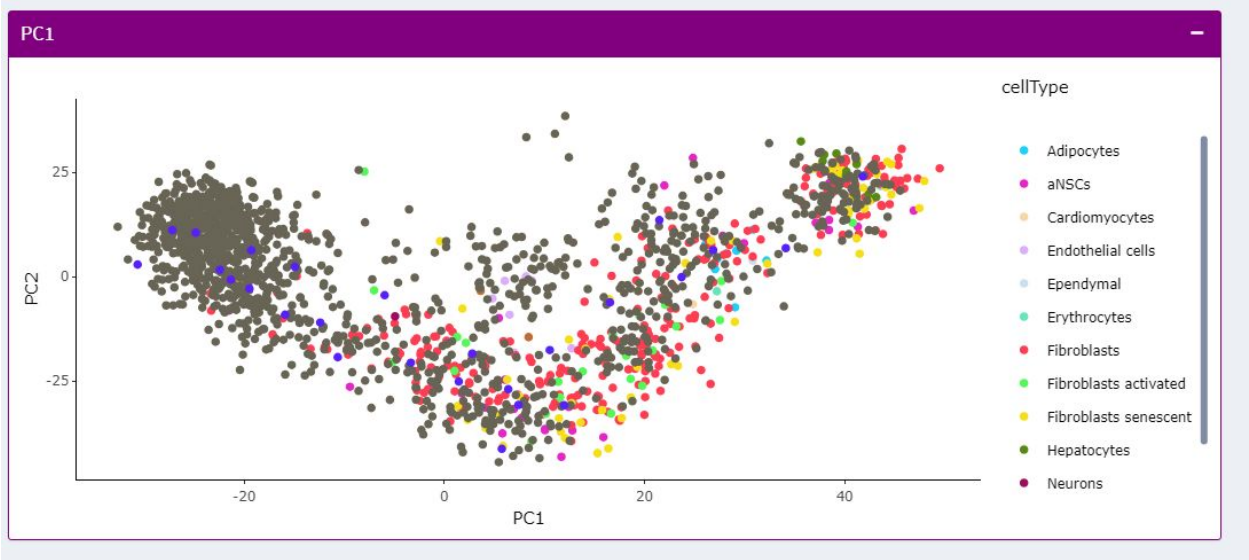
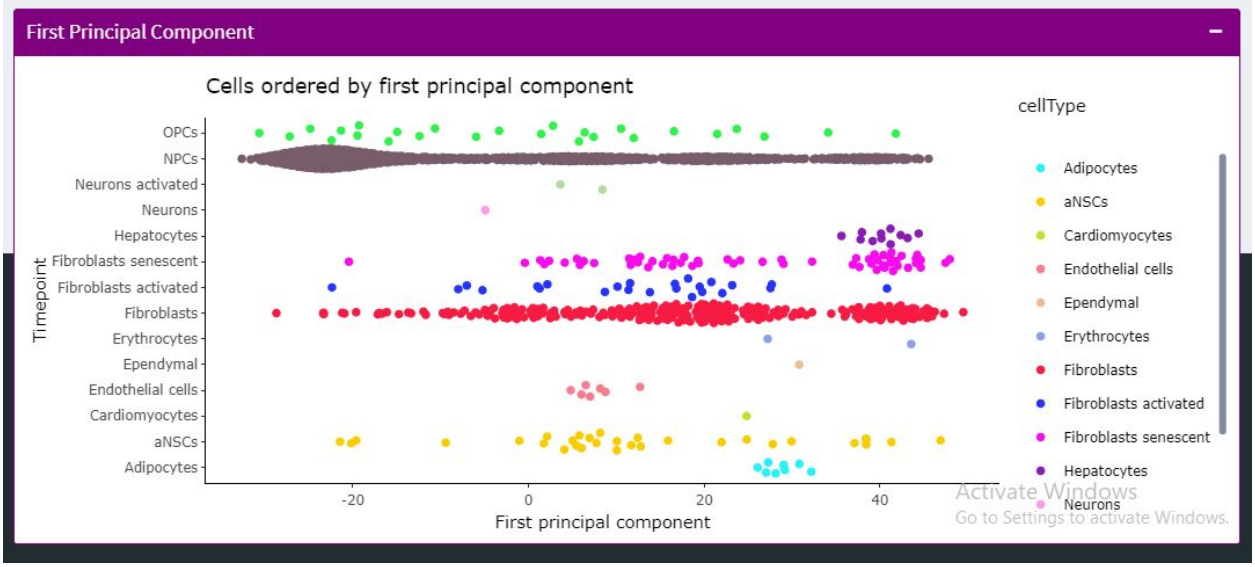
