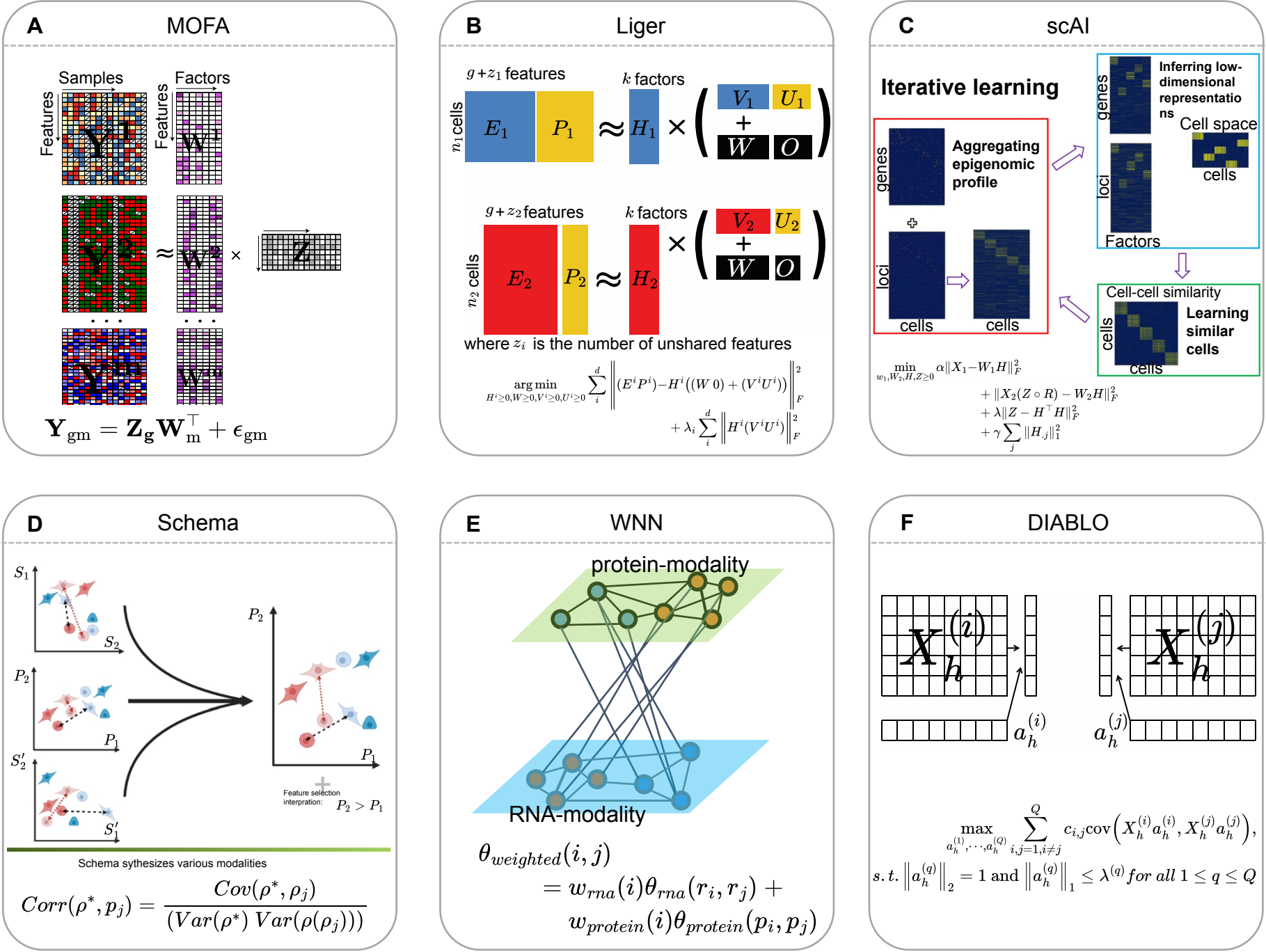
A
MOFA
Samples
Factors
Features
Features
$\mathbf{Y}^1$
$\mathbf{W}^1$
$\mathbf{Y}^2$
$\mathbf{W}^2$
$\mathbf{Z}$
$\mathbf{Y}^m$
$\mathbf{W}^m$
$\mathbf{Y}_{\mathrm{gm}} = \mathbf{Z}_{\mathbf{g}}\mathbf{W}_{\mathrm{m}}^{\top} + \epsilon_{\mathrm{gm}}$
B
Liger
$g+z_1$ features
k factors
n_1 cells
E_1
P_1
H_1
V_1
U_1
W
O
$g+z_2$ features
k factors
n_2 cells
E_2
P_2
H_2
V_2
U_2
W
O
where z_i is the number of unshared features
$\arg\min_{H^i\geq 0, W\geq 0, V^i\geq 0, U^i\geq 0} \sum_i^d \left\| (E^iP^i) - H^i((W\ 0) + (V^iU^i)) \right\|_F^2 + \lambda_i \sum_i^d \left\| H^i(V^iU^i) \right\|_F^2$
C
scAI
Iterative learning
genes
Aggregating epigenomic profile
loci
cells
cells
genes
Inferring low-dimensional representations
Cell space
cells
loci
Factors
Cell-cell similarity
cells
cells
Learning similar cells
$\min_{w_1,W_2,H,Z\geq 0} \alpha\|X_1 - W_1H\|_F^2 + \|X_2(Z\circ R) - W_2H\|_F^2 + \lambda\|Z - H^{\top}H\|_F^2 + \gamma\sum_j \|H_{.j}\|_1^2$
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
$X_h^{(i)}$
$X_h^{(j)}$
$a_h^{(i)}$
$a_h^{(j)}$
$\max_{a_h^{(1)},\cdots,a_h^{(Q)}} \sum_{i,j=1,i\neq j}^{Q} c_{i,j}\mathrm{cov}\left(X_h^{(i)}a_h^{(i)}, X_h^{(j)}a_h^{(j)}\right),$
$s.t.\ \left\|a_h^{(q)}\right\|_2 = 1$ and $\left\|a_h^{(q)}\right\|_1 \leq \lambda^{(q)}$ for all $1 \leq q \leq Q$