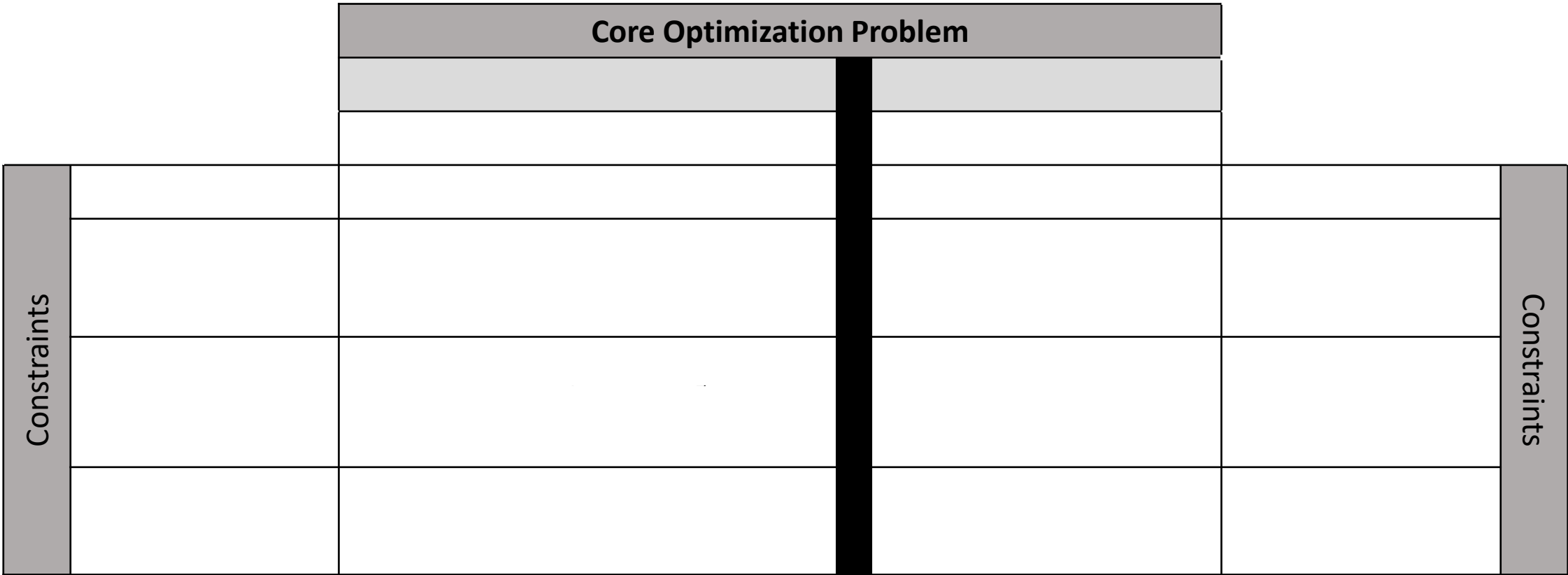
$$f(\mathbf{w}_1^s, \dots, \mathbf{w}_L^s) \leq f(\mathbf{w}_1^{s+1}, \dots, \mathbf{w}_L^{s+1})$$

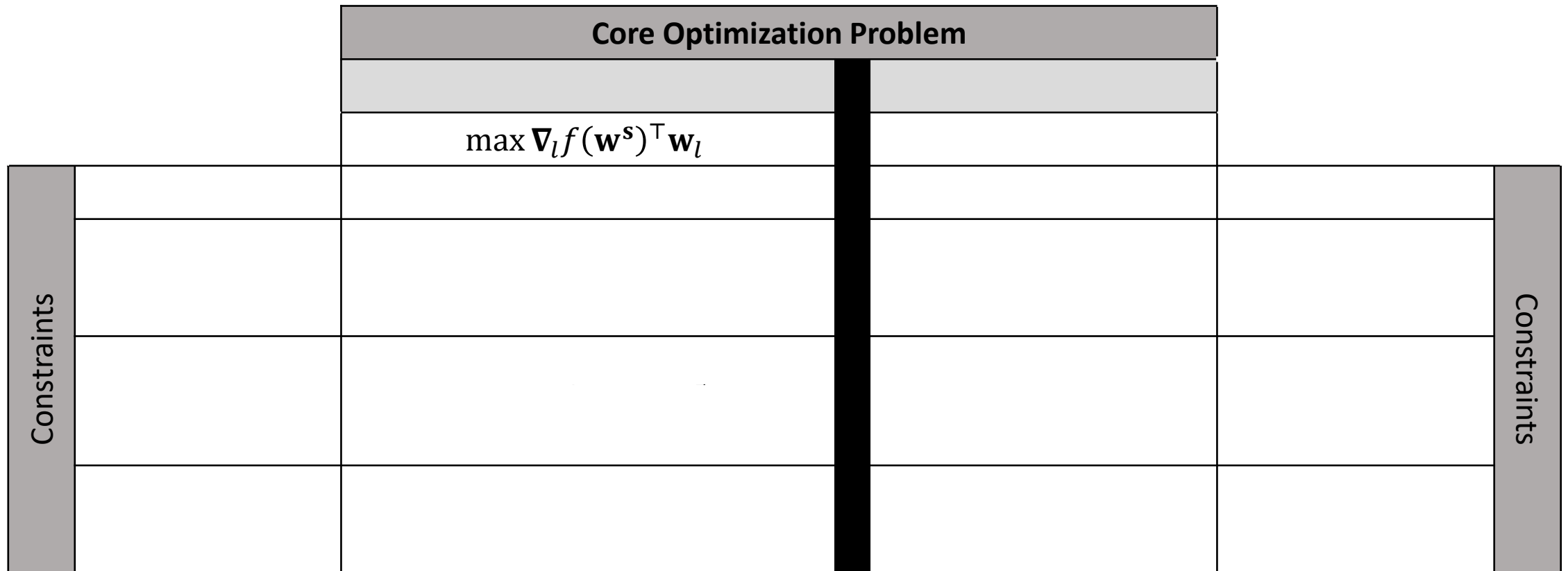
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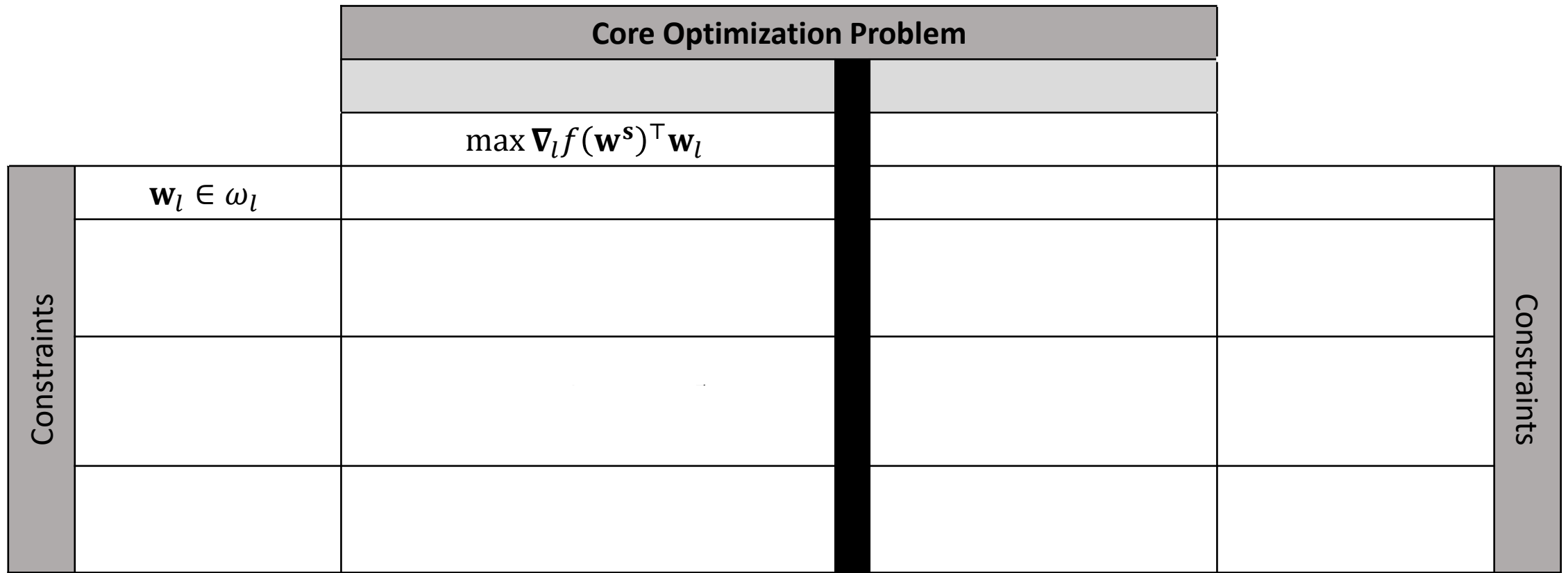
- ❖ The sequence $\{\mathbf{w}^s\}$ is asymptotically regular:

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- ❖ At convergence, a stationary point is obtained.







$$\omega_l = \{ \mathbf{w}_l \in \mathbb{R}^{J_l}; \mathbf{w}_l^\top \mathbf{M}_l \mathbf{w}_l = 1 \}$$



		Core Optimization Problem			
		$\max \nabla_l f(\mathbf{w}^s)^T \mathbf{w}_l$			
		RGCCA ^{1,2}			
Constraints	$\mathbf{w}_l \in \omega_l$				
				Constraints	

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1. (Tenenhaus and Tenenhaus, 2011) 2. (Tenenhaus, Tenenhaus and Groenen, 2017)



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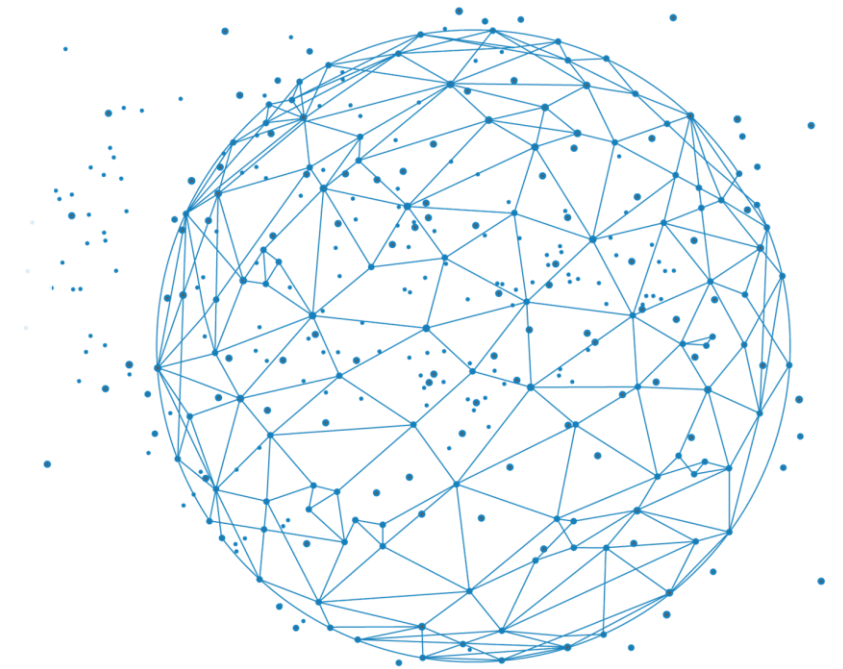
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Constraints	$\mathbf{w}_l \in \omega_l$	RGCCA ^{1,2}	
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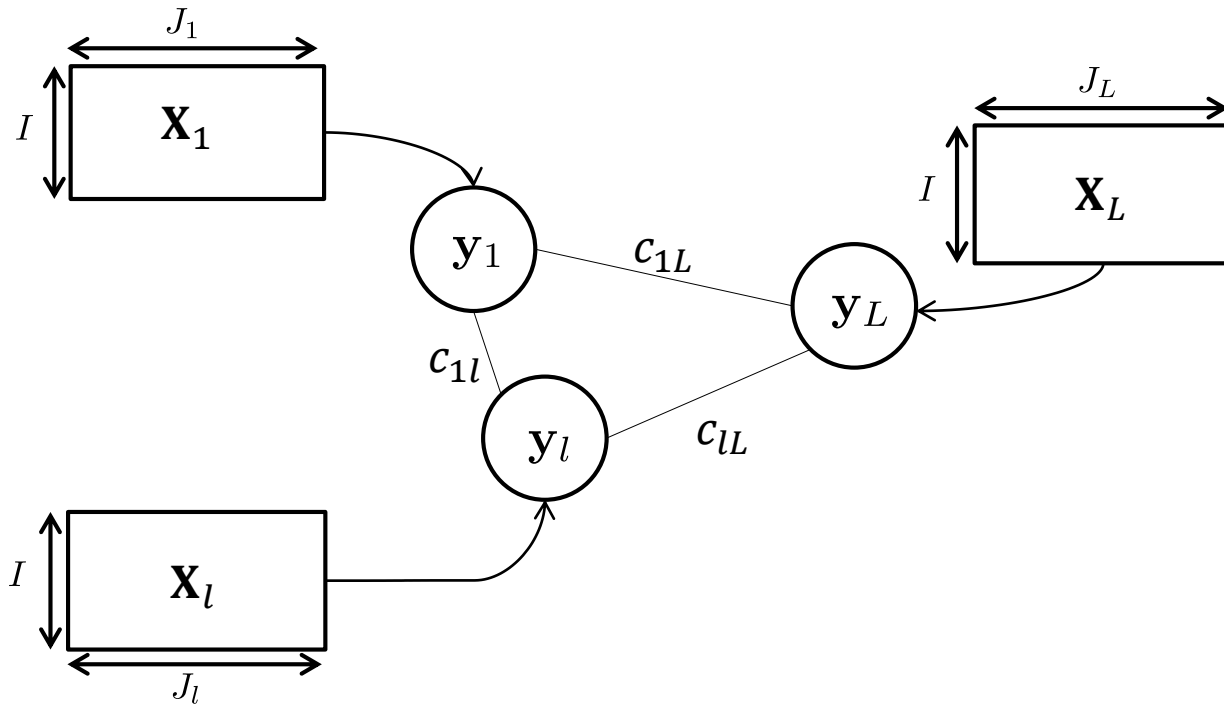
1. (Tenenhaus and Tenenhaus, 2011) 2. (Tenenhaus, Tenenhaus and Groenen, 2017) 3. (Tenenhaus et al., 2014)

1. Introduction of the case study
2. Unsupervised analysis with one-block: Principal Component Analysis (PCA)
3. Unsupervised analysis with two-blocks:
Partial Least Squares (PLS) and Canonical Correlation Analysis (CCA)
4. Unsupervised analysis with L -blocks:
Regularized Generalized Canonical Correlation Analysis (RGCCA)
5. Supervised analysis with RGCCA
6. Variable selection in RGCCA:
Sparse Generalized Canonical Correlation Analysis (SGCCA)
7. **The flexible Optimization Framework of RGCCA**

- ❖ The general principal
- ❖ Extension to multi-way analysis
- ❖ From Sequential to Global



