# Low-Rank Joint Subspace Construction for Multimodal Data Clustering

Aparajita Khan March 14, 2019



Common set of n samples M sets of observations

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 $\mathbf{X_1} \in \mathbb{R}^{n imes d_1}$ 

 $\mathbf{X_2} \in \mathbb{R}^{n imes d_2}$ 

 $\mathbf{X}_{\mathbf{M}} \in \mathbb{R}^{n imes d_M}$ 

 $n \ll d_m$ , for m = 1, ..., M

. . .

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. . .

#### Cluster the n samples considering information from M different modalities/views





Statistical hypothesis testing based Rank Estimation

$$\mathbf{X_m} = \mathbf{\Xi_m} + \mathbf{Z_m}, \text{ signal } \mathbf{\Xi_m} \sim \sum_{j=1}^{k} \pi_j \mathcal{N}(\mu_j, \mathbf{\Sigma_j}), \text{ noise } \mathbf{Z_m} \sim \mathcal{N}(\mathbf{0}, \mathbf{\Lambda})$$







#### **Multivariate Normality based Relevance Estimation**

Relevance 
$$\mathcal{R}_{l}(\mathbf{X_{m}}) = \frac{1}{2} \left[ 1 + \frac{H_{r_{m}} - F_{\chi^{2}}^{-1}((1-\alpha), r_{m})}{\max\{H_{r_{m}}, F_{\chi^{2}}^{-1}((1-\alpha), r_{m})\}} \right]$$

 $H_{r_m}$ 









# Data sets:Colorectal carcinoma (CRC)[307 samples, 2 clusters]Cervical carcinoma (CESC)[124 samples, 3 clusters]Lower grade glioma (LGG)[267 samples, 3 clusters]Stomach adenocarcinoma (STAD)[199 samples, 4 clusters]

Modalities: DNA Methylation Gene Expression Micro-RNA Expression Protein Expression

**Importance of Noise-Free Approximation** 



 Performance of selected proposed joint subspace is better than taking fullrank subspace from each modality

#### **Importance of Integration**



- Proposed method performs better than all the individual modalities in all 4 data sets
- Very high performance for LGG and STAD data sets

#### **Comparison with Existing Approaches**

![](_page_14_Figure_2.jpeg)

- Performance of proposed better than existing in all data sets, especially for STAD data set
- PCA and SNF have next best performance

## Conclusion

- Statistical hypothesis testing to estimate rank of subspaces
- Multivariate Normality based relevance of individual modalities
- Select only relevant modalities
- Select only complementary information between two modalities

A. Khan and P. Maji, "Low-Rank Joint Subspace Construction for Cancer Subtype Discovery," IEEE/ACM Transactions on Computational Biology and Bioinformatics. (Accepted)

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# THANK YOU!

![](_page_17_Picture_2.jpeg)

![](_page_17_Picture_3.jpeg)