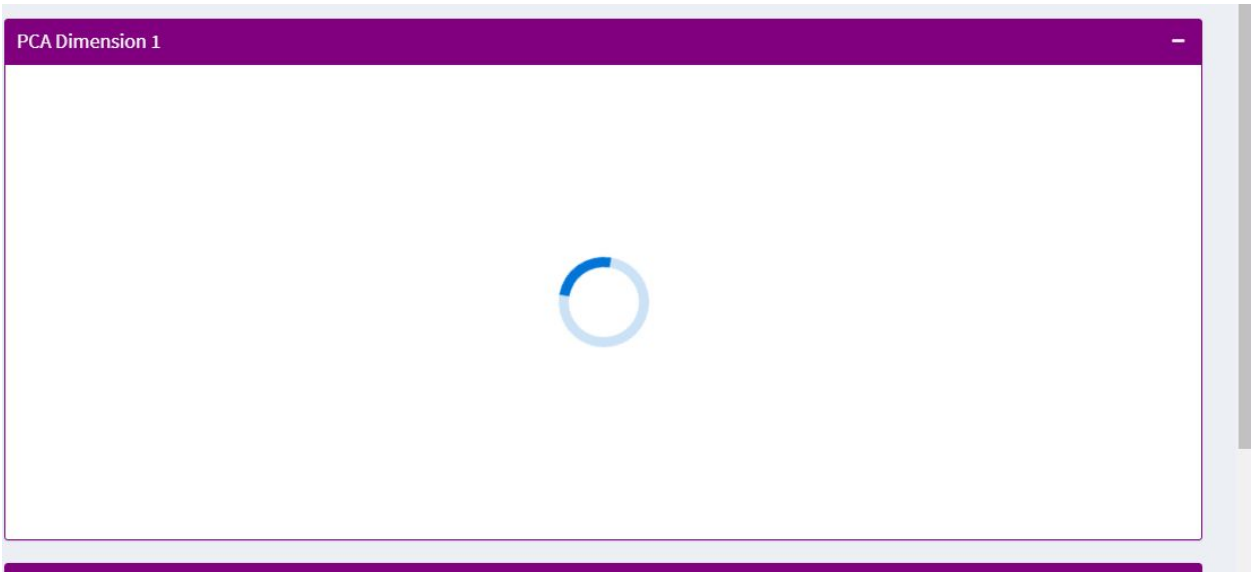
First Look:



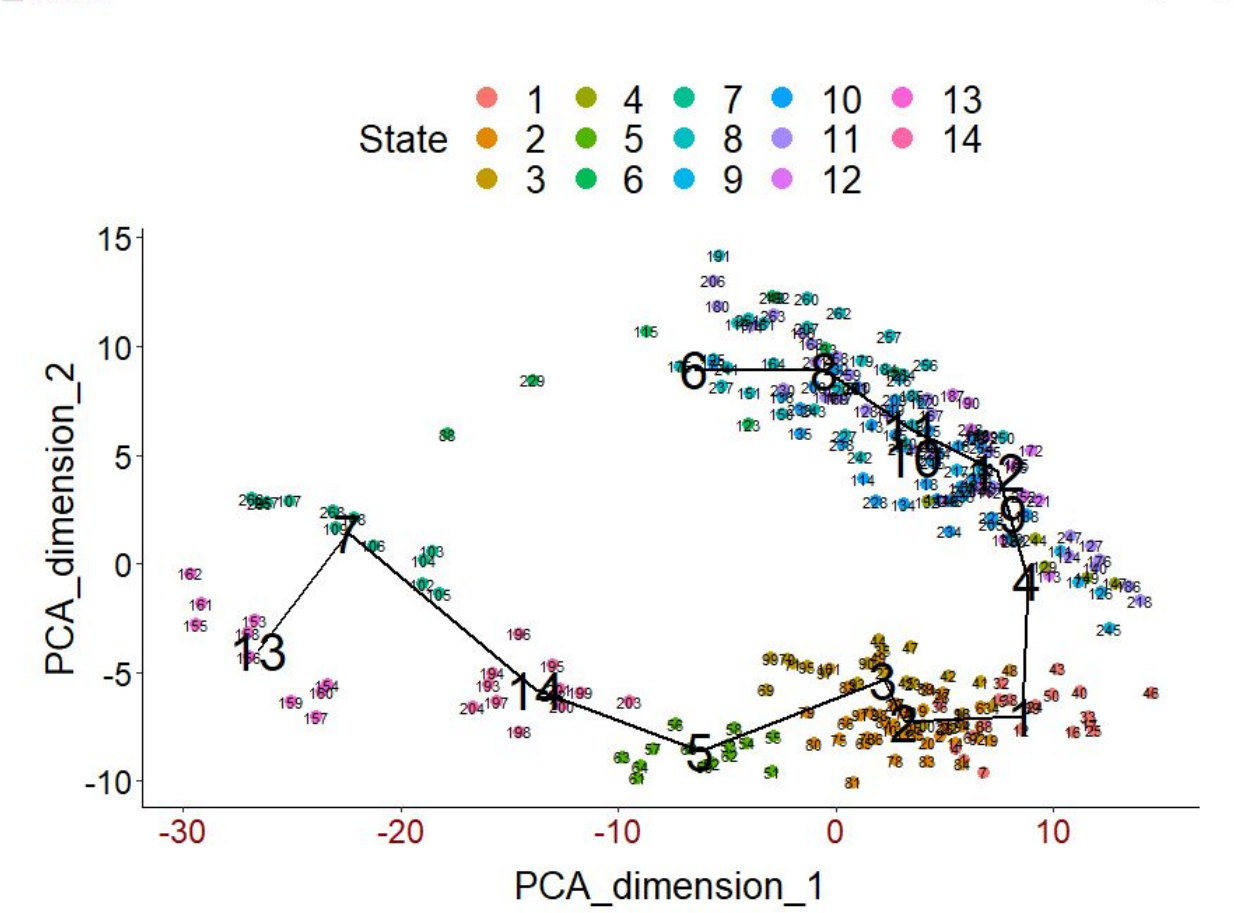


For Slingshot:

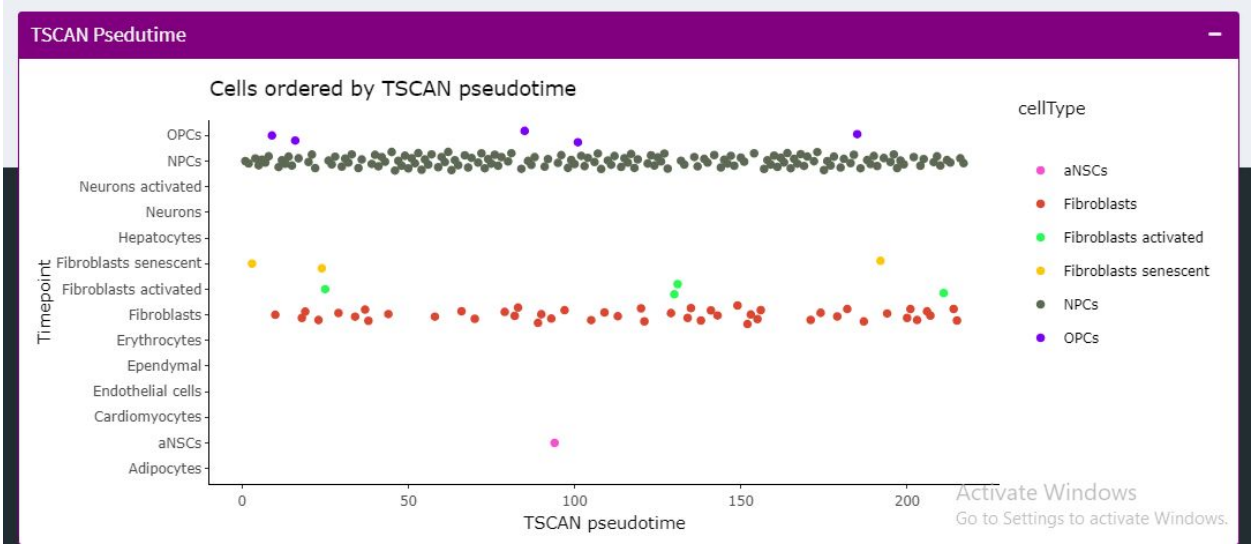
For TSCAN:



