	Droplet Pre-processing	Normalisation	Integration	Reduction	Clustering	Trajectory Inference	Benchmarking	Platform	Misc
IBRAP	Scrublet DecontX	Scanpy (CPM), TPM, Scran, SCTransform	BBKNN, Scanorama, CCA, Harmony	PCA, Diffusion Maps, t-SNE, UMAP, LargeVis	Kmeans, PAM, SC3, louvain, louvain with multilevel refinement, smart local moving, leiden, singleR, scType	Slingshot	ASW (biological & Batch), ARI, NMI, Connectivity, Dunn index	R	CellTalker (cell-cell communication) ssGSEA (Gene set enrichment)
ASAP	None	CPM, DESeq2, voom, log2, SCTransform	ComBat, fastMNN, Limma	PCA, UMAP, t-SNE	Kmeans, PAM, SC3, louvain, louvain with multilevel refinement, smart local moving, leiden	None	None	Web	None
scCancer	SoupX, Scds	Lognorm	CCA, Harmony, Liger	PCA, t-SNE, UMAP	Louvain	None	None	R	GSVA (gene set enrichment) NMF Custom cell interaction analysis
Scanpy	Scrublet	CPM	ComBat, BBKNN, Scanorama, MNN	PCA, Diffusion Maps. T-SNE, UMAP	Louvain, leiden, ingest	PAGA	None	Python	Differential Expression Enrichment
Seurat	None	Lognorm, SCTransform	CCA	PCA, ICA, t-SNE, UMAP	louvain, louvain with multilevel refinement, smart local moving, leiden	None	None	R	None
Pegasus	None	Counts per 100,000	Harmony, Scanorama	PCA, Diffusion Maps, FLE	Louvain, leiden	FLE-based	kBET, kSIM	Python/ Web	None

	Droplet Pre-processing	Normalisation	Integration	Reduction	Clustering	Trajectory Inference	Benchmarking	Platform	Misc
IBRAP	Scrublet DecontX	Scanpy (CPM), TPM, Scran, SCTransform	BBKNN, Scanorama, CCA, Harmony	PCA, Diffusion Maps, t-SNE, UMAP, LargeVis	Kmeans, PAM, SC3, louvain, louvain with multilevel refinement, smart local moving, leiden, singleR, scType	Slingshot	ASW (biological & Batch), ARI, NMI, Connectivity, Dunn index	R	CellTalker (cell-cell communication) ssGSEA (Gene set enrichment)