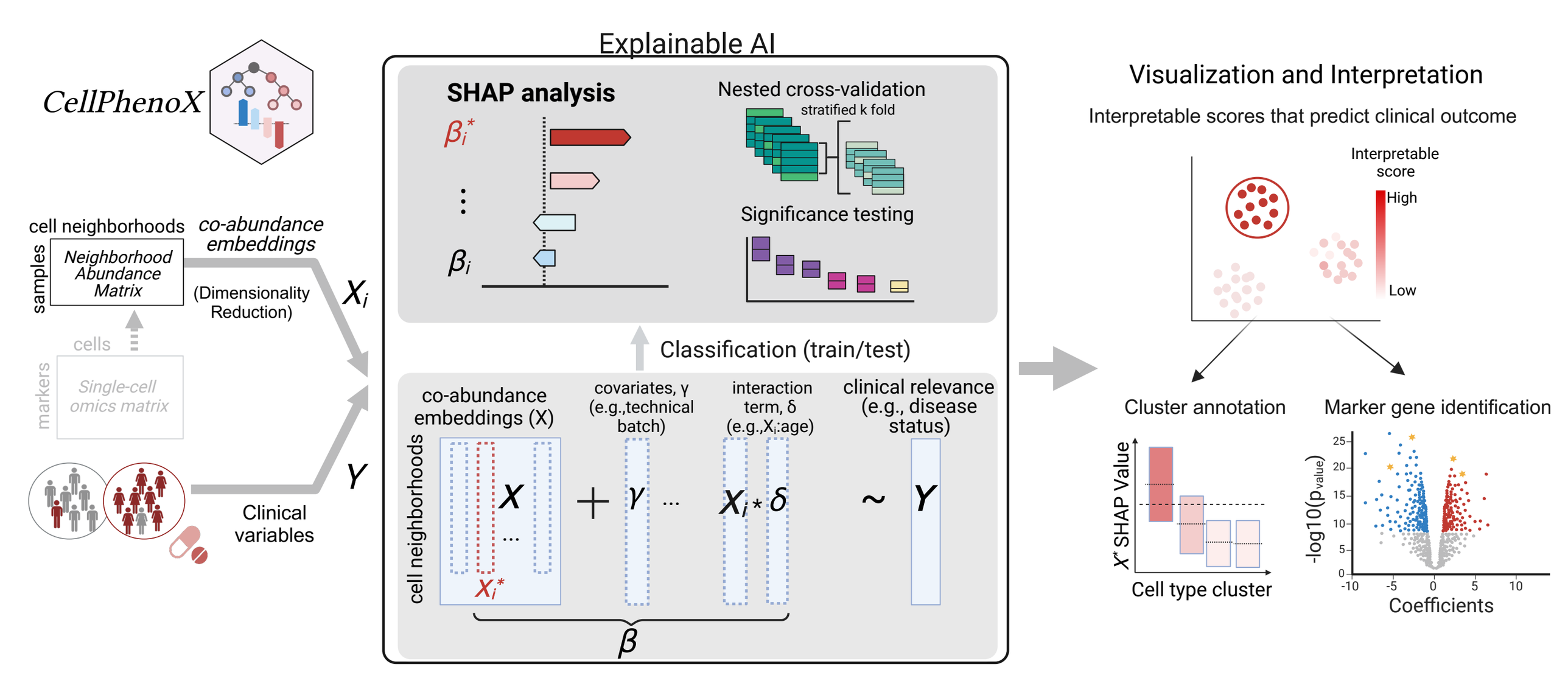
CellPhenoX
cell neighborhoods
co-abundance embeddings
samples
Neighborhood Abundance Matrix
(Dimensionality Reduction)
X_i
cells
markers
Single-cell omics matrix
Y
Clinical variables
Explainable AI
SHAP analysis
β_i^*
β_i
Nested cross-validation
stratified k fold
Significance testing
Classification (train/test)
co-abundance embeddings (X)
covariates, γ (e.g.,technical batch)
interaction term, δ (e.g.,X_i:age)
clinical relevance (e.g., disease status)
cell neighborhoods
X
X_i^*
γ
$X_i * \delta$
Y
β
Visualization and Interpretation
Interpretable scores that predict clinical outcome
Interpretable score
High
Low
Cluster annotation
Marker gene identification
X^* SHAP Value
Cell type cluster
$-\log10(p_{value})$
Coefficients