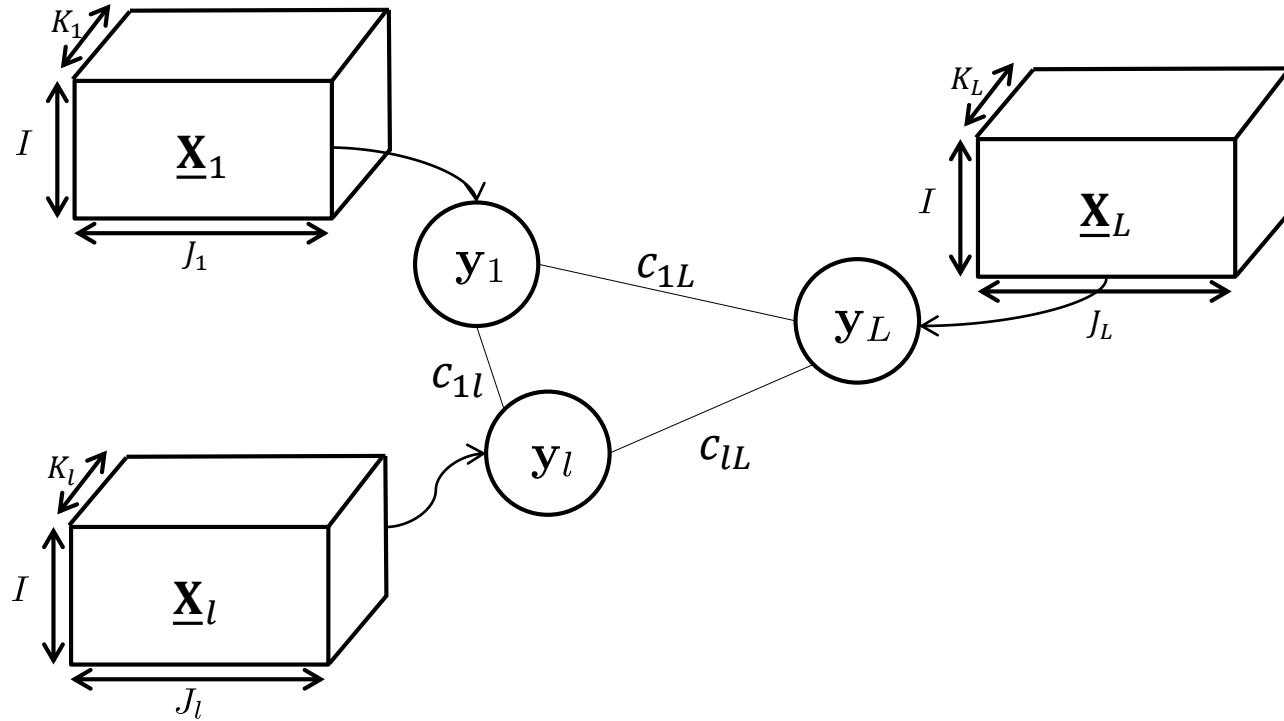
From RGCCA to Multiway GCCA



$$\max_{\mathbf{w}_1, \dots, \mathbf{w}_L} \sum_{k,l=1}^L c_{kl} g(\text{Cov}(\mathbf{X}_k \mathbf{w}_k, \mathbf{X}_l \mathbf{w}_l))$$

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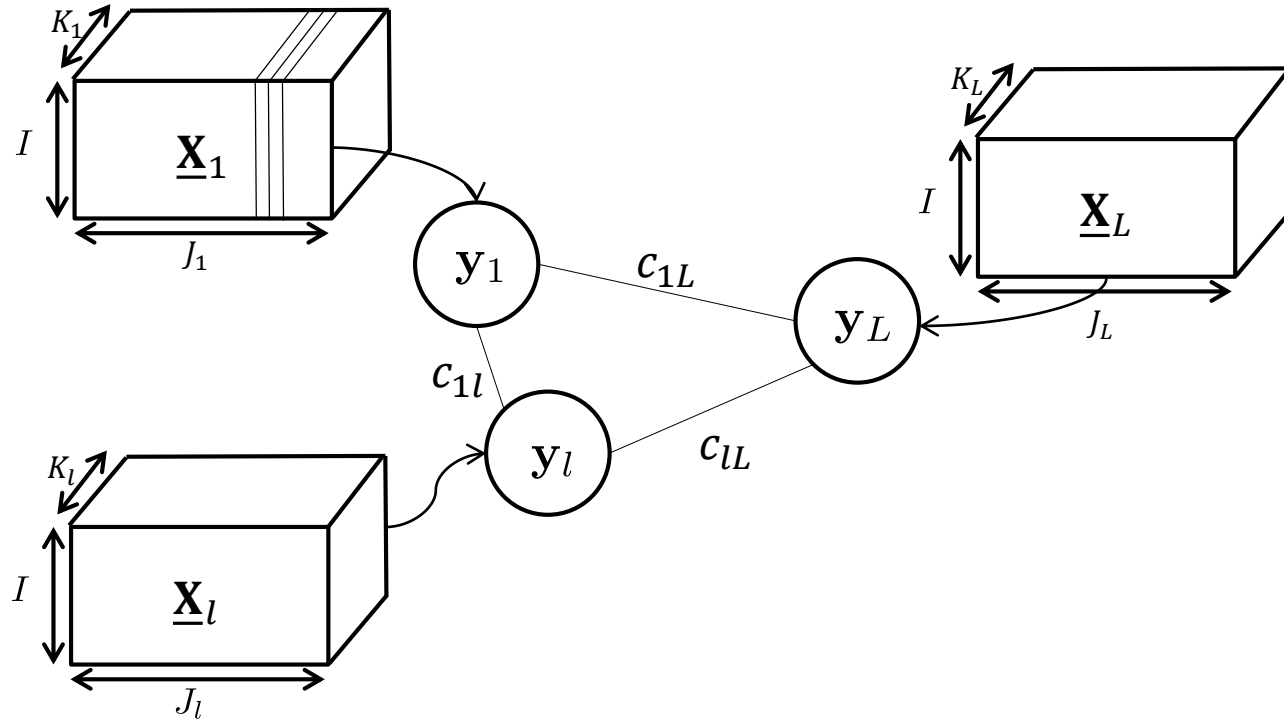
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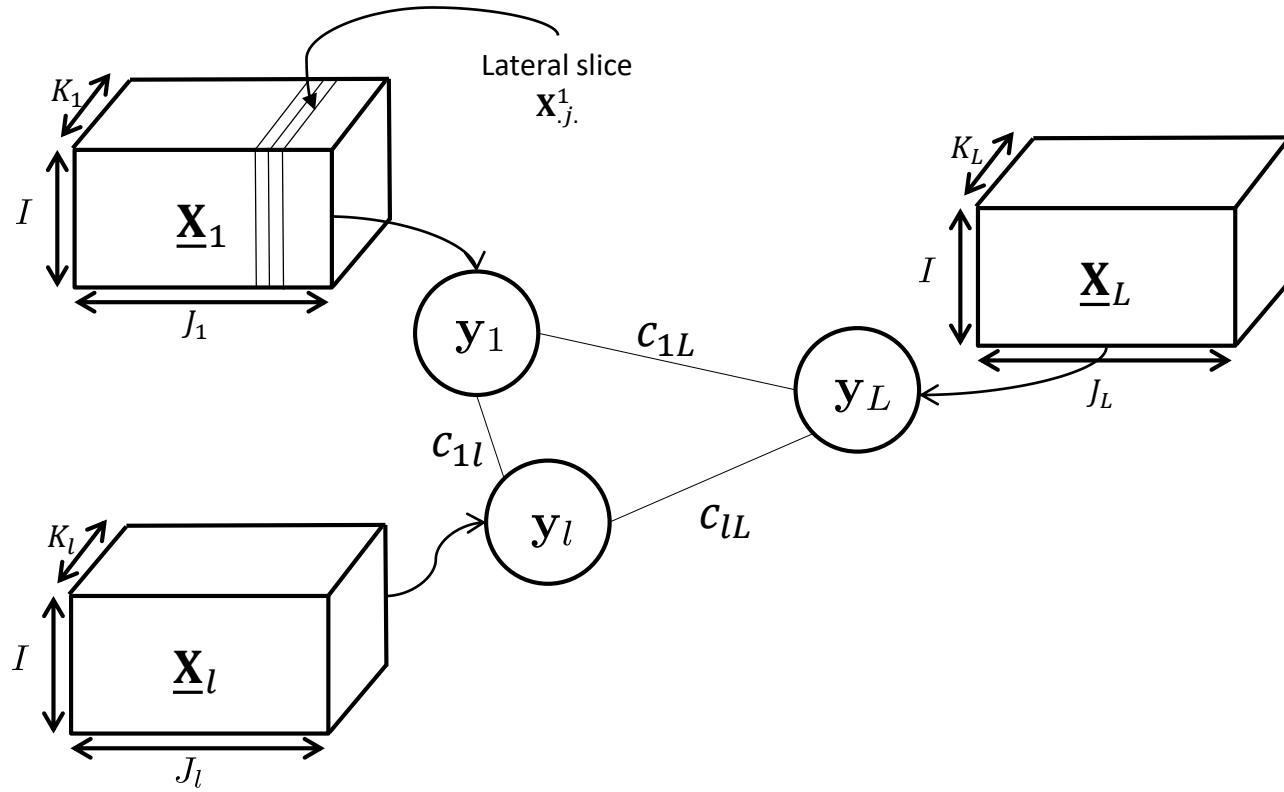
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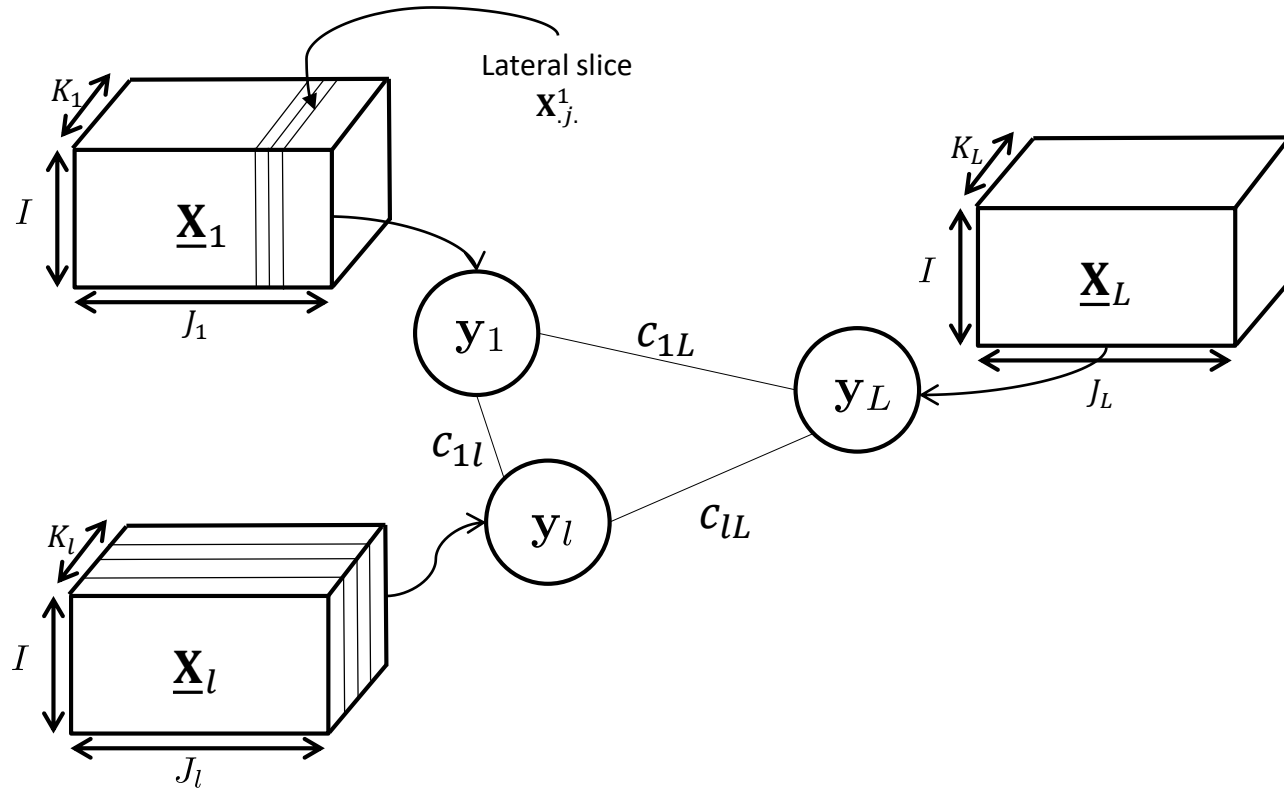
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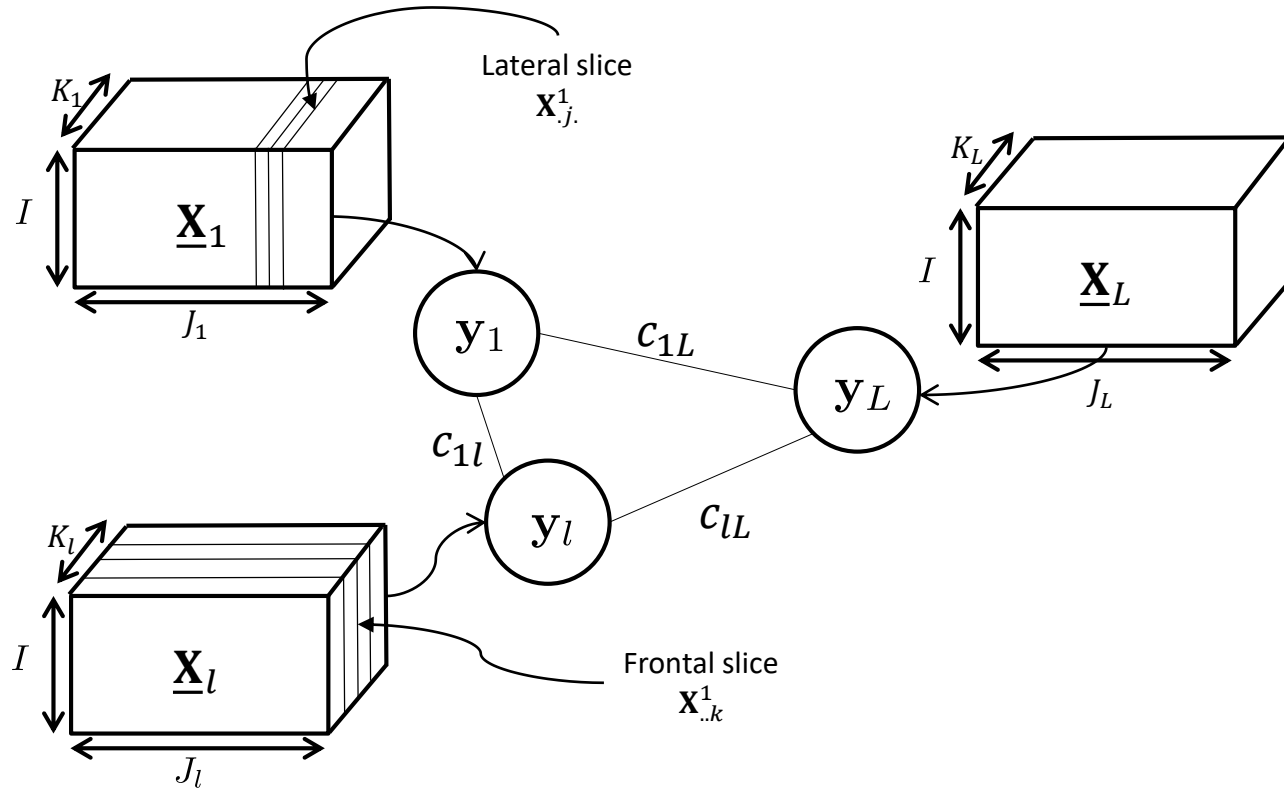
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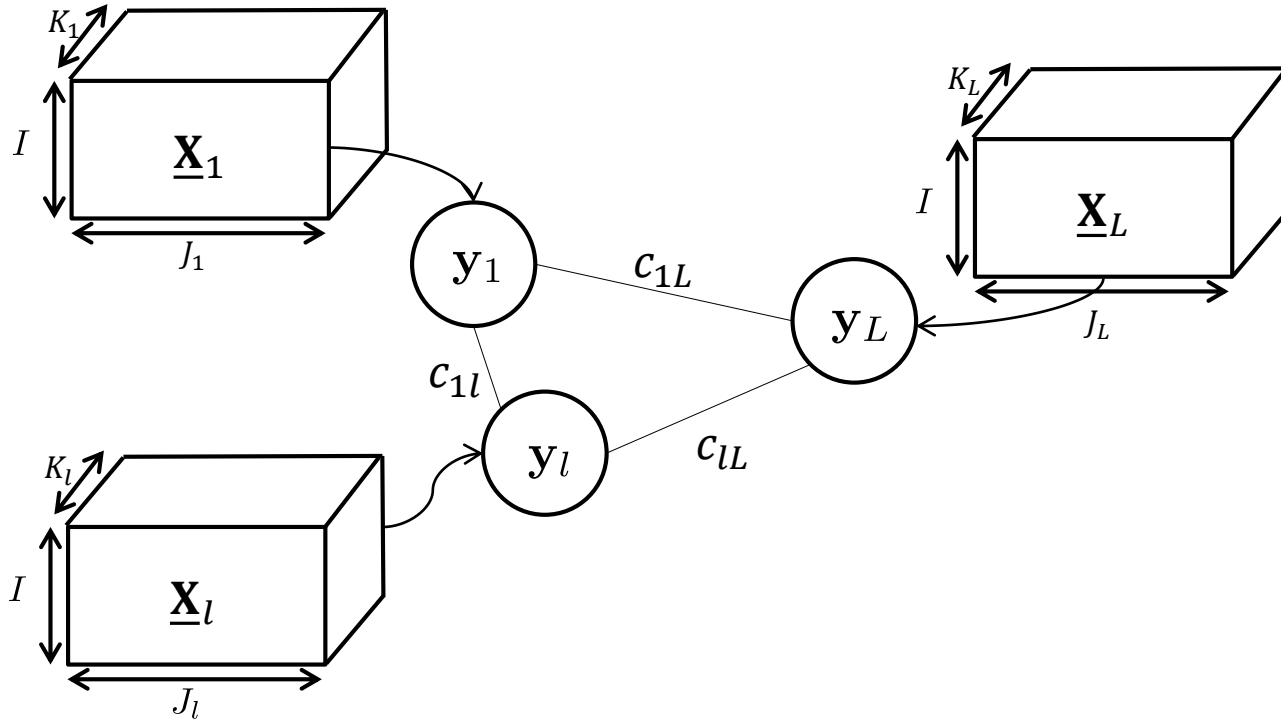
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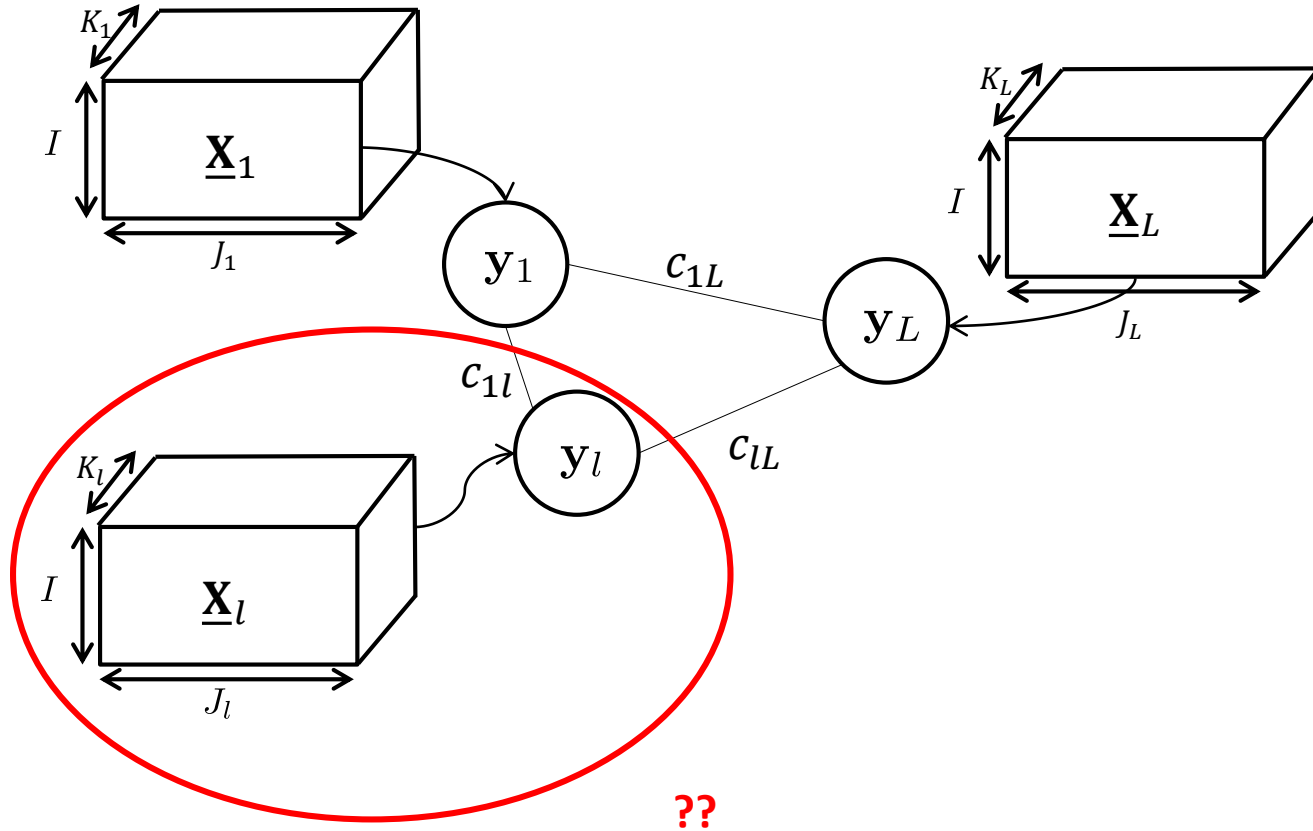
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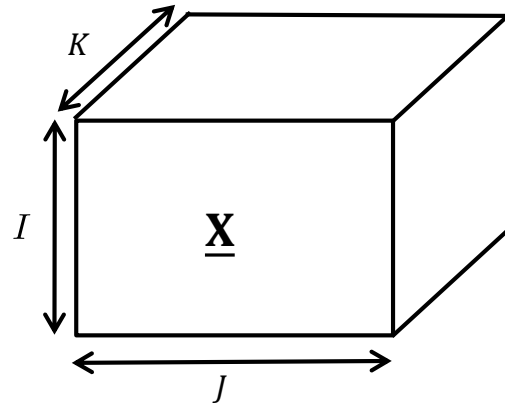
From RGCCA to Multiway GCCA



