Multi-omic data integration using joint Non-negative Matrix Factorization approaches for identification of relevant biological events in low-grade glioma

- Low-grade glioma is a brain cancer with heterogeneous behavior

1. We implemented a variant of joint matrix factorization (MjNMF)

2. We used observational (***TCGA***) and experimental data (***CCLE***)

3. Clusters of patients have different survival characteristics and gene signatures

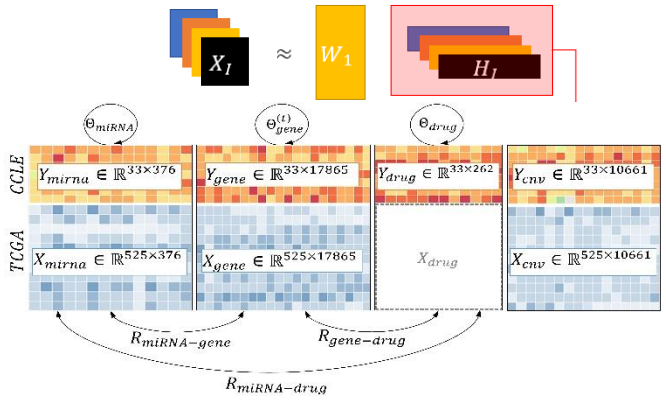
4. Association patients-cell lines showed ***similar biological pathways***

5. We identified miRNA signatures for patients with low and high sensitivity to drugs

NMF does not solve the integration problem, joint Non-negative Matrix Factorization (*jNMF*) does.

$$\min_{W,H_I} \sum_I \|X_I - WH_I\|_F^2 \quad s.t. W \geq 0, H_I \geq 0$$

jNMF is an extension of NMF for multiple inputs (X_I)



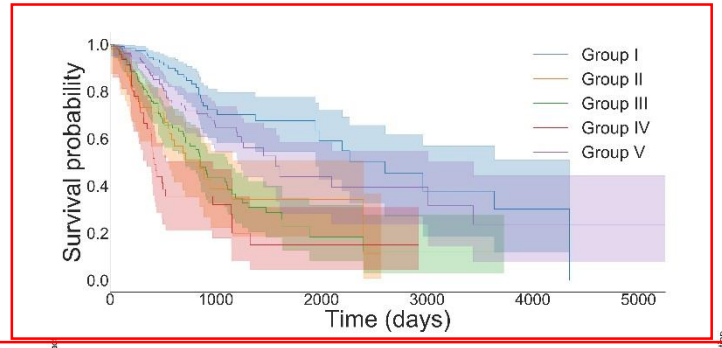
1. Multidimensional-jNMF

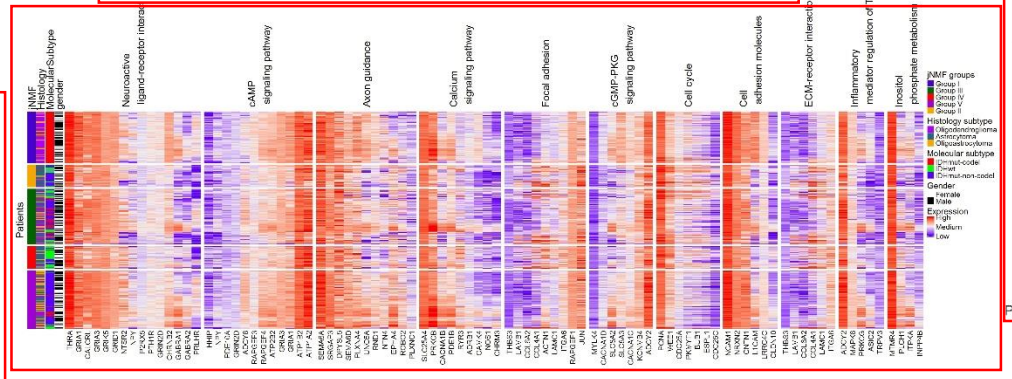
$$min \quad F(W_1, W_2, H_1, \ldots, H_I) =$$
$$\|X_I - W_1H_I\|_F^2 + \|Y_I - W_2H_I\|_F^2 + \|Y_{drug} - W_2H_{drug}\|_F^2$$
$$-\lambda_1 \sum_I \sum_t Tr\left(H_I\Theta_I^{(t)}H_I^T\right) - \lambda_2 \sum_{I\neq J} Tr\left(H_IR_{IJ}H_J^T\right)$$
$$+\gamma_1\|W_1\|_F^2 + \gamma_2\|W_2\|_F^2 + \delta_1\left(\sum_I \sum_j \|h_j^I\|_1^2\right)$$

2.

* Co-Modules ** Cluster Patient-Cell Lines *** Drug repurposing (AUC)

3.





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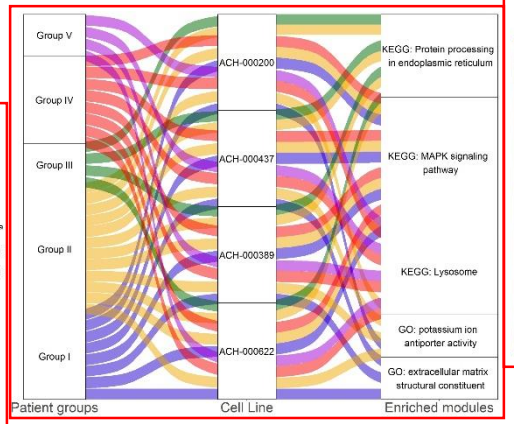
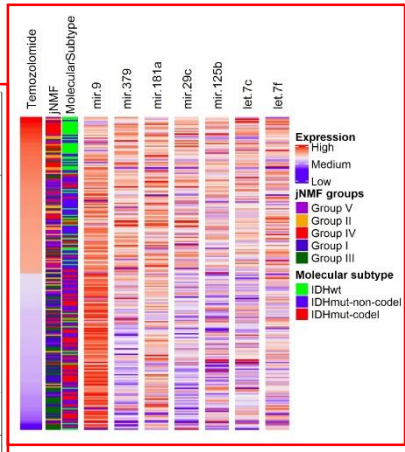


5.



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