Identifiable Shared Component Analysis of Unpaired Multimodal Mixtures

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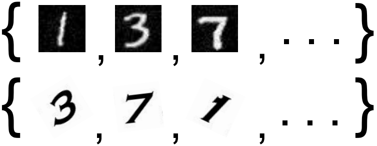
Shared Component Analysis (SCA)



Modality 1

Modality 2

$$\boldsymbol{x}^{(q)} = \boldsymbol{A}^{(q)}\boldsymbol{z}^{(q)}, \quad \boldsymbol{z}^{(q)} = \begin{bmatrix}\boldsymbol{c} \\ \boldsymbol{p}^{(q)}\end{bmatrix}, \ \forall q = 1, 2. \tag{1}$$

- $\boldsymbol{c} \in \mathbb{R}^{d_{\mathrm{C}}}$: shared component
- $\boldsymbol{p}^{(q)} \in \mathbb{R}^{d_{\mathrm{P}}^{(q)}}, q = 1, 2$: private component
- $\boldsymbol{A}^{(q)} \in \mathbb{R}^{d^{(q)} \times (d_{\mathrm{C}} + d_{\mathrm{P}}^{(q)})}, q = 1, 2$ is the mixing matrix

Unaligned SCA: Identify $\boldsymbol{c}$ from unaligned samples $\{\boldsymbol{x}_i^{(1)}\}_{i=1}^{M}$ and $\{\boldsymbol{x}_i^{(2)}\}_{i=1}^{N}$

Existing Works on Identifiable SCA and Challenges

Aligned SCA

- Require paired samples $(\boldsymbol{x}_i^{(1)}, \boldsymbol{x}_i^{(2)})_{i=1}^{N}$, e.g., [Ibrahim et al., 2021],
- Formulated as canonical component analysis (CCA).

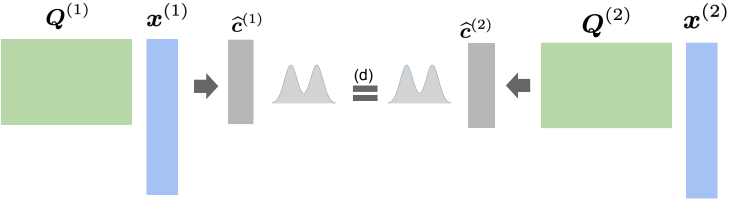
Unaligned SCA

- Stringent conditions for identifiability, such as component-wise independence [Sturma et al., 2024].

Proposed Method

$$\begin{aligned} \text{find} \quad & \boldsymbol{Q}^{(q)} \in \mathbb{R}^{d_{\mathrm{C}} \times d^{(q)}}, \; q = 1, 2, && \text{(2a)} \\ \text{subject to} \quad & \boldsymbol{Q}^{(1)} \boldsymbol{x}^{(1)} \overset{\text{(d)}}{=\!=} \boldsymbol{Q}^{(2)} \boldsymbol{x}^{(2)}, && \text{(2b)} \\ & \boldsymbol{Q}^{(q)} \mathbb{E}\left[\boldsymbol{x}^{(q)} (\boldsymbol{x}^{(q)})^{\top} \right] (\boldsymbol{Q}^{(q)})^{\top} = \boldsymbol{I} \quad q = 1, 2, && \text{(2c)} \end{aligned}$$

"$\overset{\text{(d)}}{=\!=}$" means matched distributions



Identifiability of Unaligned SCA

Theorem 1 (Informal) Sufficiently different $p(\boldsymbol{z}^{(1)})$ and $p(\boldsymbol{z}^{(2)}) \implies$ identifiability of $\boldsymbol{c}$ (i.e., $\boldsymbol{Q}^{(q)}\boldsymbol{x}^{(q)} = \boldsymbol{\Theta}\boldsymbol{c}$) if one of the following holds,

1. Individual components of $\boldsymbol{c}$ are statistically independent and non-Gaussian,
2. Support of $p(\boldsymbol{c})$ is a hyper-rectangle.

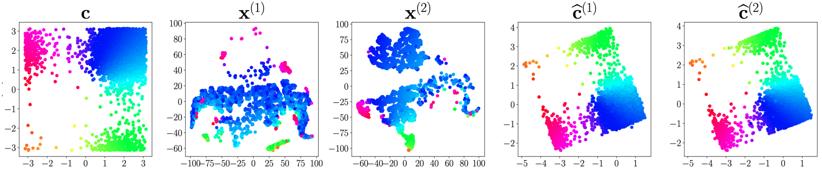


Figure: Validation of Theorem 1. Result shows $\widehat{\boldsymbol{c}}^{(1)} \approx \widehat{\boldsymbol{c}}^{(2)}$

Synthetic experiment detail:

- Shared component $\mathbb{R}^2$ - Vonmises distribution. $\boldsymbol{p}^{(q)} \in \mathbb{R}^1$ from Laplace and Uniform distribution

Enhanced Identifiability via Structural Constraints

Homogeneous Domains (i.e., $\boldsymbol{A}^{(q)} = \boldsymbol{A}\ \forall q = 1, 2$)

Theorem 2 (Informal) Sufficiently different $p(\boldsymbol{z}^{(1)})$ and $p(\boldsymbol{z}^{(2)})$ with same mixing matrix $\implies$ identifiability of $\boldsymbol{c}$ (i.e., $\boldsymbol{Q}\boldsymbol{x}^{(q)} = \boldsymbol{\Theta}\boldsymbol{c}$).