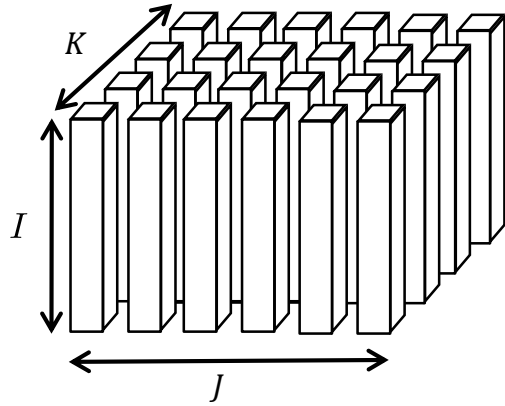
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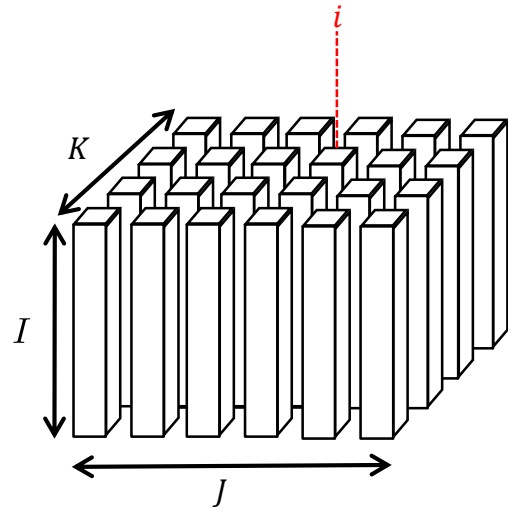
How Multiway is handled ?



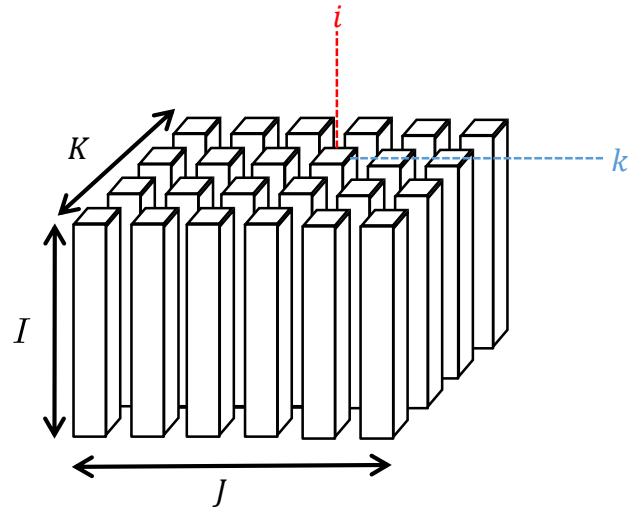
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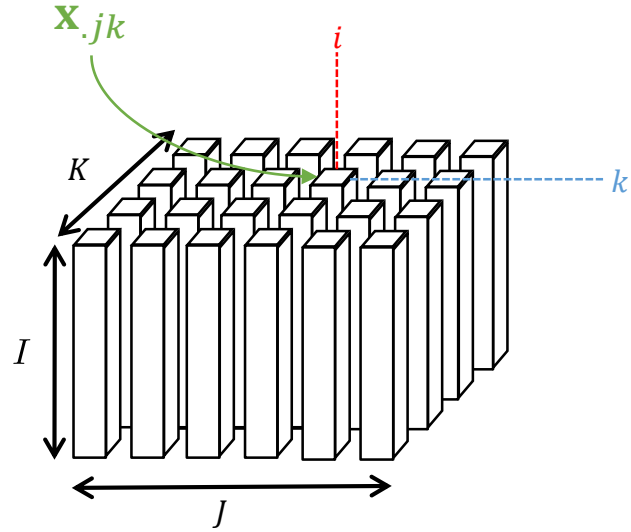
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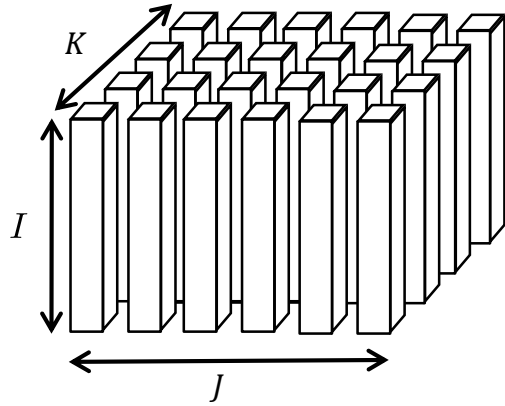
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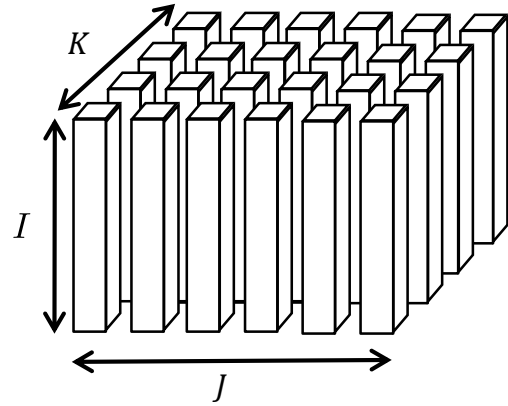
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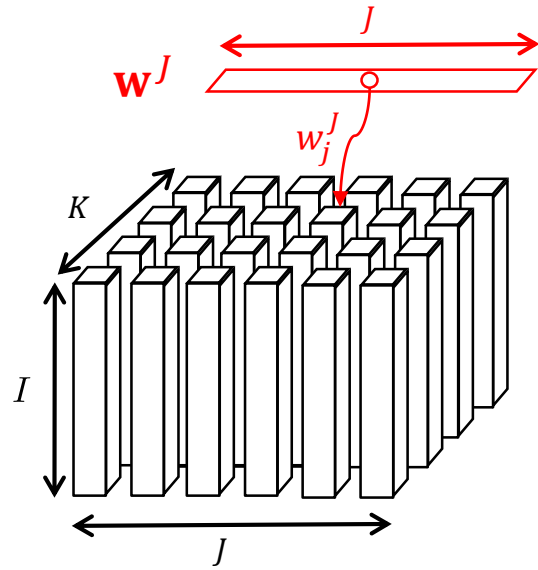
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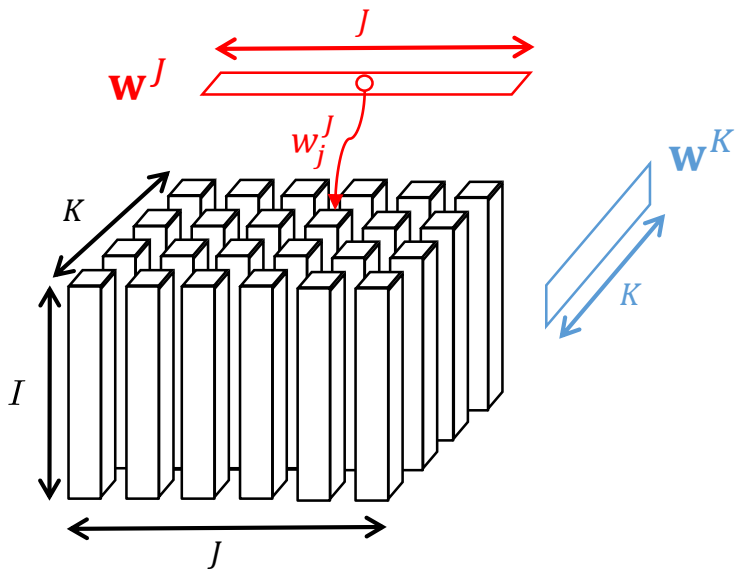
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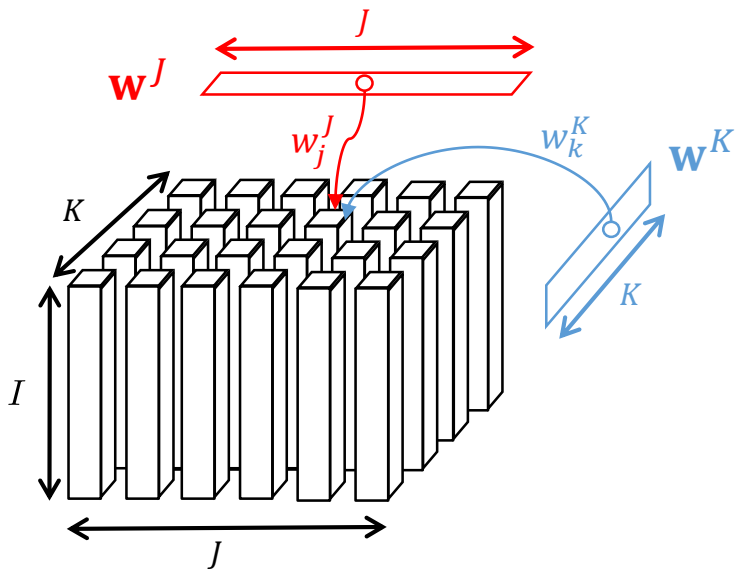
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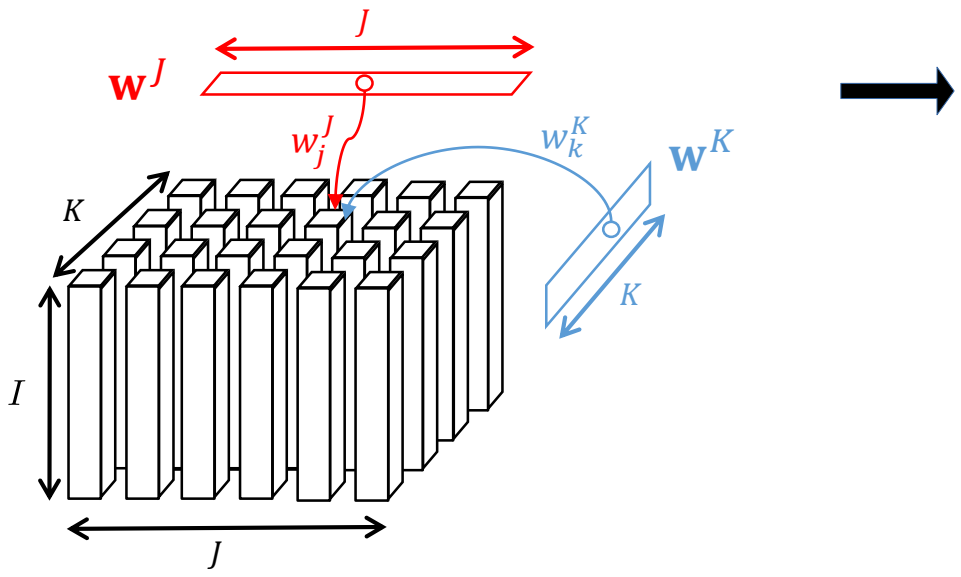
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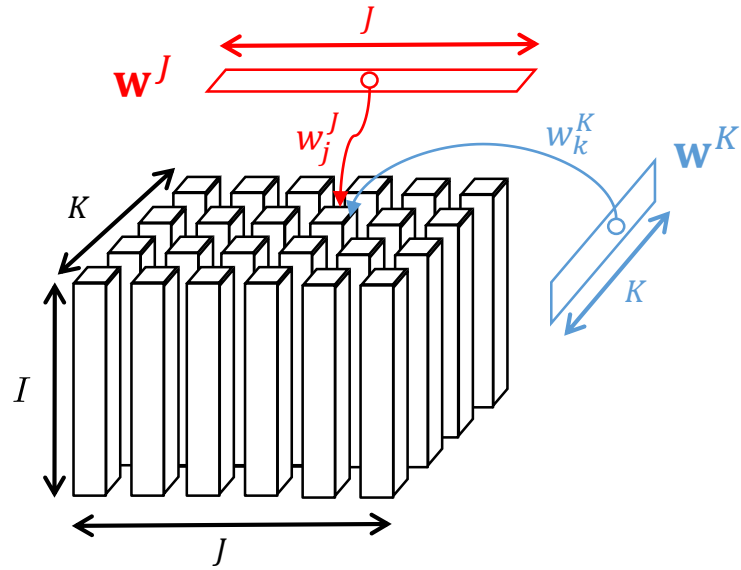
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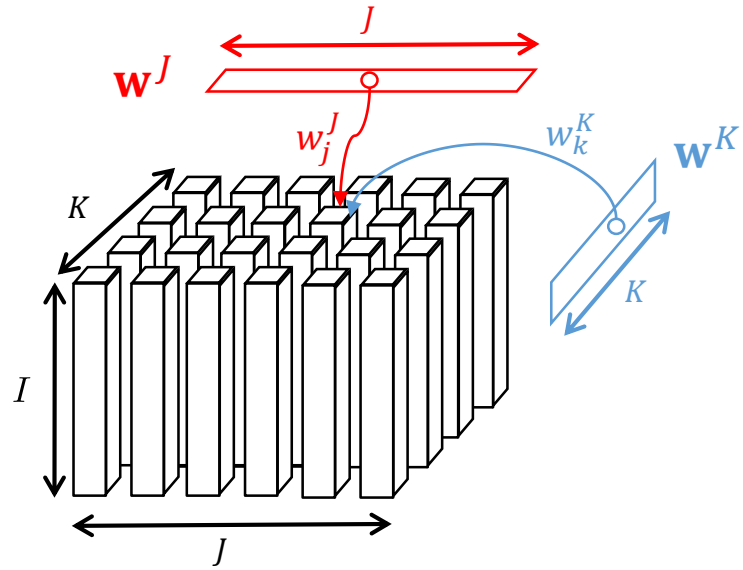