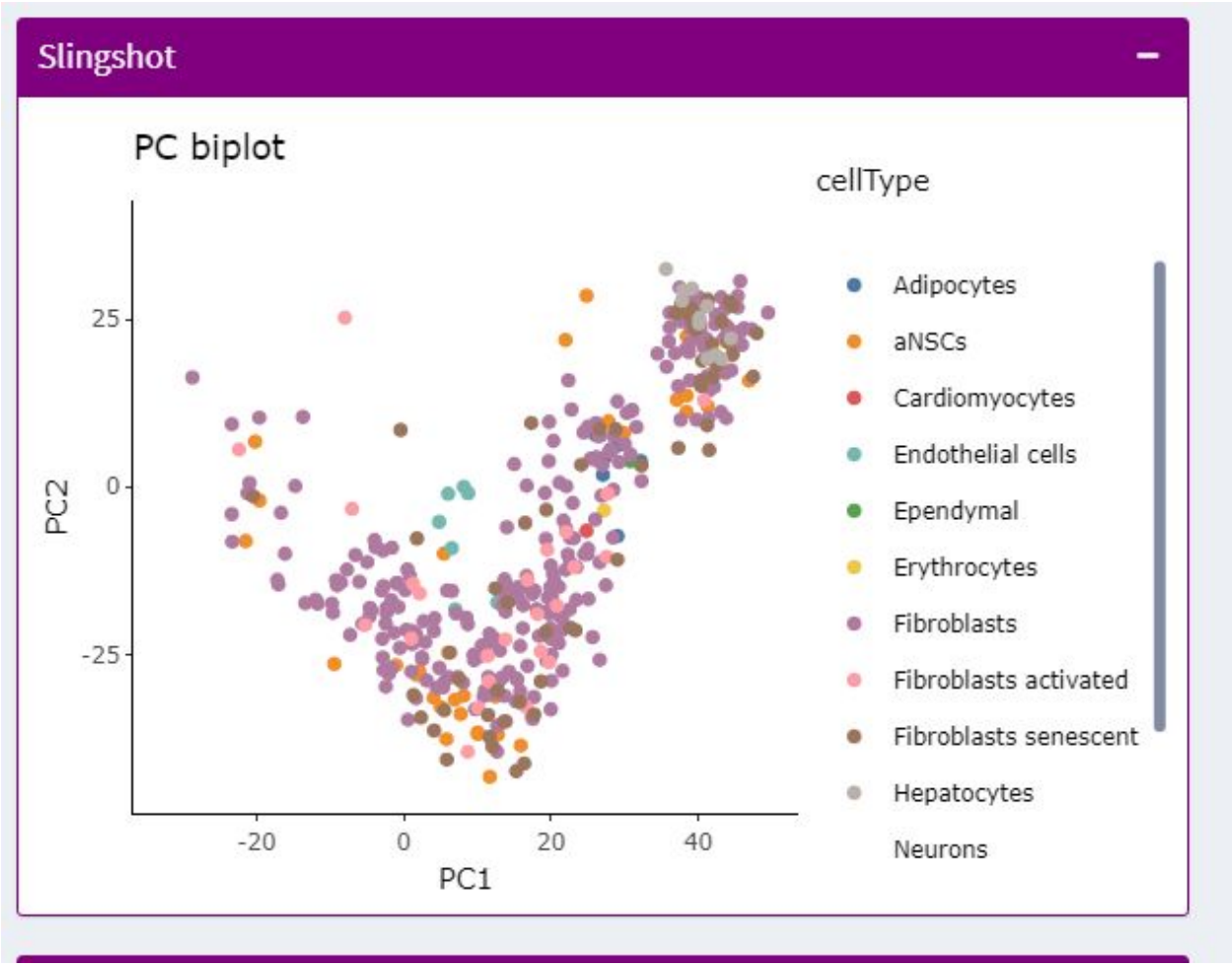
But this one works in normal R properly:

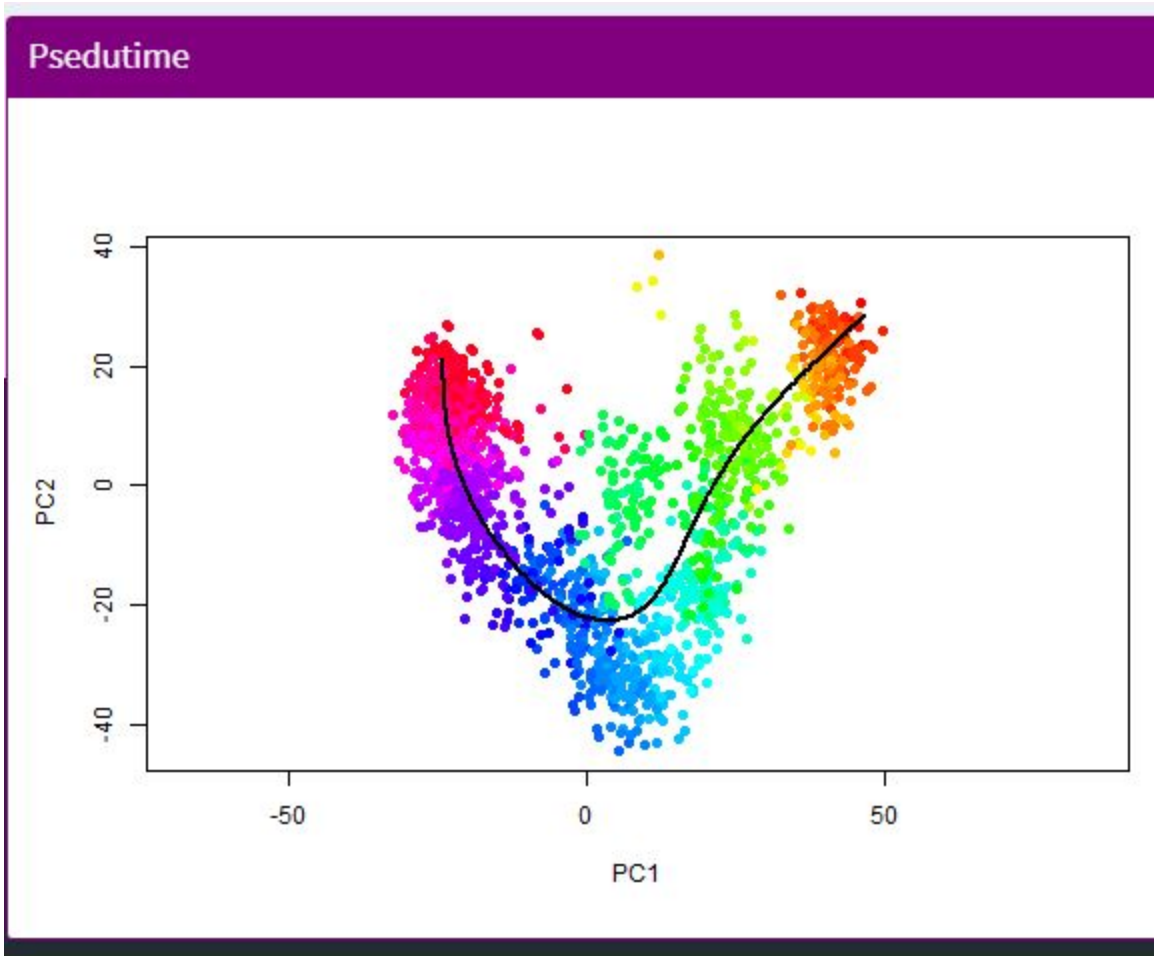


TSCAN Pseudotime:

