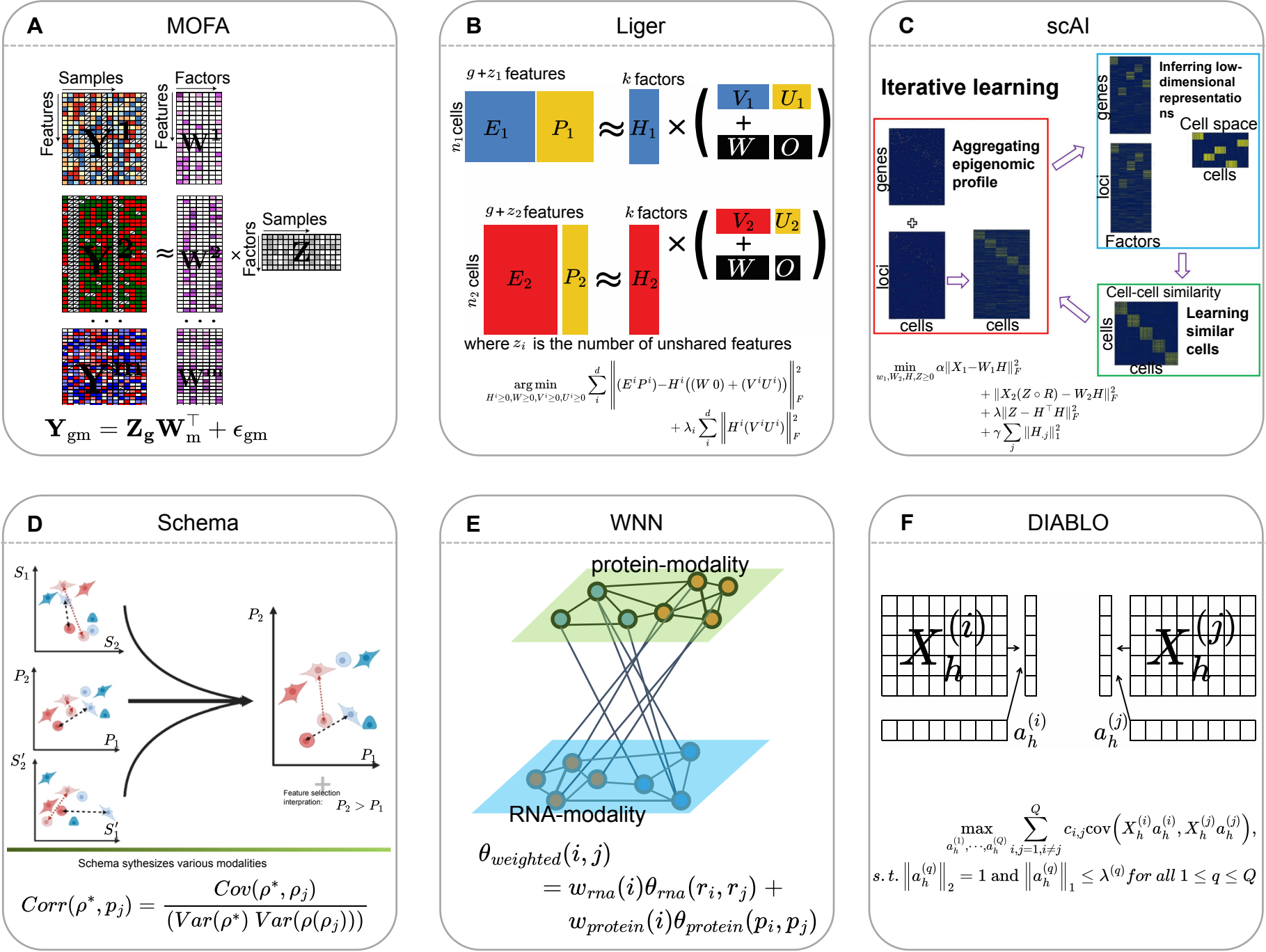
A
MOFA
Samples
Factors
Features
Features
Samples
Factors
$\mathbf{Y}_{gm} = \mathbf{Z}_g \mathbf{W}_m^\top + \epsilon_{gm}$
B
Liger
$g + z_1$ features
k factors
n_1 cells
E_1 P_1 $\approx$ H_1 $\times$ V_1 U_1 + W O
$g + z_2$ features
k factors
n_2 cells
E_2 P_2 $\approx$ H_2 $\times$ V_2 U_2 + W O
where z_i is the number of unshared features
$\arg\min_{H^i \geq 0, W \geq 0, V^i \geq 0, U^i \geq 0} \sum_i^d \left\| (E^i P^i) - H^i((W\ 0) + (V^i U^i)) \right\|_F^2 + \lambda_i \sum_i^d \left\| H^i (V^i U^i) \right\|_F^2$
C
scAI
Iterative learning
genes
Aggregating epigenomic profile
loci
cells
cells
genes
Inferring low-dimensional representations
Cell space
loci
cells
Factors
Cell-cell similarity
cells
Learning similar cells
cells
$\min_{w_1, W_2, H, Z \geq 0} \alpha \|X_1 - W_1 H\|_F^2 + \|X_2(Z \circ R) - W_2 H\|_F^2 + \lambda \|Z - H^\top H\|_F^2 + \gamma \sum_j \|H_{,j}\|_1^2$
D
Schema
S_1
S_2
P_2
P_1
S_2'
S_1'
P_2
P_1
Feature selection interpration: $P_2 > P_1$
Schema sythesizes various modalities
$Corr(\rho^*, p_j) = \frac{Cov(\rho^*, \rho_j)}{(Var(\rho^*)\ Var(\rho(\rho_j)))}$
E
WNN
protein-modality
RNA-modality
$\theta_{weighted}(i,j) = w_{rna}(i)\theta_{rna}(r_i, r_j) + w_{protein}(i)\theta_{protein}(p_i, p_j)$
F
DIABLO
$X_h^{(i)}$
$a_h^{(i)}$
$X_h^{(j)}$
$a_h^{(j)}$
$\max_{a_h^{(1)}, \cdots, a_h^{(Q)}} \sum_{i,j=1, i \neq j}^{Q} c_{i,j} \mathrm{cov}\left(X_h^{(i)} a_h^{(i)}, X_h^{(j)} a_h^{(j)}\right)$,
$s.t. \left\|a_h^{(q)}\right\|_2 = 1$ and $\left\|a_h^{(q)}\right\|_1 \leq \lambda^{(q)}$ for all $1 \leq q \leq Q$