How Multiway is handled ?



$$y = \sum_{j=1}^J \sum_{k=1}^K w_k^K w_j^J x_{.jk}$$

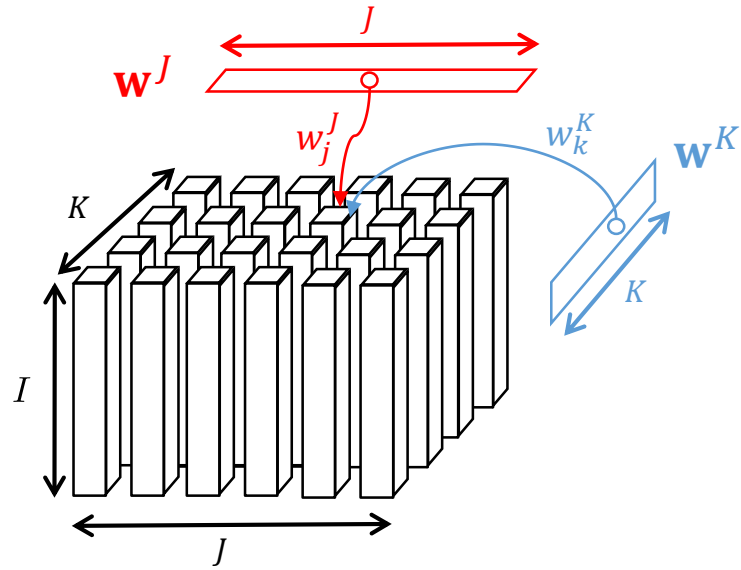
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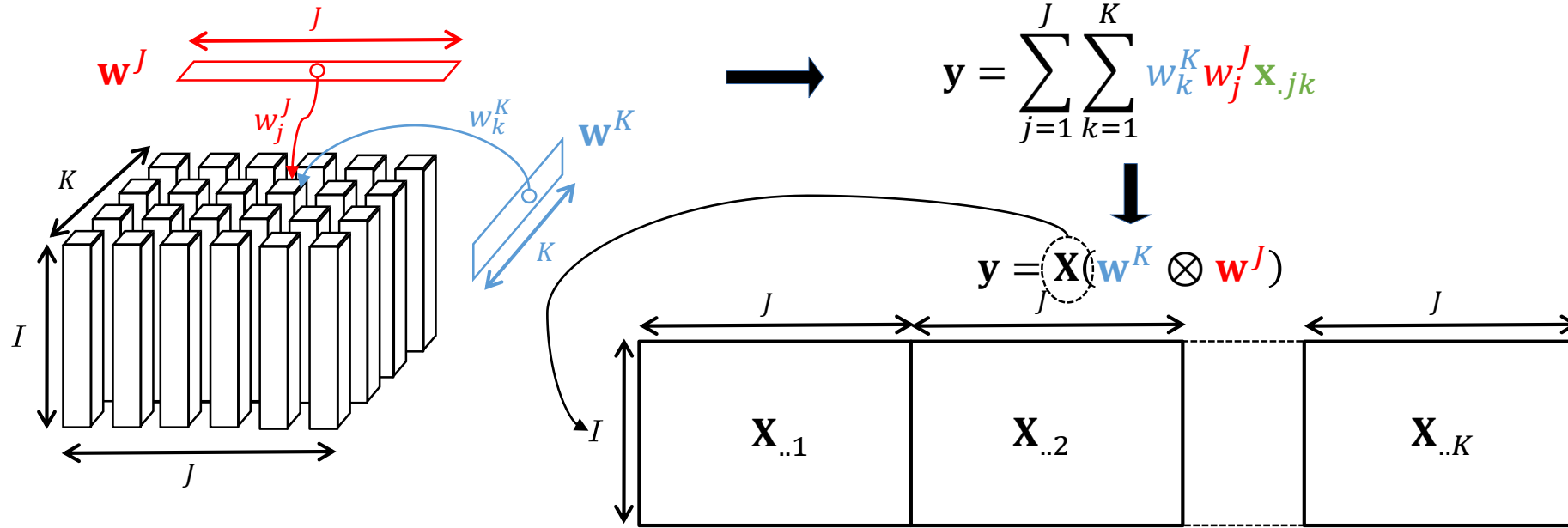
How Multiway is handled ?



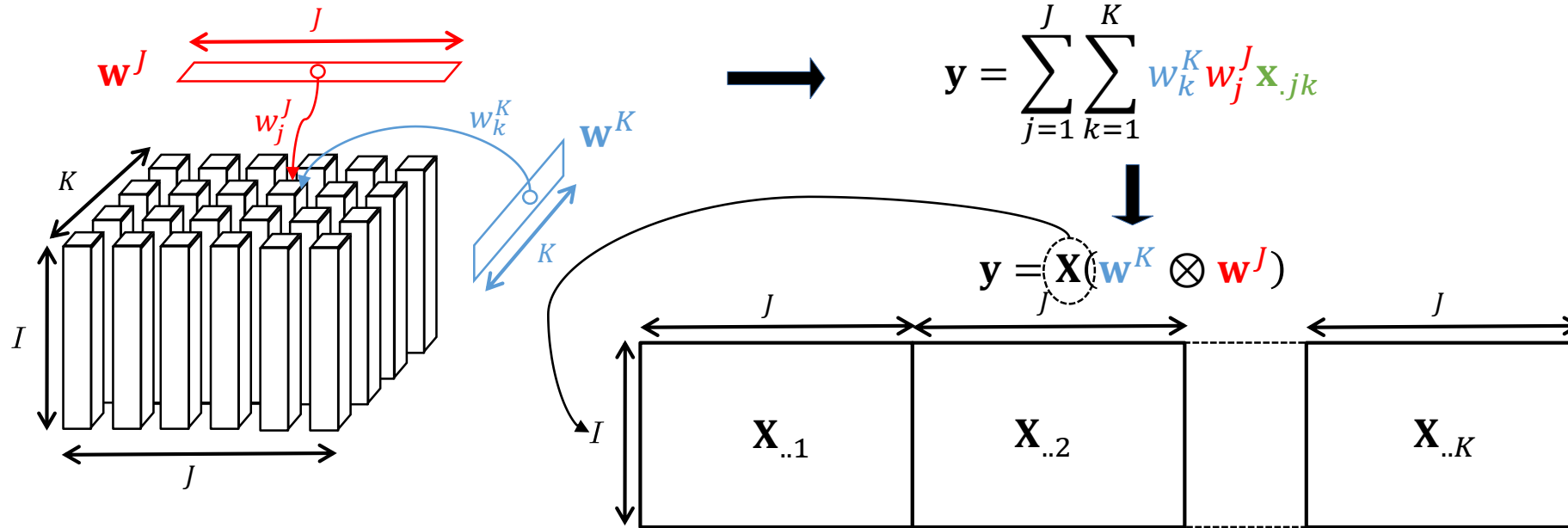
$$y = \sum_{j=1}^J \sum_{k=1}^K w_k^K w_j^J x_{.jk}$$

$$y = \mathbf{X}(\mathbf{w}^K \otimes \mathbf{w}^J)$$

How Multiway is handled ?

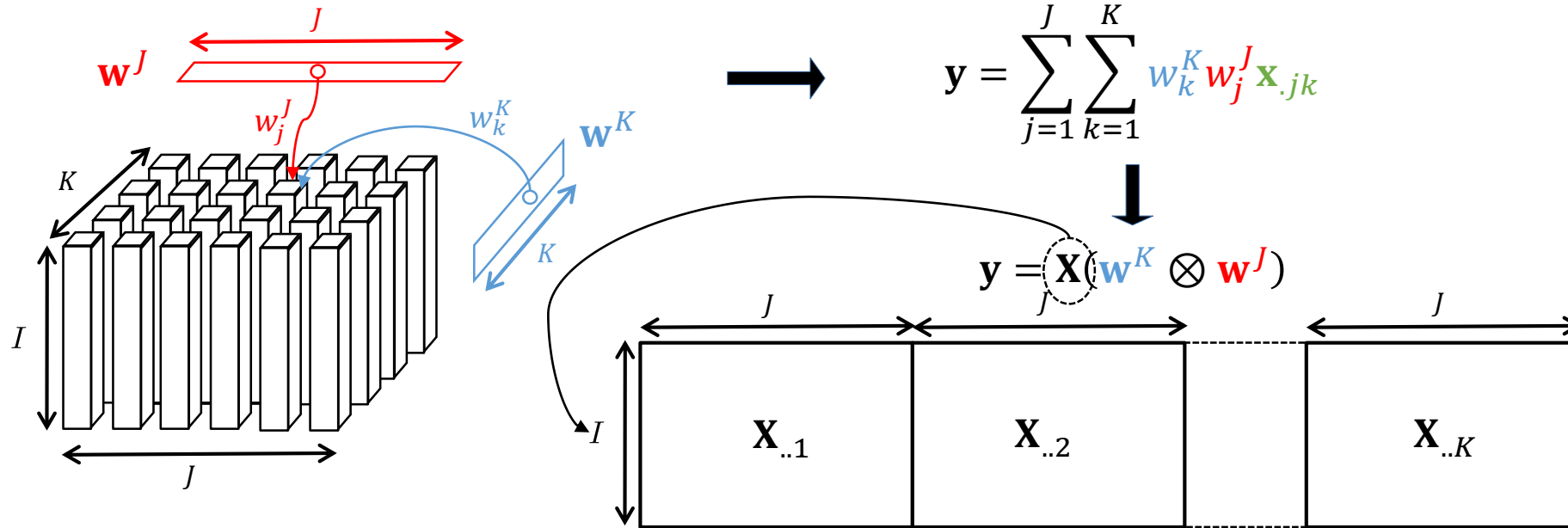


How Multiway is handled ?



