Parameter name	Description	Range of tested values			
KNN graph	Underlying k-NN graph, generated from simulated or real scRNA-seq datasets	Clusters [dyntoy]	1D trajectory [dyntoy]	Branching trajectory [dyntoy]	Mouse gastrulation atlas [Pijuan-Sala et al. 2019]
DA population	cell population selected as centroid for differential abundance region	M1	M1	M1	Caudal_neurectoderm
		M2	M2	M2	Erythroid2
		M3	M3	M3	Gut
			M4	M4	Somitic_mesoderm
			M5	M5	Pharyngeal_mesoderm
			M6	M6	Erythroid1
			M7	M7	Mesenchyme
				M8	ExE_endoderm
				M9	
				M10	
Logit parameter	Coefficient of logit transformation	0.5	0.5	0.5	0.5
Max C1 probability	maximum probability of Condition 1	0.75 - 0.95	0.75-0.95	0.75-0.95	0.75-0.95
Seed for label sampling	Random seed for sampling of condition labels and assignment to replicates	43, 44, 45	43, 44, 45	43, 44, 45	43, 44, 45
Batch effect magnitude	Standard deviation of gaussian vector added to all cells in the same batch	0	0	0	0, 0.25, 0.5, 0.75, 1
	Total # simulations	54	126	180	810