Table 2a: Simulated single-cell data/algorithms

Title	Algorithm	# Cells	Simulation methods	Reference
Splatter	DCA, DeepImpute, PERMUDA, scDeepCluster, scVI, scScope, solo	~2000	Splatter/R	[78]
CIDR	sclGAN	50	CIDR simulation	[54]
NB+dropout	Dhaka	500	Hierachical model of NB/Gamma + random dropout	
Bulk RNA-seq	SAUCIE	1076	1076 CCLE bulk RNAseq + dropout conditional on expression level	
SIMLR	scScope	1 million	SIMLR, high-dimensional data generated from latent vector	[43]