Interest in taking into account 3-way structure with the Kronecker product:

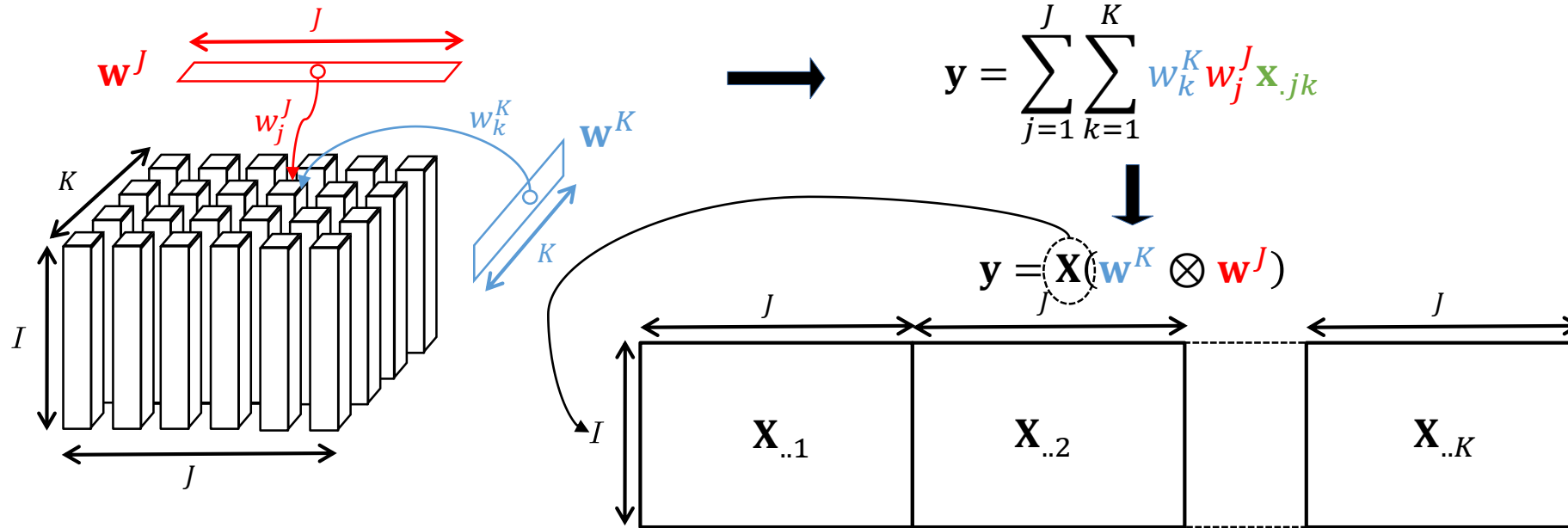
How Multiway is handled ?



Interest in taking into account 3-way structure with the Kronecker product:

- ❖ Gain in interpretability thanks to vector weights specific to each dimension.

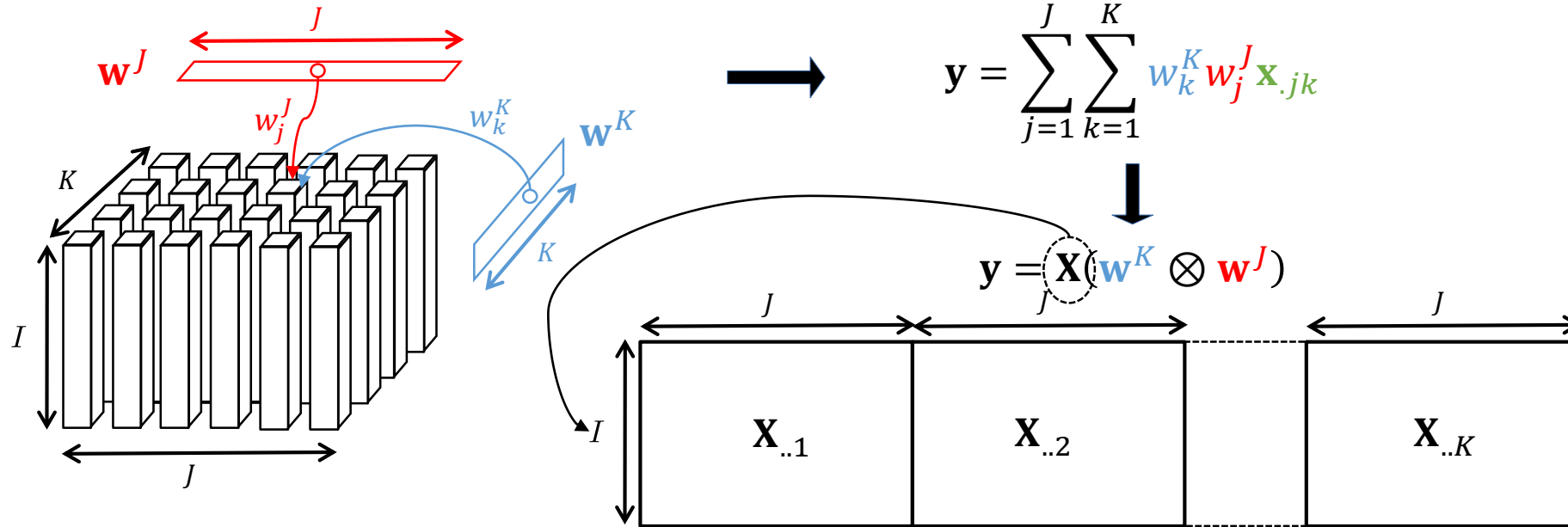
How Multiway is handled ?



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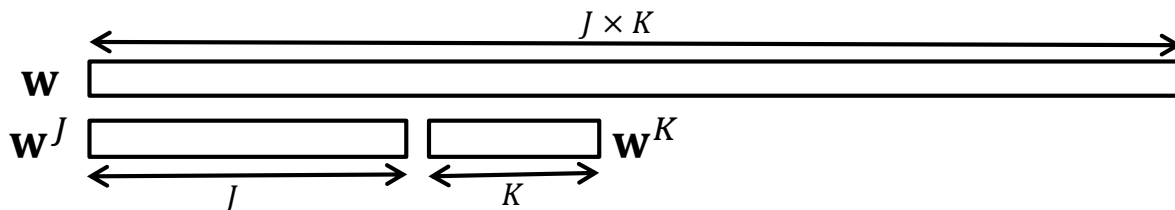
- ❖ Gain in interpretability thanks to vector weights specific to each dimension.
- ❖ Less weights to estimate: from $J \times K$ to $J + K$.

How Multiway is handled ?

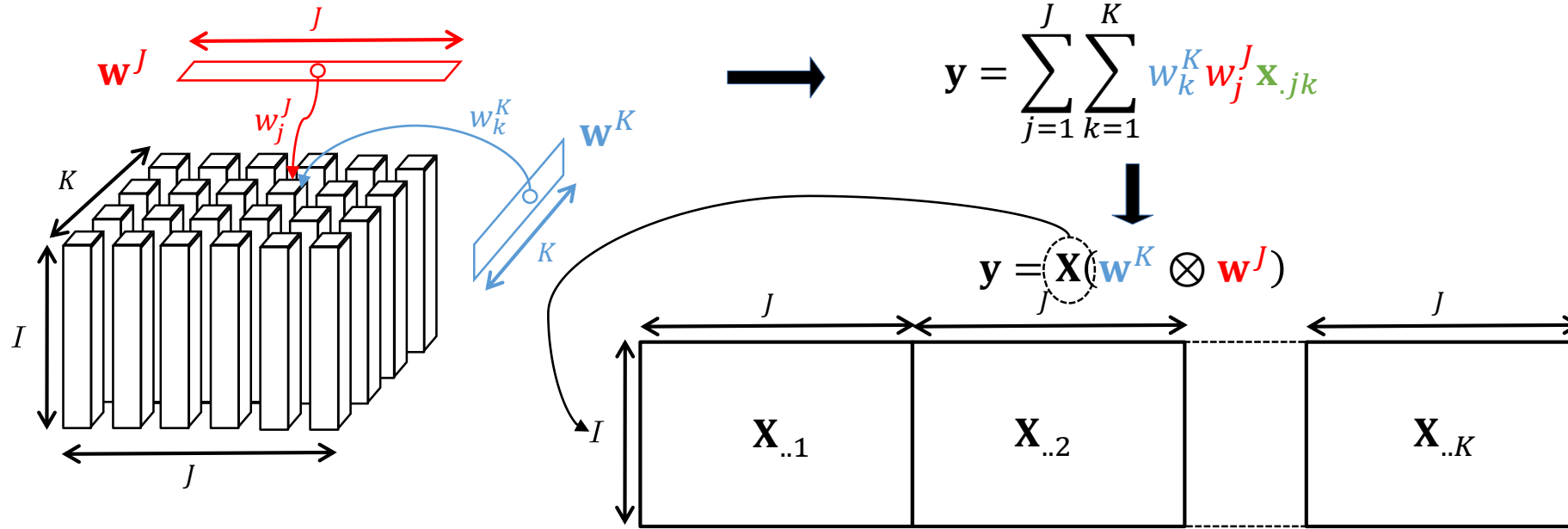


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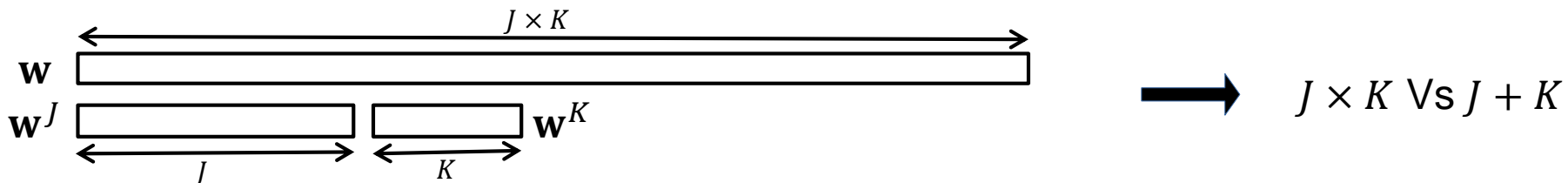


How Multiway is handled ?

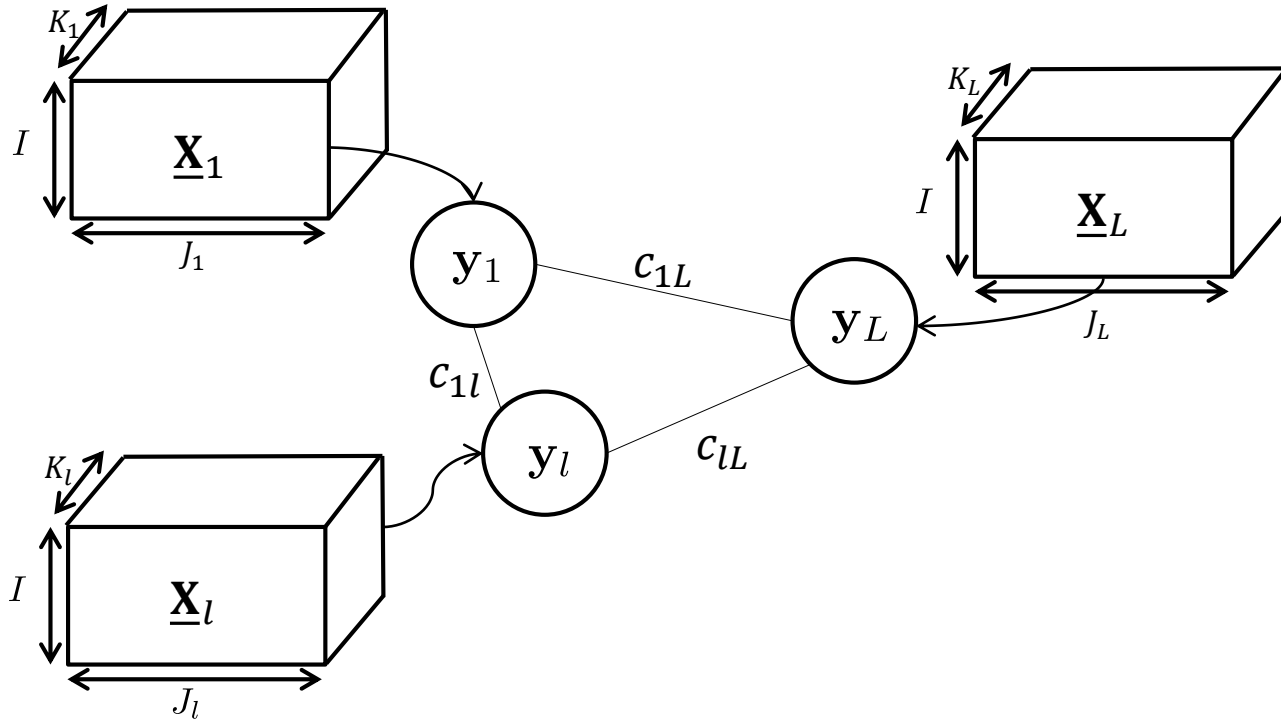


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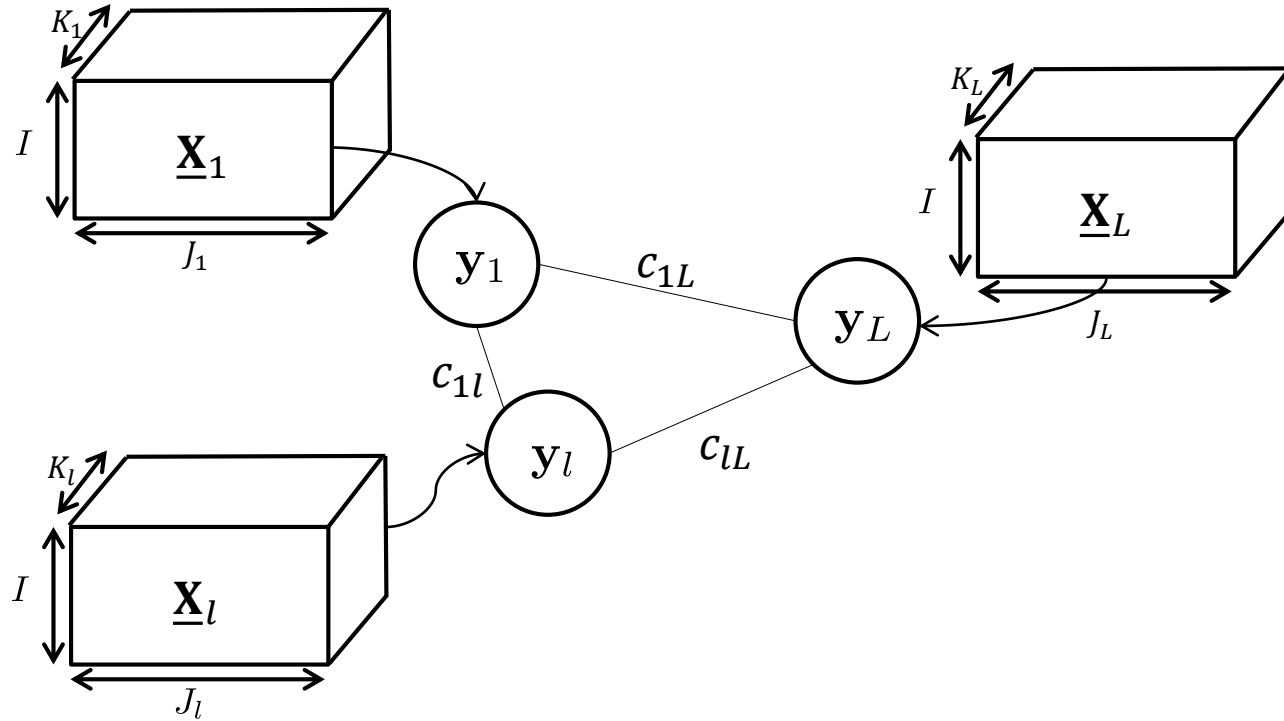
Multiway Generalized Canonical Correlation Analysis (MGCCA)



$$\max_{\mathbf{w}_1, \dots, \mathbf{w}_L} \sum_{k,l=1}^L c_{kl} g(\text{Cov}(\mathbf{X}_k \mathbf{w}_k, \mathbf{X}_l \mathbf{w}_l))$$