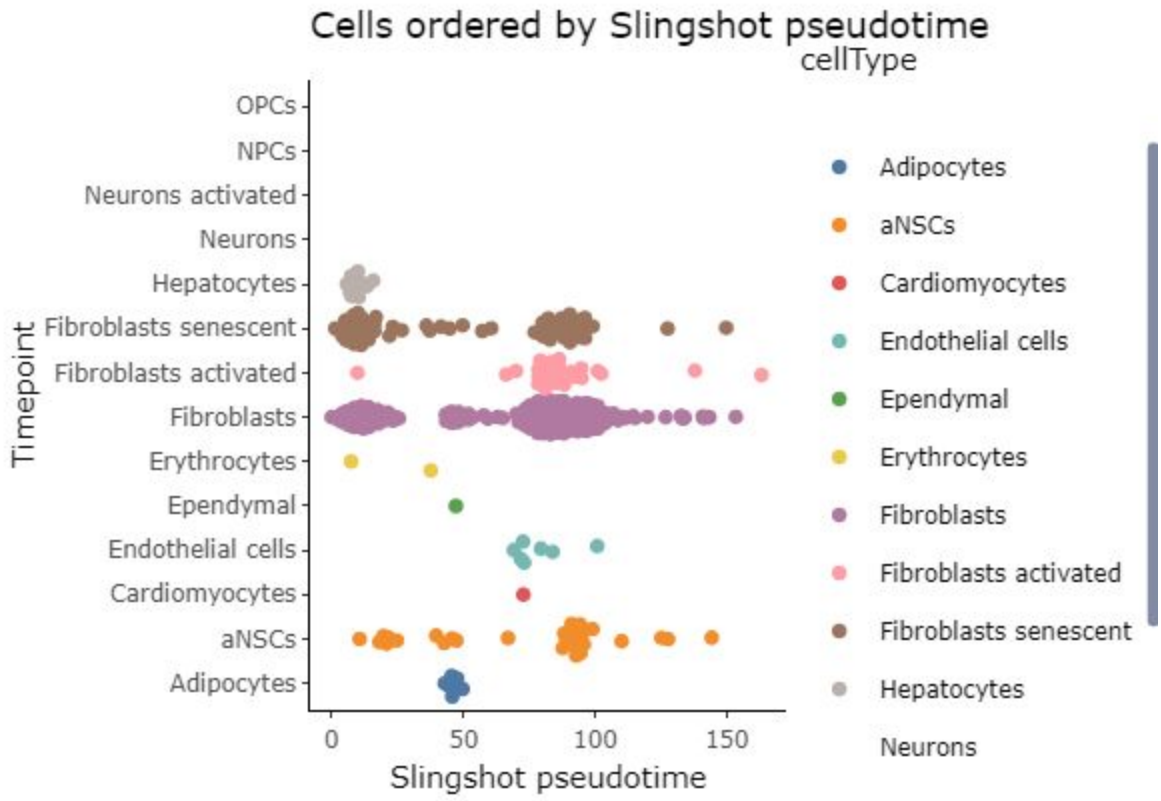


Slingshot:


Slingshot
PC biplot
cellType
Adipocytes
aNSCs
Cardiomyocytes
Endothelial cells
Ependymal
Erythrocytes
Fibroblasts
Fibroblasts activated
Fibroblasts senescent
Hepatocytes
Neurons
PC2
25
0
-25
-20
0
20
40
PC1


