

1

Single Cell Data

- HALO
- QuPath
- CSV files
- Visiopharm
- IMC



Single cell data

2

Data Ingestion

- Add new annotations
- Manual phenotyping
- Subsampling
- Pin color mapping

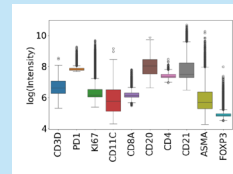
	phenotype_code	phenotype_name
	STRING	STRING
1	CD30+CD4+FOXP3+	Regulatory T Cell
2	CD30+CD4+	Helper T Cell
3	CD30+CD8A+	Cytotoxic T Cell
4	CD30+	T Cell
5	CD20+	B Cell
6	CD21+CD20-	Follicular Dendritic Cell

Manual phenotyping via phenotypes codes

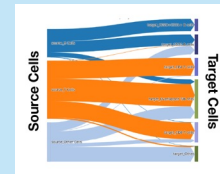
3

Visualization

- Histogram
- Boxplot
- Heatmap
- Hierarchical clustering
- Relational heatmap
- Sankey plot
- Scatter plot



Distribution of annotations or features

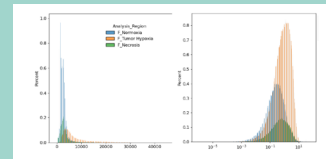


Relation analysis between annotations

4

Data Preprocessing

- Arcsinh transformation
- Z-score normalization
- Quantile normalization
- Batch correction
- Rescaling

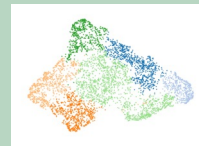


Feature expression before vs. after z-score normalization

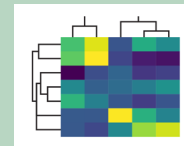
5

Clustering and Phenotyping

- Phenograph clustering
- tSNE/UMAP
- UTAG clustering
- Spatial UMAP



Clustering and phenotyping identification

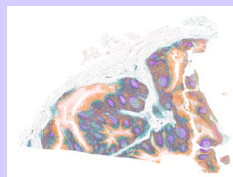


Hierarchical clustering and feature expression

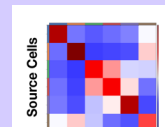
6

Spatial Analysis

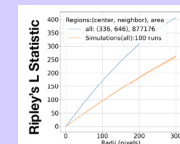
- Interactive spatial plot
- Nearest neighbor
- Cluster interaction matrix
- Neighborhood enrichment
- Ripley's L
- Spatial hypothesis testing



Spatial distribution



Neighborhood enrichment



Ripley's L