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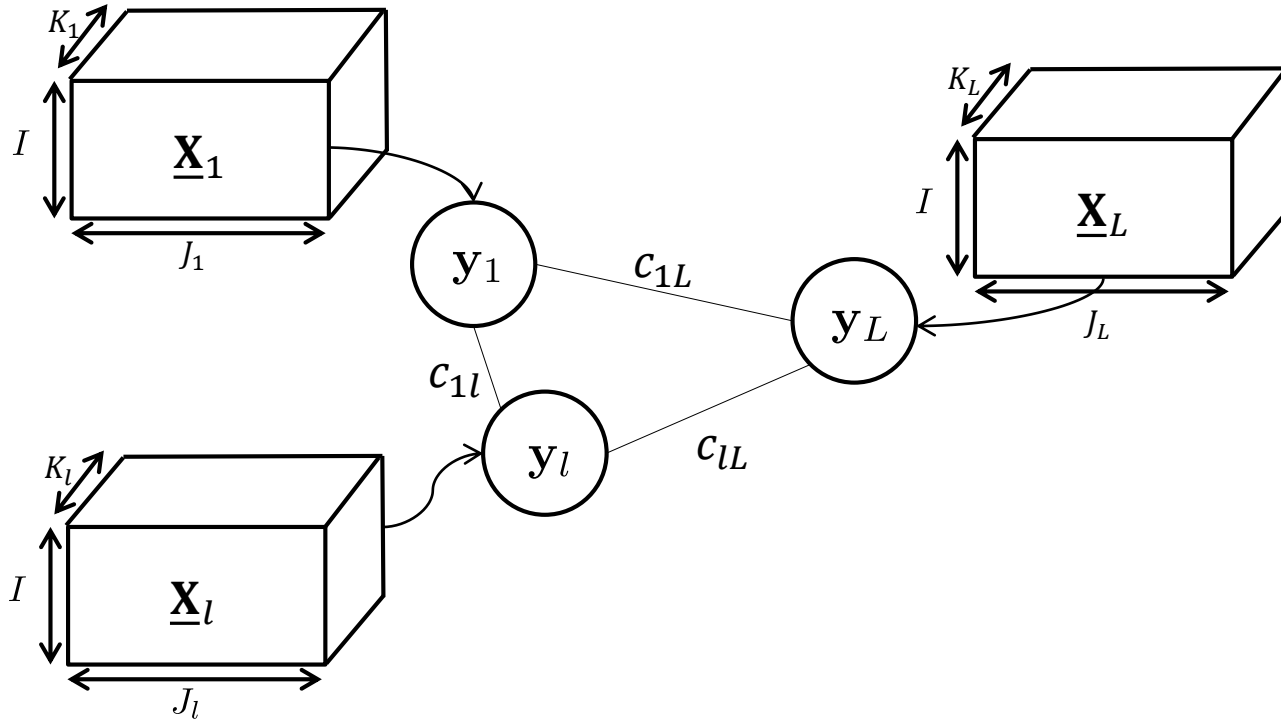
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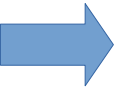
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Multiway Generalized Canonical Correlation Analysis (MGCCA)

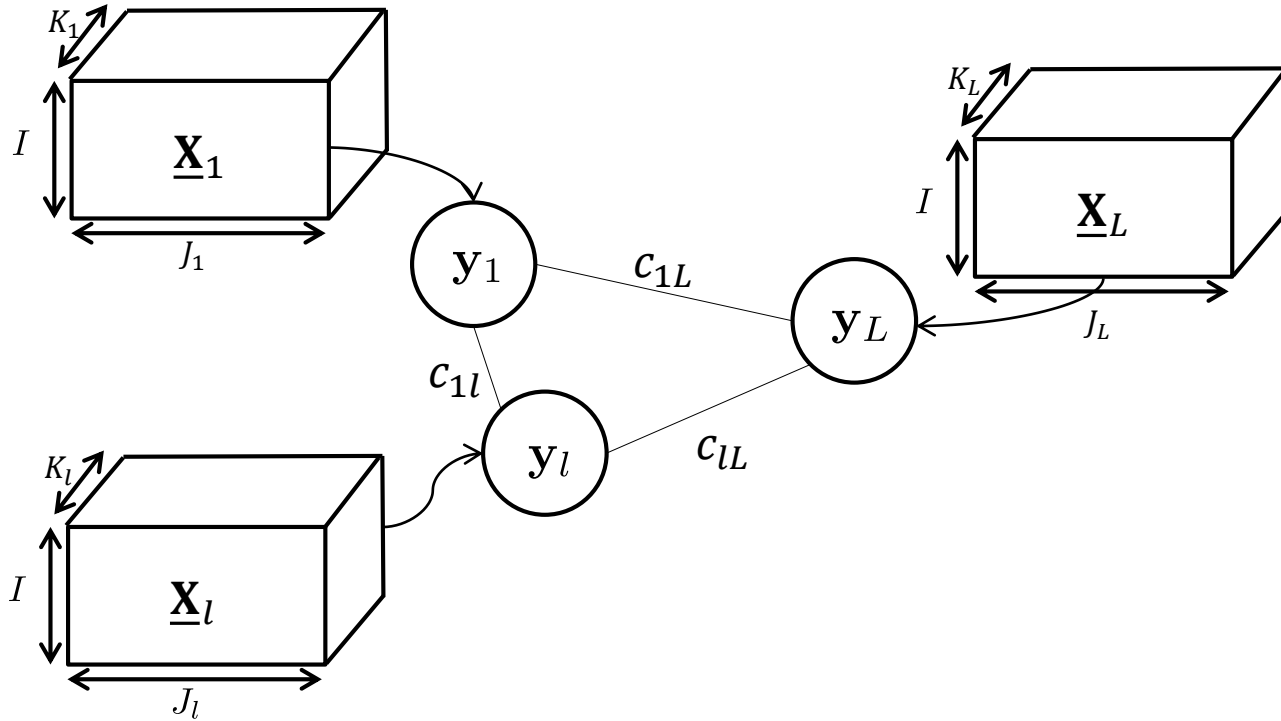


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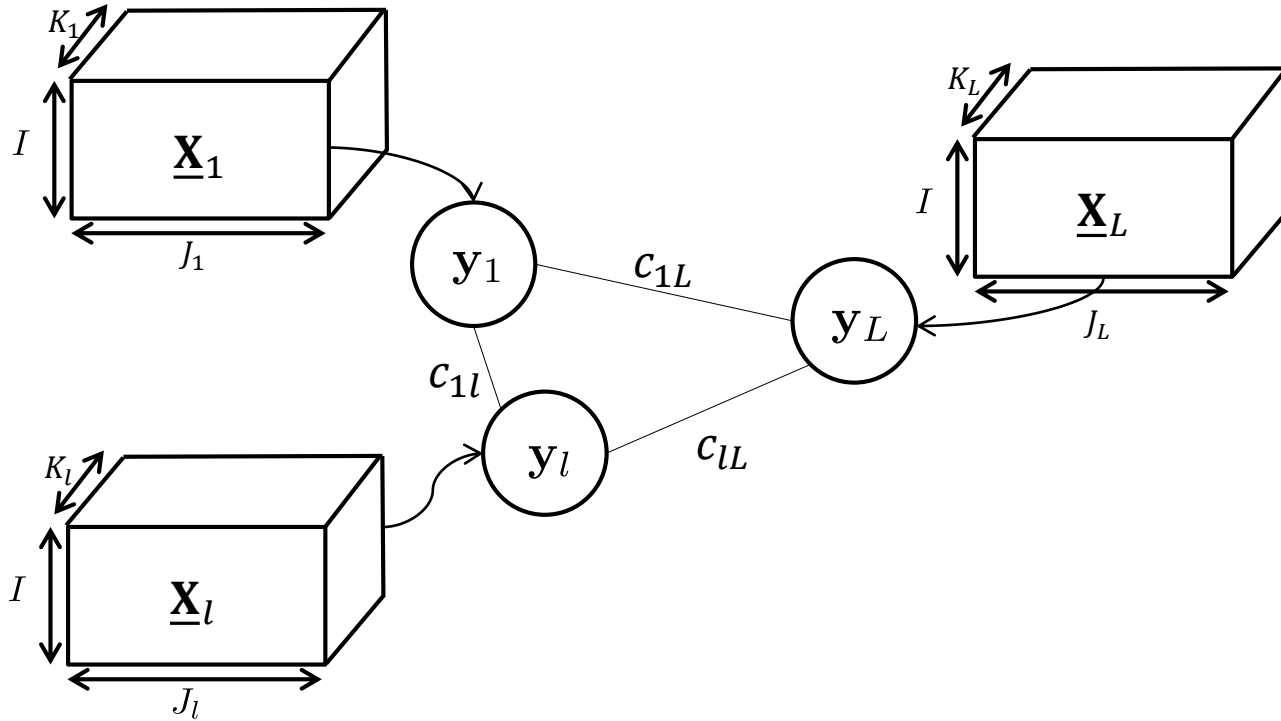


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➔ Example of such data: Electro-EncephaloGrams.

Multiway Generalized Canonical Correlation Analysis (MGCCA)

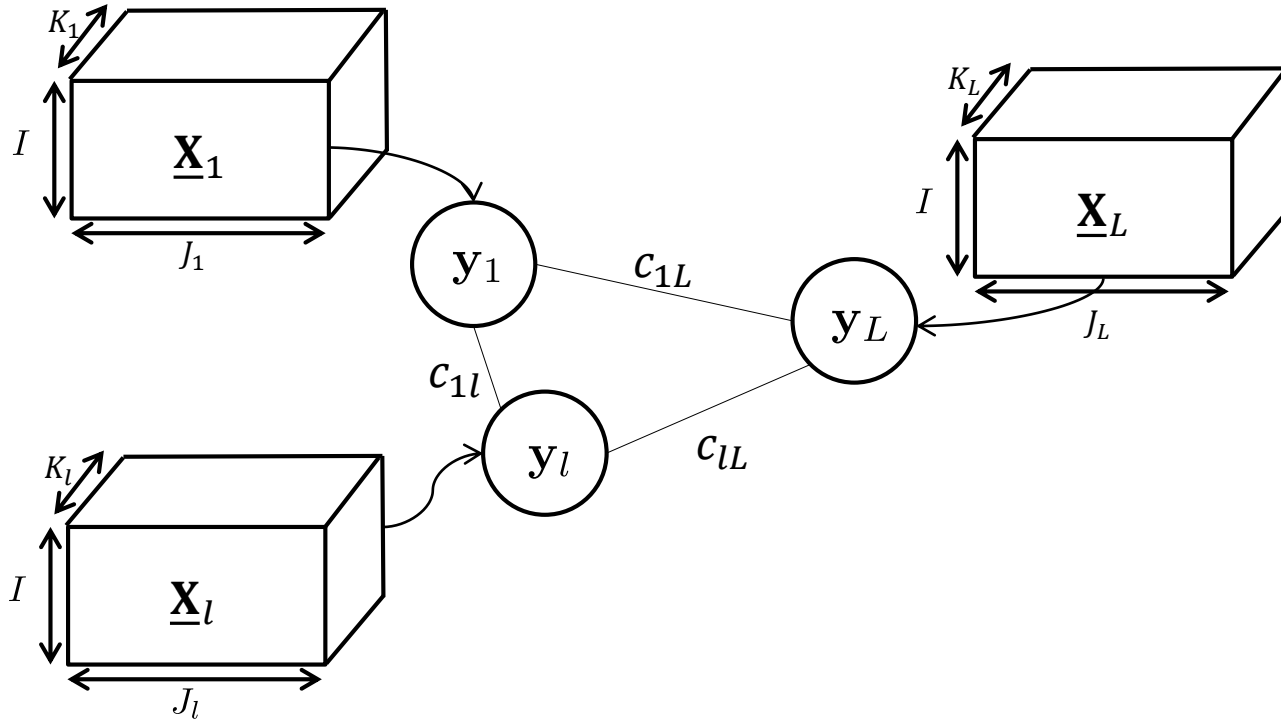


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Idea of the Algorithm:

Multiway Generalized Canonical Correlation Analysis (MGCCA)



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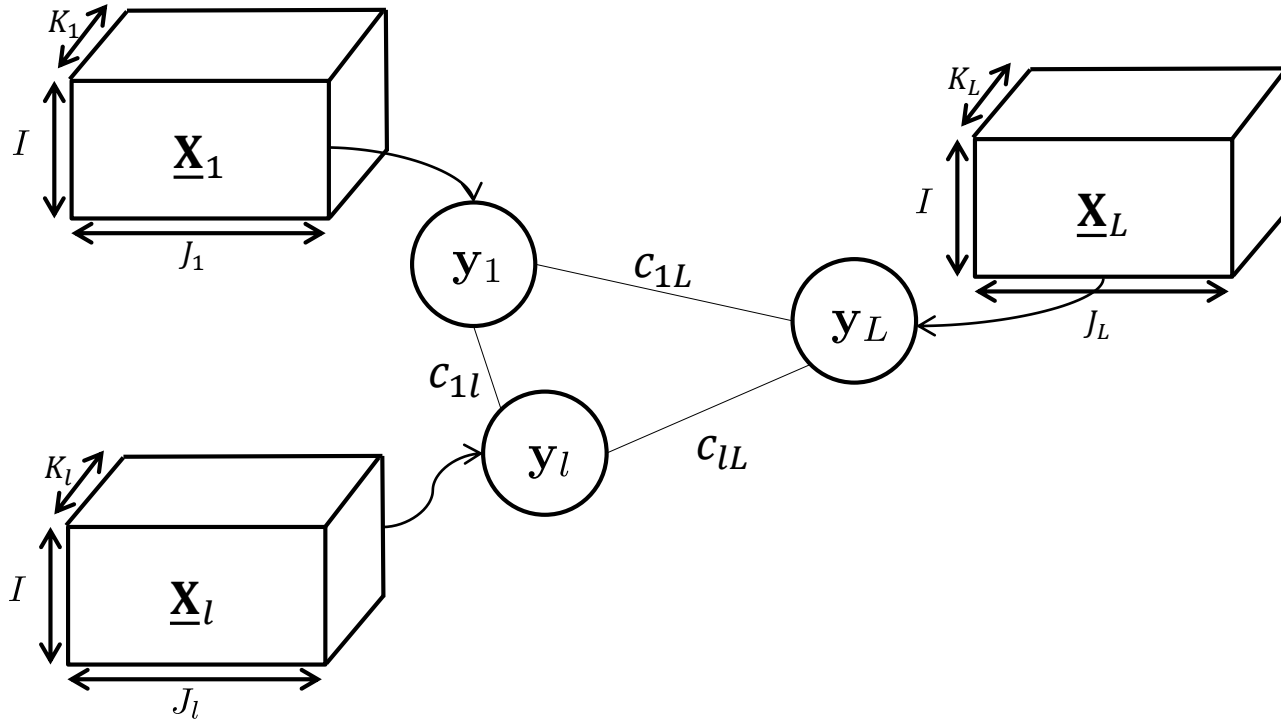
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1. Block Coordinate Ascent (BCA).