Weakly Supervised Cases (i.e., $\boldsymbol{Q}^{(1)}\boldsymbol{x}_\ell^{(1)} = \boldsymbol{Q}^{(2)}\boldsymbol{x}_\ell^{(2)},\ \ell \in \{(\boldsymbol{x}_\ell^{(1)}, \boldsymbol{x}_\ell^{(2)})\}_{\ell=1}^{D}$)

Theorem 3 (Informal) Sufficiently different $p(\boldsymbol{z}^{(1)})$ and $p(\boldsymbol{z}^{(2)})$ with $D \geq d_{\mathrm{C}}$ paired samples $\implies$ identifiability of $\boldsymbol{c}$ (i.e., $\boldsymbol{Q}^{(q)}\boldsymbol{x}^{(q)} = \boldsymbol{\Theta}\boldsymbol{c}$).

Experiments : Domain Adaptation

Table: Classification accuracy on the target domain of *office-Home* dataset (ResNet50 embedding).

source → target	`ResNet`	`DANN`	`MDD`	`MCC`	`SDAT`	`ELS`	`Proposed`
Ar → Cl	42.0 ± 0.2	46.7 ± 0.2	47.4 ± 0.3	44.4 ± 0.3	47.3 ± 0.4	48.5 ± 0.2	**51.0** ± 0.3
Ar → Pr	69.2 ± 0.1	70.2 ± 0.4	72.8 ± 0.4	72.4 ± 0.2	71.1 ± 0.3	71.0 ± 0.3	**75.8** ± 0.1
Ar → Rw	80.2 ± 0.3	81.2 ± 0.4	81.2 ± 0.1	80.3 ± 0.3	80.5 ± 0.1	80.8 ± 0.4	**82.5** ± 0.2
Cl → Ar	60.7 ± 0.4	60.8 ± 0.3	62.4 ± 0.1	59.2 ± 0.4	57.6 ± 0.2	59.8 ± 0.1	**62.7** ± 0.4
Cl → Pr	71.0 ± 0.1	69.8 ± 0.3	70.0 ± 0.4	**71.1** ± 0.4	66.5 ± 0.1	68.5 ± 0.2	72.5 ± 0.3
Cl → Rw	74.8 ± 0.2	73.3 ± 0.1	74.1 ± 0.1	**76.2** ± 0.2	70.7 ± 0.1	71.7 ± 0.1	75.8 ± 0.1
Pr → Ar	60.6 ± 0.2	62.2 ± 0.1	64.3 ± 0.1	59.2 ± 0.1	62.5 ± 0.4	60.9 ± 0.2	**64.4** ± 0.3
Pr → Cl	44.8 ± 0.1	48.8 ± 0.1	48.0 ± 0.3	46.2 ± 0.2	49.0 ± 0.3	49.6 ± 0.3	**50.4** ± 0.1
Pr → Rw	79.6 ± 0.1	80.3 ± 0.4	79.6 ± 0.3	80.3 ± 0.2	80.0 ± 0.1	79.2 ± 0.1	**81.7** ± 0.2
Rw → Ar	70.1 ± 0.2	71.5 ± 0.1	71.4 ± 0.3	67.8 ± 0.2	71.6 ± 0.4	71.3 ± 0.4	**72.6** ± 0.1
Rw → Cl	45.8 ± 0.2	50.9 ± 0.2	50.3 ± 0.1	50.0 ± 0.2	51.4 ± 0.1	50.7 ± 0.1	**53.2** ± 0.1
Rw → Pr	80.7 ± 0.1	80.6 ± 0.4	81.1 ± 0.1	81.2 ± 0.1	80.7 ± 0.1	79.8 ± 0.3	**82.9** ± 0.3
Average	64.9 ± 0.1	66.3 ± 0.2	66.8 ± 0.2	65.6 ± 0.2	65.7 ± 0.2	65.9 ± 0.2	**68.7** ± 0.2

Experiments: Cross-lingual Information Retrieval & Single Cell Sequence alignment

Table: Average precision P@1 of cross-language information retrieval.

source → target	`Adv` - NN	`proposed` - NN	`Adv` - CSLS	`proposed` - CSLS
en→es	61.3	**66.4**	70.2	**74.9**
es→en	55.4	**65.3**	67.6	**75.6**
en→it	48.2	**54.4**	60.8	**67.7**
it→en	**55.2**	51.9	63.8	**66.0**
en→fr	**63.6**	60.2	72.6	**73.7**
fr→en	55.4	**58.4**	64.1	**71.4**
en→de	51.4	**56.7**	59.3	**67.6**
de→en	42.5	**57.0**	51.0	**59.3**
en→ru	32.7	**34.9**	38.6	**41.4**
ru→en	27.6	**41.6**	35.0	**50.8**
en→ar	12.6	**22.7**	16.7	**29.1**
ar→en	15.7	**26.9**	20.1	**35.6**
en→vi	2.1	**10.4**	7.7	**22.8**
vi→en	2.7	**17.3**	4.4	**33.0**
Average	37.6	**44.5**	45.1	**54.9**

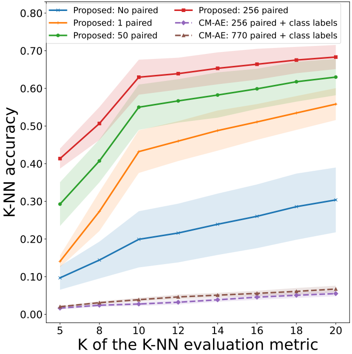


Figure: k-NN accuracy for single-cell sequence alignment.

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