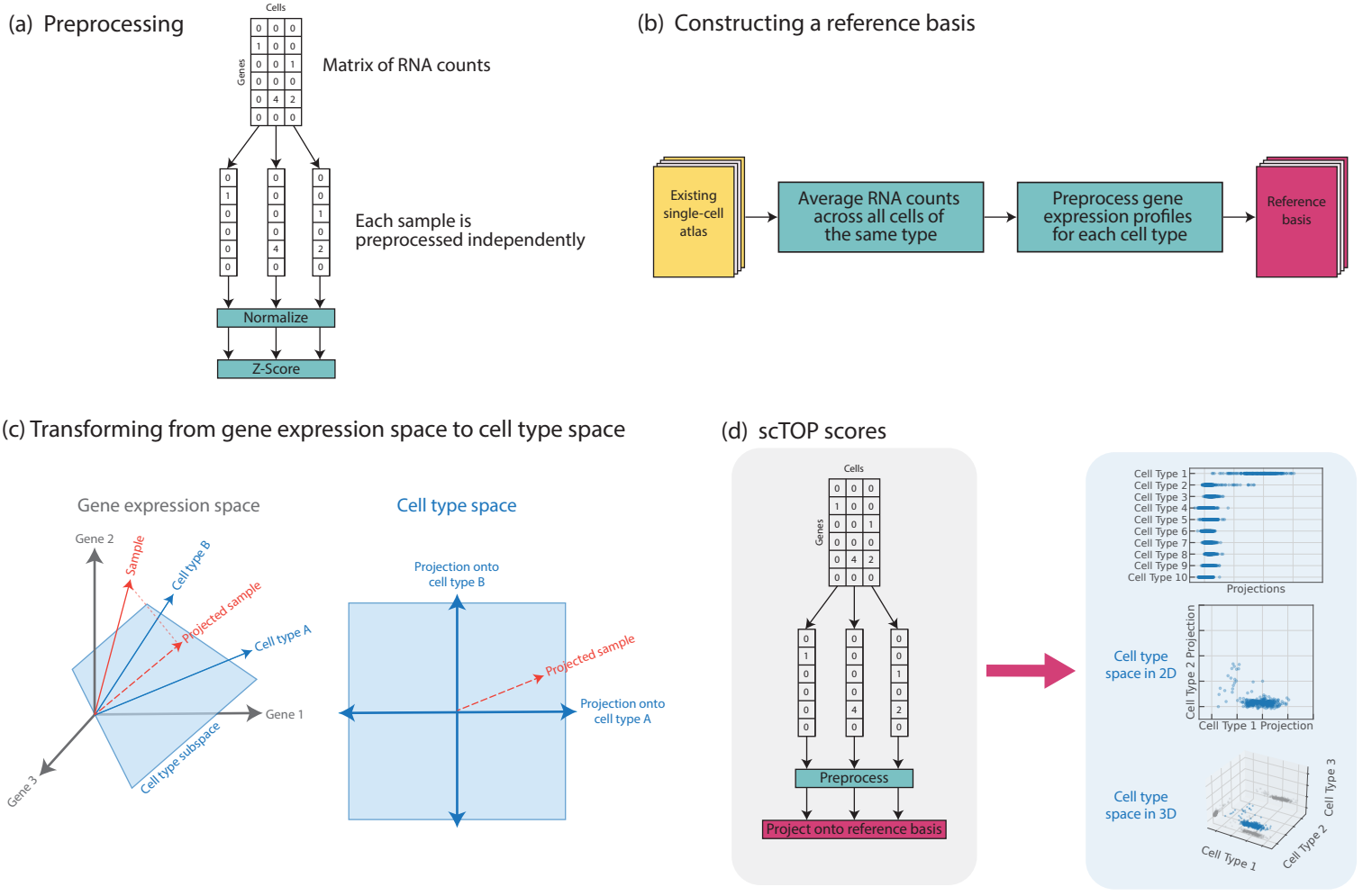
(a) Preprocessing
Cells
Genes
Matrix of RNA counts
Each sample is preprocessed independently
Normalize
Z-Score
(b) Constructing a reference basis
Existing single-cell atlas
Average RNA counts across all cells of the same type
Preprocess gene expression profiles for each cell type
Reference basis
(c) Transforming from gene expression space to cell type space
Gene expression space
Gene 2
Gene 1
Gene 3
Sample
Cell type B
Projected sample
Cell type A
Cell type subspace
Cell type space
Projection onto cell type B
Projected sample
Projection onto cell type A
(d) scTOP scores
Cells
Genes
Preprocess
Project onto reference basis
Cell Type 1
Cell Type 2
Cell Type 3
Cell Type 4
Cell Type 5
Cell Type 6
Cell Type 7
Cell Type 8
Cell Type 9
Cell Type 10
Projections
Cell type space in 2D
Cell Type 2 Projection
Cell Type 1 Projection
Cell type space in 3D
Cell Type 3
Cell Type 2
Cell Type 1