Multiway Generalized Canonical Correlation Analysis (MGCCA)



$$\max_{\mathbf{w}_1, \dots, \mathbf{w}_L} \sum_{k,l=1}^L c_{kl} g(\text{Cov}(\mathbf{X}_k \mathbf{w}_k, \mathbf{X}_l \mathbf{w}_l))$$

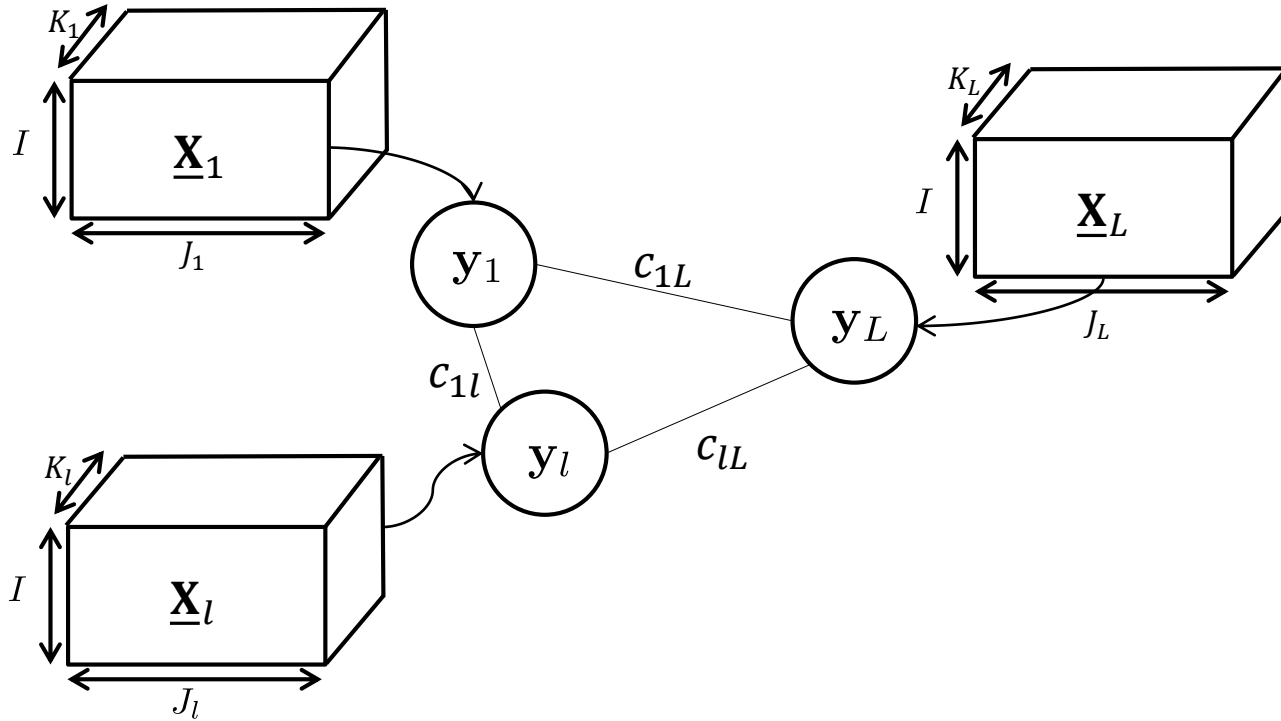
$$\text{s. t. } \begin{cases} \mathbf{w}_l^T \mathbf{M}_l \mathbf{w}_l = 1 \\ \mathbf{w}_l = \mathbf{w}_l^K \otimes \mathbf{w}_l^J \end{cases}, l = 1, \dots, L.$$

Example of such data: Electro-EncephaloGrams.

Idea of the Algorithm:

1. Block Coordinate Ascent (BCA).
2. MM principle: each update is a SVD of a specific matrix of size $K_l \times J_l$.

Multiway Generalized Canonical Correlation Analysis (MGCCA)



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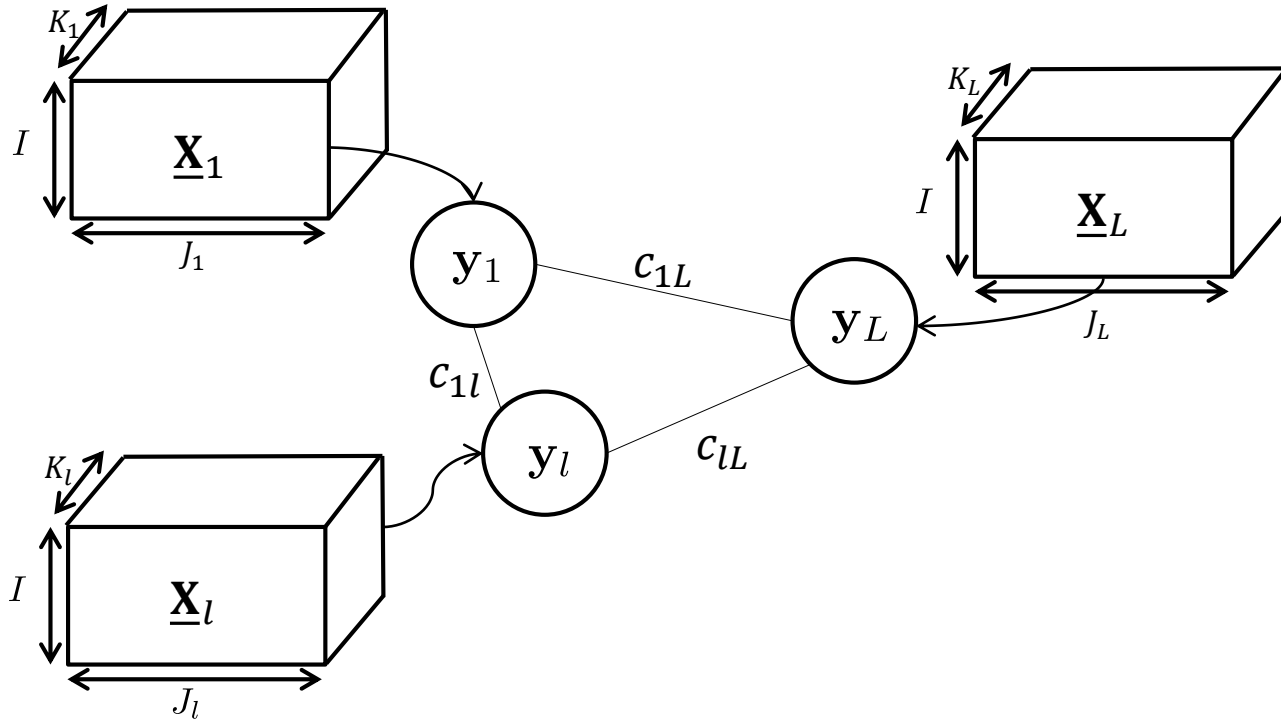
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Global convergence of this algorithm was shown.

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Idea of the Algorithm:

1. Block Coordinate Ascent (BCA).
2. MM principle: each update is a SVD of a specific matrix of size $K_l \times J_l$.

New extension with Tensor GCCA

Global convergence of this algorithm was shown.



		Core Optimization Problem			
			$\max \nabla_l f(\mathbf{w}^s)^\top \mathbf{w}_l$		
Constraints	$\mathbf{w}_l \in \omega_l$		RGCCA ^{1,2}		
	$\begin{cases} \ \mathbf{w}_l\ _2^2 = 1 \\ \ \mathbf{w}_l\ _1 \leq s_l \end{cases}$		SGCCA ³		
					Constraints

$$\omega_l = \{\mathbf{w}_l \in \mathbb{R}^{J_l}; \mathbf{w}_l^\top \mathbf{M}_l \mathbf{w}_l = 1\}$$

1. (Tenenhaus and Tenenhaus, 2011) 2. (Tenenhaus, Tenenhaus and Groenen, 2017) 3. (Tenenhaus et al., 2014)



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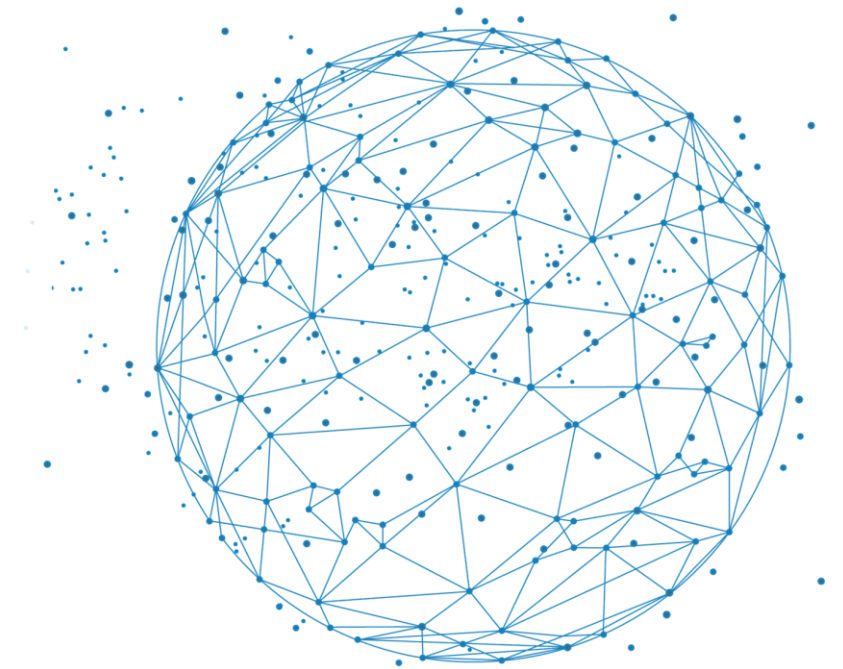
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1. Introduction of the case study
2. Unsupervised analysis with one-block: Principal Component Analysis (PCA)
3. Unsupervised analysis with two-blocks:
Partial Least Squares (PLS) and Canonical Correlation Analysis (CCA)
4. Unsupervised analysis with L -blocks:
Regularized Generalized Canonical Correlation Analysis (RGCCA)
5. Supervised analysis with RGCCA
6. Variable selection in RGCCA:
Sparse Generalized Canonical Correlation Analysis (SGCCA)
7. **The flexible Optimization Framework of RGCCA**

- ❖ The general principal
- ❖ Extension to multi-way analysis
- ❖ From Sequential to Global





$$\operatorname{argmax}_{\mathbf{w}_1, \dots, \mathbf{w}_L} \sum_{k,l=1}^L c_{kl} \quad g \left(\operatorname{Cov} \left(\mathbf{X}_k \mathbf{w}_k, \mathbf{X}_l \mathbf{w}_l \right) \right)$$
$$\text{s. t. } \left\{ \begin{array}{l} \mathbf{w}_l^\top \mathbf{M}_l \mathbf{w}_l = 1 \\ , l = 1, \dots, L. \end{array} \right.$$

Where:

❖ $\mathbf{w}_l \in \mathbb{R}^{J_l}$ is a block-weight vector.

Optimization criterion: From Sequential to Global



$$\operatorname{argmax}_{\mathbf{w}_1^{(1)}, \dots, \mathbf{w}_L^{(1)}} \sum_{k,l=1}^L c_{kl} \quad g \left(\operatorname{Cov} \left(\mathbf{X}_k \mathbf{w}_k^{(1)}, \mathbf{X}_l \mathbf{w}_l^{(1)} \right) \right)$$
$$\text{s. t.} \begin{cases} \mathbf{w}_l^{(1)\top} \mathbf{M}_l \mathbf{w}_l^{(1)} = 1 \\ , l = 1, \dots, L. \end{cases}$$

Where:

❖ $\mathbf{w}_l^{(1)} \in \mathbb{R}^{J_l}$ is a **the first** block-weight vector.



$$\operatorname{argmax}_{\mathbf{w}_1^{(2)}, \dots, \mathbf{w}_L^{(2)}} \sum_{k,l=1}^L c_{kl} \quad g \left(\operatorname{Cov} \left(\mathbf{X}_k \mathbf{w}_k^{(2)}, \mathbf{X}_l \mathbf{w}_l^{(2)} \right) \right)$$
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Where:

- ❖ $\mathbf{w}_l^{(1)} \in \mathbb{R}^{J_l}$ is a **the first** block-weight vector.
- ❖ $\mathbf{w}_l^{(2)} \in \mathbb{R}^{J_l}$ is a **the second** block-weight vector.



$$\operatorname{argmax}_{\mathbf{w}_1^{(2)}, \dots, \mathbf{w}_L^{(2)}} \sum_{k,l=1}^L c_{kl} \quad g \left(\operatorname{Cov} \left(\mathbf{X}_k \mathbf{w}_k^{(2)}, \mathbf{X}_l \mathbf{w}_l^{(2)} \right) \right)$$
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- ❖ ...



$$\operatorname{argmax}_{\mathbf{w}_1^{(1)}, \dots, \mathbf{w}_L^{(1)}} \sum_{k,l=1}^L c_{kl} \quad g \left(\operatorname{Cov} \left(\mathbf{X}_k \mathbf{w}_k^{(1)}, \mathbf{X}_l \mathbf{w}_l^{(1)} \right) \right)$$

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$$\operatorname{argmax}_{\mathbf{w}_1^{(r)}, \dots, \mathbf{w}_L^{(r)}} \sum_{k,l=1}^L c_{kl} \sum_{r=1}^R g \left(\operatorname{Cov} \left(\mathbf{X}_k \mathbf{w}_k^{(r)}, \mathbf{X}_l \mathbf{w}_l^{(r)} \right) \right)$$

Where:

❖ $\mathbf{w}_l^{(r)} \in \mathbb{R}^{J_l}$ is a the r^{th} block-weight vector.



$$\operatorname{argmax}_{\mathbf{W}_1, \dots, \mathbf{W}_L} \sum_{k,l=1}^L c_{kl} \operatorname{Trace} \left(g(\operatorname{Cov}(\mathbf{X}_k \mathbf{W}_k, \mathbf{X}_l \mathbf{W}_l)) \right)$$

Where:

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- ❖ $\mathbf{W}_l = [\mathbf{w}_l^{(1)}, \dots, \mathbf{w}_l^{(R)}] \in \mathbb{R}^{J_l \times R}$ is a **block-weight matrix**.



$$\operatorname{argmax}_{\mathbf{W}_1, \dots, \mathbf{W}_L} \sum_{k,l=1}^L c_{kl} \operatorname{Trace} \left(g(\operatorname{Cov}(\mathbf{X}_k \mathbf{W}_k, \mathbf{X}_l \mathbf{W}_l)) \right)$$

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Following the optimization framework of RGCCA, the core optimization problem is:

$$\underset{\mathbf{W}_l, \mathbf{W}_l^T \mathbf{M}_l \mathbf{W}_l = \mathbf{I}_R}{\operatorname{argmax}} \operatorname{Trace}(\nabla_l f(\mathbf{W}^s)^T \mathbf{W}_l)$$



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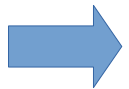


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Closed form solution: the rank- R Singular Value Decomposition (SVD) of a specific matrix of dimension $J_l \times R$.



