

Method	Parameters	Values - clusters	Values - 1D trajectory	Values - branching trajectory	Values - mouse gastrulation	Significance threshold
Milo	K	15	20	20	50	10% FDR
	d	30	30	30	30	
	prop	0.1	0.1	0.1	0.1	
MELD	K	NA	NA	NA	50	NA
	d	NA	NA	NA	30	
Cydar	tol	0.8	6	6	1	10% FDR
	downsample	3	3	3	3	
	d	30	30	30	30	
DAseq	k.vector	15-500, steps of 50	20-500, steps of 50	20-500, steps of 50	50-500, steps of 50	DA score > permutation threshold (pred.thres = NULL)
	d	30	30	30	30	
Louvain + GLM	k	15	20	20	50	10% FDR
	d	30	30	30	30	