#### Multi-view Spectral Clustering and Generation from a Shared Latent Space

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#### Unsupervised Multi-view Learning

#### Unsupervised Multi-view Learning

- Real-world data can be collected from different sources, e.g.,
  - Newspaper articles in multiple languages,
  - Multi-omic data: genomics, transcriptomics, methylomics...
- Aim: fuse information from multiple views to gain greater insights compared to considering a single view.

#### Unsupervised Multi-view Learning

- Real-world data can be collected from different sources, e.g.,
  - Newspaper articles in multiple languages,
  - Multi-omic data: genomics, transcriptomics, methylomics...
- Aim: fuse information from multiple views to gain greater insights compared to considering a single view.
- Multi-view dimensionality reduction: the multi-view dataset is reduced to a lower-dimensional space to compactly represent the heterogeneous data. Applications:
  - Multi-view generation and domain translation: generation of new samples in multiple views simultaneously or generation of missing views.
  - Multi-view clustering: using several views can reveal structures not seen with a single data source (e.g., cancer subtypes can be defined based on gene expression and DNA methylation together).

#### Generative Multi-view Kernel PCA

#### **Motivation**



(reproduced from [Yang et al., 2021])

Multi-view data integration and domain translation: each view represents a different modality of the same population of cells.

#### Kernel Principal Component Analysis (KPCA)



(reproduced from [Mika et al., 1999])

- Nonlinear extension of PCA.
- Linear PCA is performed in the feature space induced by the feature map φ.

Primal problem [Suykens et al., 2002]:

$$\min_{w,e} \frac{1}{2} \|w\|^2 - \frac{1}{2\lambda} \sum_{i=1}^N e_i^2 \quad \text{s.t.} \quad e_i = w^T \phi(x_i)$$

#### **Dualization of Kernel PCA**

Obtain upper bound to primal objective using Fenchel–Young inequality  $\frac{1}{2\lambda}e^{T}e + \frac{\lambda}{2}h^{T}h \ge e^{T}h$  [Suykens, 2017]; [Tonin, Patrinos, and Suykens, 2021] :

$$J_{p} = \frac{\eta}{2} \operatorname{Tr} W^{T} W - \frac{1}{2\lambda} \sum_{i=1}^{N} e_{i}^{T} e_{i} \quad \text{s.t.} \quad e_{i} = W^{T} \phi(x_{i})$$

$$\leq -\sum_{i=1}^{N} e_{i}^{T} h_{i} + \frac{\lambda}{2} \sum_{i=1}^{N} h_{i}^{T} h_{i} + \frac{\eta}{2} \operatorname{Tr} \left( W^{T} W \right) \quad \text{s.t.} \quad e_{i} = W^{T} \phi(x_{i})$$

$$= -\sum_{i=1}^{N} \phi(x_{i})^{T} W h_{i} + \frac{\lambda}{2} \sum_{i=1}^{N} h_{i}^{T} h_{i} + \frac{\eta}{2} \operatorname{Tr} \left( W^{T} W \right) \triangleq J$$

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#### **RKM Dual Problem of Kernel PCA**

Stationary points of *J*:

$$\begin{cases} \frac{\partial J}{\partial h_i} = 0 \implies W^T \phi(x_i) = \lambda h_i, \forall i = 1, \dots, N, \\ \frac{\partial J}{\partial W} = 0 \implies W = \frac{1}{\eta} \sum_{i=1}^N \phi(x_i) h_i^T. \end{cases}$$

Substituting the expression for W in the first equation gives the eigenvalue problem:

$$\frac{1}{\eta} \mathbf{K} \mathbf{H}^{\mathsf{T}} = \mathbf{H}^{\mathsf{T}} \mathbf{\Lambda},$$

where

#### Multi-view Kernel PCA

Consider two views and two corresponding feature maps  $\phi_1 : \Omega_x \to \mathcal{H}_x$  and  $\phi_2 : \Omega_y \to \mathcal{H}_y$ . The multi-view KPCA objective is [Pandey, Schreurs, and Suykens, 2021]:

$$J_{\text{MV-KPCA}} = \sum_{i=1}^{N} -\phi_1(x_i)^T U h_i - \phi_2(y_i)^T V h_i + \frac{\lambda}{2} h_i^T h_i + \frac{\eta_1}{2} \operatorname{Tr} \left( U^T U \right) + \frac{\eta_2}{2} \operatorname{Tr} \left( V^T V \right), \quad \text{second view}$$

where

► *U*, *V* are the unknown interconnection matrices,

•  $h_i$  is the latent variable of a common subspace  $\mathcal{H} \subseteq \mathcal{H}_x \oplus \mathcal{H}_y$ . Training corresponds to the following eigenvalue problem:

$$\left(\frac{1}{\eta_1}K_1+\frac{1}{\eta_2}K_2\right)H^T=H^T\Lambda,$$

where  $K_1, K_2$  are the kernel matrices of the first and second view.

#### Generative Multi-view Kernel PCA

- **\checkmark Task**: given a latent variable  $h^*$ , generate data point
- $x^{\star} \in \Omega_x, y^{\star} \in \Omega_y$  in both views.

**Problem**: compute the inverse images of the feature maps  $\phi_1, \phi_2$  (*pre-image problem*).

**Solution**: use parametrized feature maps and learn both the feature maps and the pre-image maps  $\psi_1 : \mathcal{H}_x \to \Omega_x$ ,  $\psi_2 : \mathcal{H}_y \to \Omega_y$ . The parametrization depends on the data type of

each view (e.g., CNN for images, GNN for graphs, LSTM for time series, etc.)

$$\begin{split} \min_{\substack{U, V, h_i, \\ \theta_1, \theta_2, \zeta_1, \zeta_2}} J_{\text{Gen-RKM}} &= J_{\text{MV-KPCA}}^{\text{stab}} + \frac{\gamma}{2N} \bigg( \sum_{i=1}^N \big\| x_i - \psi_{1\zeta_1}(\phi_{1\theta_1}(x_i)) \big\|^2 \\ &+ \sum_{i=1}^N \big\| y_i - \psi_{2\zeta_2}(\phi_{2\theta_2}(y_i)) \big\|^2 \bigg) \end{split}$$

#### Generative Multi-view Kernel PCA



(reproduced from [Pandey, Schreurs, and Suykens, 2021])

Gen-RKM schematic. The single subspace  $\mathcal{H} \subseteq \mathcal{H}_x \bigoplus \mathcal{H}_y$  is shared between the two views  $\Omega_x, \Omega_y$ . The  $\phi_1, \phi_2$  are the viewspecific feature maps,  $\psi_1, \psi_2$  are the pre-image maps. The interconnection matrices U, V capture the view-specific dependencies between the shared latent variables and the mapped data sources.

#### Generative Multi-View Kernel PCA: Disentanglement



Each row shows the generated images corresponding to the **traversal** in the latent space plotted in the first column. [Pandey, Schreurs, and Suykens, 2021] **Interpretability**: changing one latent variable affects only one generative factor. Application: separate biological factors.

# Generative Multi-View Kernel PCA: Multi-view Generation



Multi-view generation on the Sketchy dataset showing labels, images, and sketches generated together from the single latent space  $\mathcal{H}$  **shared** among all views. [Pandey, Schreurs, and Suykens, 2021]

#### Multi-View Kernel Spectral Clustering

### Multi-omic clustering approaches



(reproduced from [Rappoport and Shamir, 2018])

Overview of multi-omic clustering algorithms to reveal further insights into biomedical omics dataset.

#### Kernel Spectral Clustering (KSC)

Weighted KPCA with k clusters [Alzate and Suykens, 2008]:

$$\min_{w^{(l)}, b^{(l)}, e^{(l)}} \quad \frac{1}{2} \sum_{l=1}^{k-1} w^{(l)^T} w^{(l)} - \frac{1}{2N} \sum_{l=1}^{k-1} \gamma^{(l)} e^{(l)^T} D^{-1} e^{(l)}$$
  
s.t.  $e^{(l)} = \Phi w^{(l)} + b^{(l)} \vec{1}_N, \ l = 1, \dots, k-1,$ 

where

• 
$$\Phi = [\phi(x_1)^T; \dots; \phi(x_N)^T]$$
 is the feature matrix,

- *e*<sup>(*l*)</sup> ∈ ℝ<sup>N</sup> is the *l*-th clustering score with clustering indicator sign(*e*<sup>(*l*)</sup>),
- ▶ *D* is the degree matrix, motivated by the random walks model, inducing the clustering:  $D_{ii} = \sum \phi(x_i)^T \phi(x_j)$ .

