Step 3: Bilateral contrastive learning

scRNA-seq

cell 1
cell 2
cell 3
cell 4
⋮
cell n_1

X_1

gene 1, gene 2, gene 3, ⋯, gene m_1

Cell Encoder g_1

Feature Encoder f_1

Z_1

Y_1

Cell level

Feature level

Decoder h_1

$\hat{X}_1$
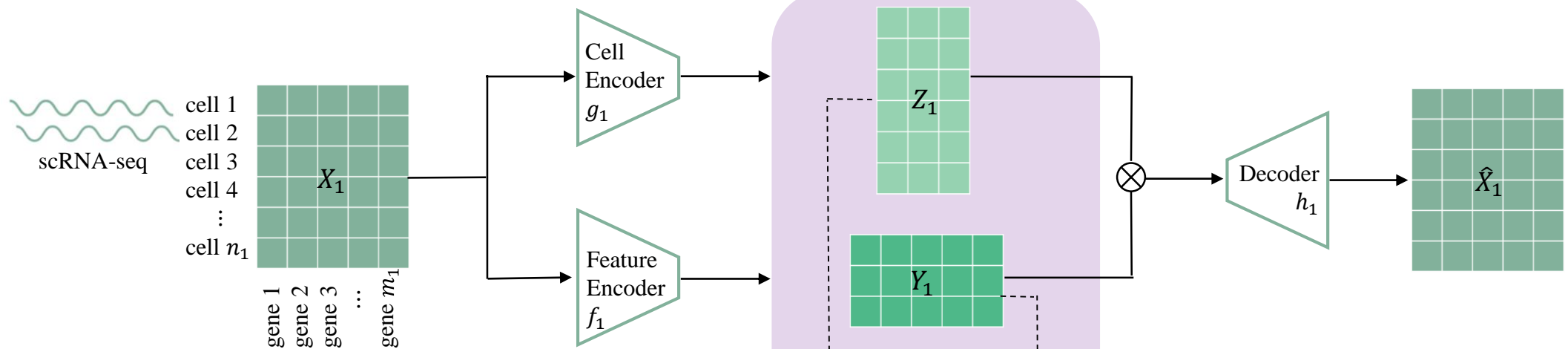
Step 2: Cell pairs and feature pairs construction

Cell pairs   Feature pairs

Transformed matrix

cell 1
cell 2
cell 3
⋮
cell n_2

X_2'

gene/protein 1, gene/protein 2, gene/protein 3, ⋯, gene/protein m_1

Feature Encoder f_2

Cell Encoder g_2

Y_2

Z_2

Decoder h_2

$\hat{X}_2'$

Bilateral contrastive loss

Reconstruction loss
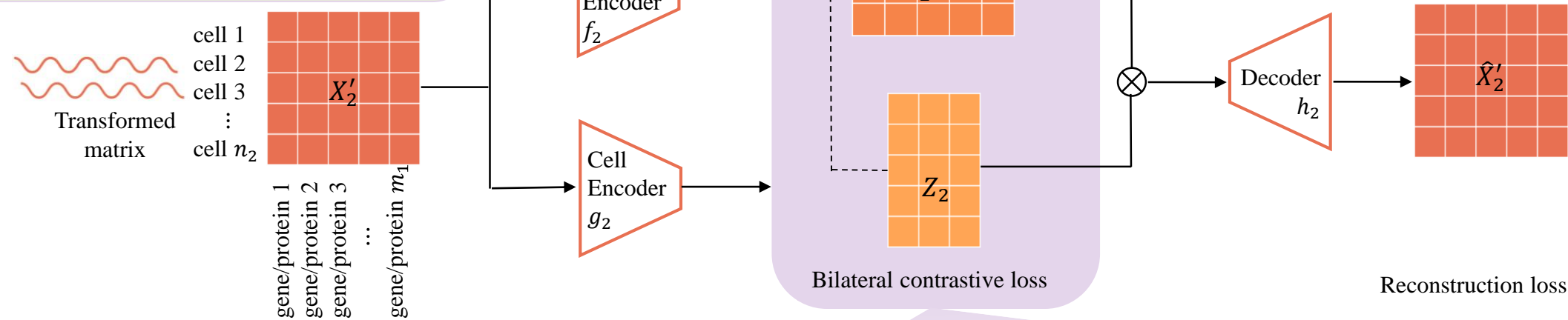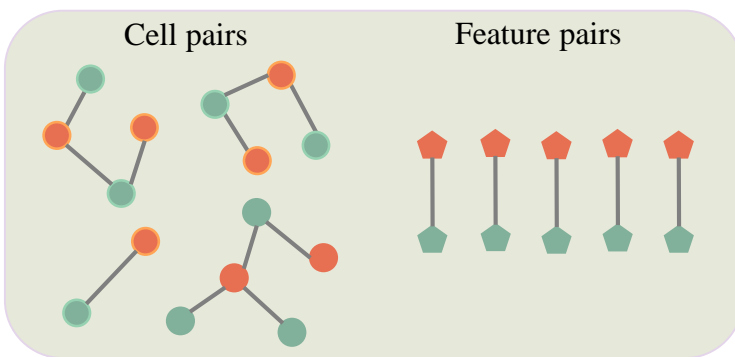
Step 1: Data transformation

Prior information

scATAC-seq

cell 1
cell 2
cell 3
⋮
cell n_2

X_2

peak/protein 1, peak/protein 2, peak/protein 3, ⋯, peak/protein p

or

Protein modality

Genes   Peaks   Proteins

Cell level   Feature level

Positive pairs (Pull close)

Negative pairs (Push away)