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❖ A single optimization problem allows to extract all components simultaneously.



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Cons:



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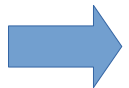
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Closed form solution: the rank- R Singular Value Decomposition (SVD) of a specic matrix of dimension $J_l \times R$.



Pros:

- ❖ A single optimization problem allows to extract all components simultaneously.
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- ❖ It is possible now to add constraints across components.

Cons:

- ❖ In this form, we have to extract the same number of component per block.



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		$\max \nabla_l f(\mathbf{w}^s)^\top \mathbf{w}_l$	
Constraints	$\mathbf{w}_l \in \omega_l$	RGCCA ^{1,2}	
	$\begin{cases} \ \mathbf{w}_l\ _2^2 = 1 \\ \ \mathbf{w}_l\ _1 \leq s_l \end{cases}$	SGCCA ³	
	$\begin{cases} \mathbf{w}_l = \mathbf{w}_l^K \otimes \mathbf{w}_l^J \\ \mathbf{w}_l \in \omega_l \end{cases}$	MGCCA ⁴ /TGCCA ⁵	
			Constraints

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		Sequential	Global
		$\max \nabla_l f(\mathbf{w}^s)^\top \mathbf{w}_l$	
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		Sequential	Global
		$\max \nabla_l f(\mathbf{w}^s)^\top \mathbf{w}_l$	$\max \text{Tr}(\nabla_l f(\mathbf{W}^s)^\top \mathbf{W}_l)$
Constraints	$\mathbf{w}_l \in \omega_l$	RGCCA ^{1,2}	
	$\begin{cases} \ \mathbf{w}_l\ _2^2 = 1 \\ \ \mathbf{w}_l\ _1 \leq s_l \end{cases}$	SGCCA ³	
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		Sequential	Global		
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Constraints	$\mathbf{w}_l \in \omega_l$	RGCCA ^{1,2}		$\mathbf{W}_l \in \Omega_l$	Constraints
	$\begin{cases} \ \mathbf{w}_l\ _2^2 = 1 \\ \ \mathbf{w}_l\ _1 \leq s_l \end{cases}$	SGCCA ³			
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		Sequential	Global		
		$\max \nabla_l f(\mathbf{w}^s)^\top \mathbf{w}_l$	$\max \text{Tr}(\nabla_l f(\mathbf{W}^s)^\top \mathbf{W}_l)$		
Constraints	$\mathbf{w}_l \in \omega_l$	RGCCA ^{1,2}	Global RGCCA ^{6,7}	$\mathbf{W}_l \in \Omega_l$	Constraints
	$\begin{cases} \ \mathbf{w}_l\ _2^2 = 1 \\ \ \mathbf{w}_l\ _1 \leq s_l \end{cases}$	SGCCA ³			
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		Core Optimization Problem			
		Sequential	Global		
		$\max \nabla_l f(\mathbf{w}^s)^\top \mathbf{w}_l$	$\max \text{Tr}(\nabla_l f(\mathbf{W}^s)^\top \mathbf{W}_l)$		
Constraints	$\mathbf{w}_l \in \omega_l$	RGCCA ^{1,2}	Global RGCCA ^{6,7}	$\mathbf{W}_l \in \Omega_l$	Constraints
	$\begin{cases} \ \mathbf{w}_l\ _2^2 = 1 \\ \ \mathbf{w}_l\ _1 \leq s_l \end{cases}$	SGCCA ³			
	$\begin{cases} \mathbf{w}_l = \mathbf{w}_l^K \otimes \mathbf{w}_l^J \\ \mathbf{w}_l \in \omega_l \end{cases}$	MGCCA ⁴ /TGCCA ⁵		$\begin{cases} \mathbf{W}_l = \mathbf{W}_l^K \odot \mathbf{W}_l^J \\ \mathbf{W}_l \in \Omega_l \end{cases}$	

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	Structured Sparsity				

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	$\begin{cases} \ \mathbf{w}_l\ _2^2 = 1 \\ \ \mathbf{w}_l\ _1 \leq s_l \end{cases}$	SGCCA ³			
	$\begin{cases} \mathbf{w}_l = \mathbf{w}_l^K \otimes \mathbf{w}_l^J \\ \mathbf{w}_l \in \omega_l \end{cases}$	MGCCA ⁴ /TGCCA ⁵	Global MGCCA ^{6,7}	$\begin{cases} \mathbf{W}_l = \mathbf{W}_l^K \odot \mathbf{W}_l^J \\ \mathbf{W}_l \in \Omega_l \end{cases}$	
	Structured Sparsity	(i). Group-Lasso in the same framework ⁸ (ii). Other structured sparse penalties in other frameworks ^{6,9,10,11}			

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		$\max \nabla_l f(\mathbf{w}^s)^\top \mathbf{w}_l$	$\max \text{Tr}(\nabla_l f(\mathbf{W}^s)^\top \mathbf{W}_l)$		
Constraints	$\mathbf{w}_l \in \omega_l$	RGCCA ^{1,2}	Global RGCCA ^{6,7}	$\mathbf{W}_l \in \Omega_l$	
	$\begin{cases} \ \mathbf{w}_l\ _2^2 = 1 \\ \ \mathbf{w}_l\ _1 \leq s_l \end{cases}$	SGCCA ³	In progress ⁷	In progress ⁷	
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In order to take estimate non-linear links between blocks.



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Missing Values in RGCCA (Peltier et al., 2023).



<https://github.com/rgcca-factory/RGCCA>



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Arthur TENENHAUS
Laboratoire Des Signaux Et Systèmes, CentraleSupélec



Fabien GIRKA
Laboratoire Des Signaux Et Systèmes, CentraleSupélec

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Caroline PELTIER
CNRS, INRAE

Here are the contributors of the actual version of the package !!



Vincent GUILLEMOT
Institut Pasteur, Bioinformatics and Biostatistics Hub



Arnaud GLOAGUEN
Centre National de Recherche en Génomique Humaine, CEA

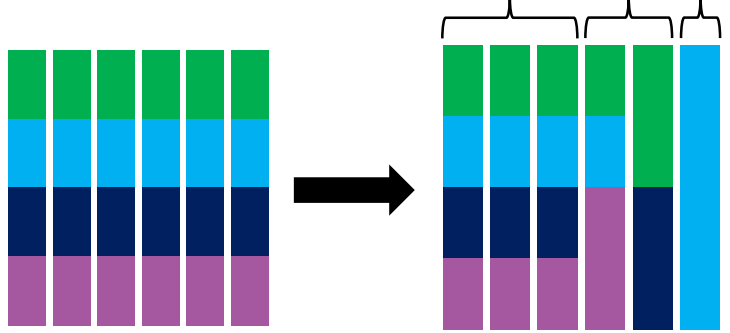
Other perspectives ?



Other perspectives ?



Axe 1: Use comon and specific information

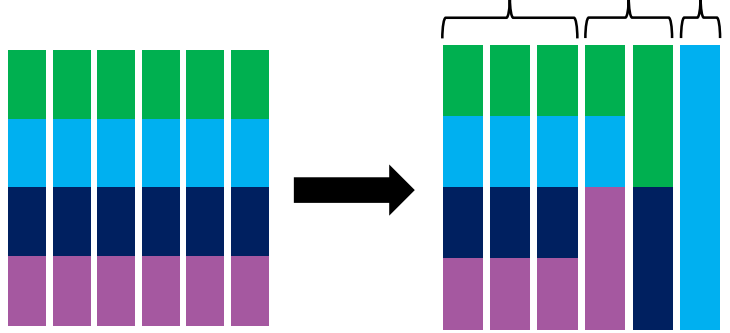


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Vary the combination of omics data from which components are built.



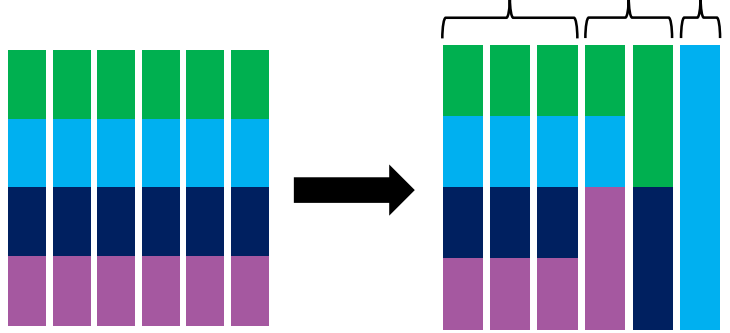
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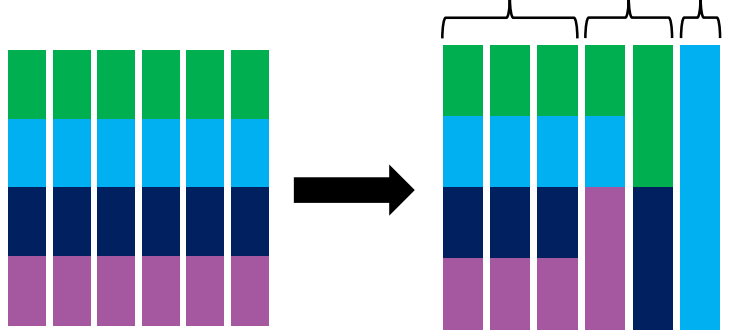


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Axe 1: Use comon and specific information

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Axe 2: Include the appartenance of each variable to a biological pathway.

Divide each omic matrix by biological pathways.
Allow to identify most important pathways (With L1 norm).

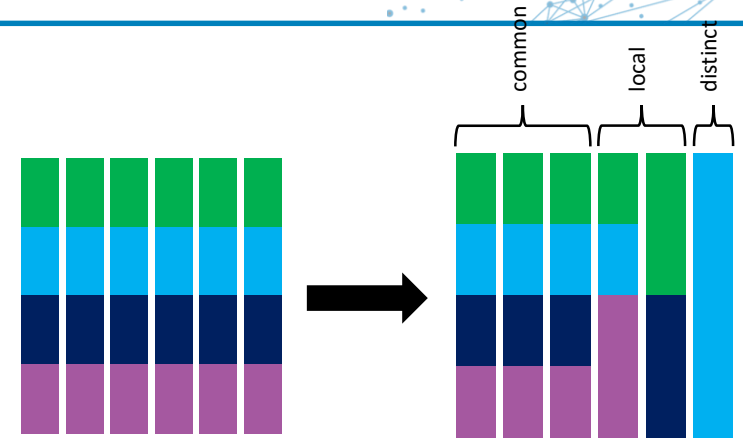


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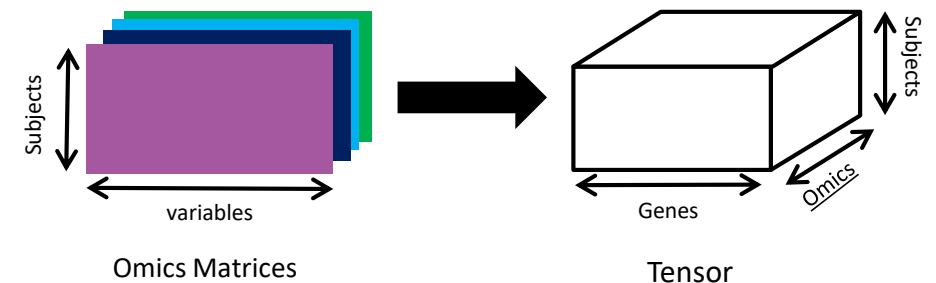
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Axe 3: Link variables across different omics

Regroup omic matrices along the third dimension (ex: by genes) to create a tensor.

Permet d'ajouter une notion biologique dans la définition du modèle



Courtesy to Vincent Le Goff.

Other perspectives ?

PhD of Vincent LE GOFF

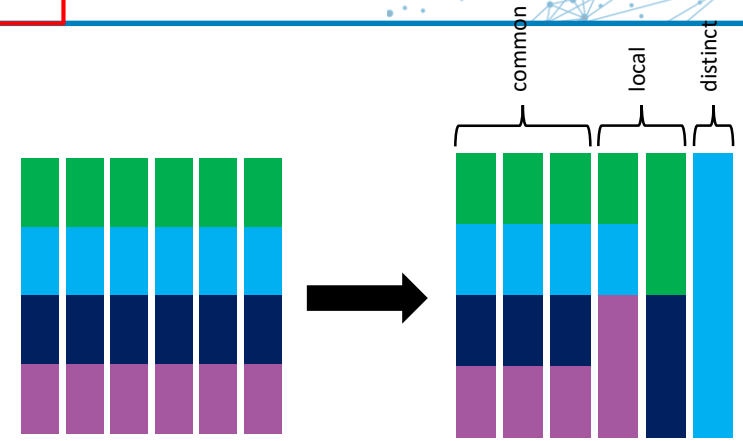
Supervised by:

- Edith Le Floch
- Vincent Guillemot
- Arnaud Gloaguen

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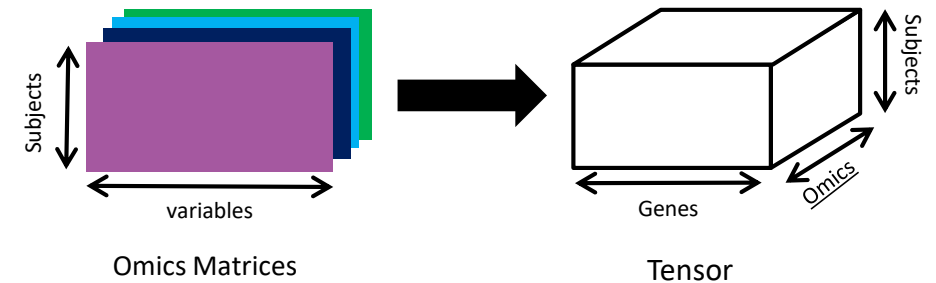
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Data (CT-ScarBip Project)

Andrée Delahaye-Duriez

Pierre-Eric Lutz

Amazigh Mokhtari

David Cohen

Bruno Etain

Cynthia Marie-Clair

El Chérif Ibrahim

Belzeaux Raoul

Gascon Gonzalo

Isabelle Mansuy

Summer School SIB/IFB:

Florence Mehl

Olivier Sand

Grégoire Rossier

Jimmy Vandel

Guillemette Marot

Marie-Galadriel Briere

Lucie Khamvongsa-Charbonnier

Morgane Terezol

Anaïs Baudot

Maxime Delmas

Jean-Clément Gallardo

Marco Pagni

Statomique:

Guillemette Marot (again !)

Christelle Hennequet-Antier

Julie Aubert

Marie-Agnès Dillies

Helene Touzet

Justine Merlan

ETBII:

Lucie Khamvongsa-Charbonnier

Hélène Chiapello

Olivier Sand

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Arthur Tenenhaus

Laurent Le Brusquet

Julien Bect

Vincent Le Goff

Edith Le Floch

Morgane Terezol

Alban Gaignard

Olivier Dameron

Pierre Larmande



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Thank you for your attention !