#### Multi-view Kernel Spectral Clustering

Extend KSC to V views with pairwise coupling terms [Houthuys, Langone, and Suykens, 2018]:

$$\min_{w^{[\nu]^{(l)}, e^{[\nu]^{(l)}}} = \frac{1}{2} \sum_{\nu=1}^{V} \sum_{l=1}^{k-1} w^{[\nu]^{(l)}} w^{[\nu]^{(l)}} w^{[\nu]^{(l)}} \\
- \frac{1}{2N} \sum_{\nu=1}^{V} \sum_{l=1}^{k-1} \gamma^{[\nu]^{(l)}} e^{[\nu]^{(l)}} D^{[\nu]^{-1}} e^{[\nu]^{(l)}} \\
- \frac{1}{2} \sum_{\nu, u=1, \nu \neq u}^{V} \sum_{l=1}^{k-1} \rho^{(l)} e^{[\nu]^{(l)}} S^{[\nu, u]} e^{[u]^{(l)}} \\
\text{s.t.} \quad e^{[\nu]^{(l)}} = \left( \Phi^{[\nu]} - \vec{1}_{N} \hat{\mu}^{[\nu]} \right) w^{[\nu]^{(l)}},$$
(1)

where

►  $S^{[v,u]} = D^{[v]^{-\frac{1}{2}}} D^{[u]^{-\frac{1}{2}}}$  couples view *v* and *u*. The **coupling term** describes the correlation between the clustering variables of two different views. Problem (1) is optimized with Lagrangian duality  $\rightarrow$  solve a *VN* × *VN* eigenvalue problem. <sub>20/28</sub>

#### Multi-view KSC - Latent Space



-0.1 0.0

0.00 0.01

Dataset with V = 3 views with image and text data

- MV-KSC achieves better separation than KSC on concatenated views
- ► MV-KSC has one latent variable for each view → less interpretability with many views

$$\begin{aligned} \text{AV-KSC with Shared Latent Space: MV-KSC-RKM} \\ \text{Obtain upper bound to weighted KPCA using the weighted} \\ \text{Fenchel-Young inequality } \frac{1}{2\lambda}e^{T}D^{-1}e + \frac{\lambda}{2}h^{T}Dh \geq e^{T}h: \\ J_{\text{KSC}} &= \frac{1}{2}\sum_{l=1}^{k-1}w^{(l)T}w^{(l)} - \frac{1}{2N}\sum_{l=1}^{k-1}\gamma^{(l)}e^{(l)T}D^{-1}e^{(l)} \quad \text{s.t.} \quad e^{(l)} = \Phi_{c}w^{(l)} \\ &\leq -\sum_{l=1}^{k-1}\left(\Phi_{c}w^{(l)}\right)^{T}h^{(l)} + \sum_{l=1}^{k-1}\frac{\lambda^{(l)}}{2}h^{(l)T}Dh^{(l)} + \frac{\eta}{2}\sum_{l=1}^{k-1}w^{(l)T}w^{(l)} \end{aligned}$$

In the <u>multi-view case</u>, we incorporate the KSC view-specific objectives with different feature map for each view and couple the views by imposing that the latent variable h is common to all views. Consequences:

- ▶ Single latent space → improved interpretability
- ► Legendre–Fenchel transformation leads to a N × N eigenvalue problem → better efficiency, independent of the number of views and of the number of features

#### MV-KSC-RKM - Shared Latent Space



Dataset with V = 3 views with image and text data

- The clusters in the common latent space are better separated
- Improved data discovery thanks to a single latent space
- Outputs not only 2D plot, but also clustering labels (unlike t-SNE, UMAP)

#### **Future Extensions**

#### Future challenges

## Encode prior knowledge in the learned disentangled latent variables

- Force the model to learn specific features such as the texture of the tissue
- Explicit feature maps for multi-view clustering, e.g., Graph Neural Networks
  - Spatial transcriptomics
- Unpaired multi-view learning
  - Different cells have different modalities

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