Psedutime
PC2
40
20
0
-20
-40
-50
0
50
PC1

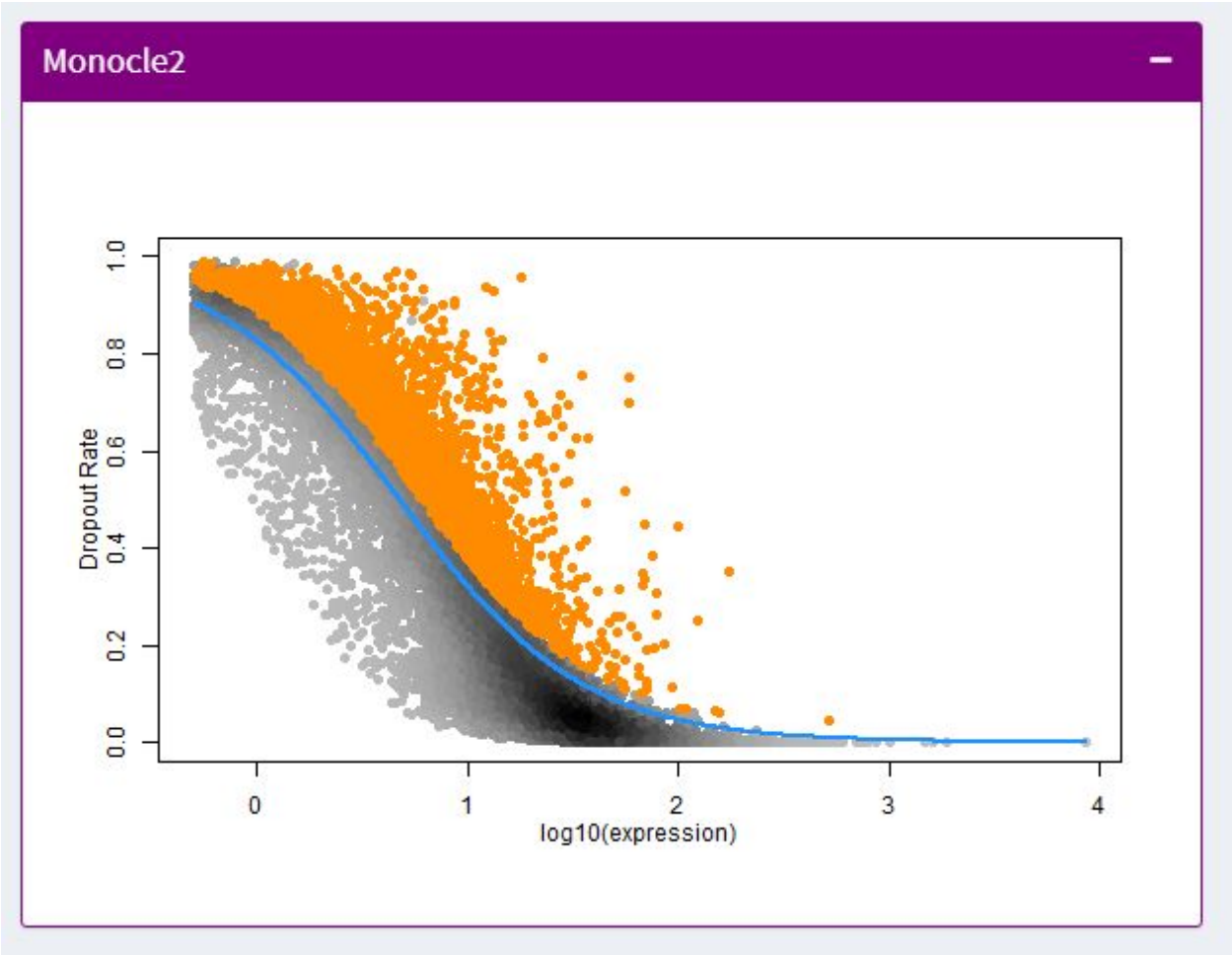
First Slingshot Psedutime



Second Slingshot Psedutime

Error: geom_point requires the following missing aesthetics: x

Monocle2:


Monocle2
Dropout Rate
0.0
0.2
0.4
0.6
0.8
1.0
0
1
2
3
4
log10(expression)

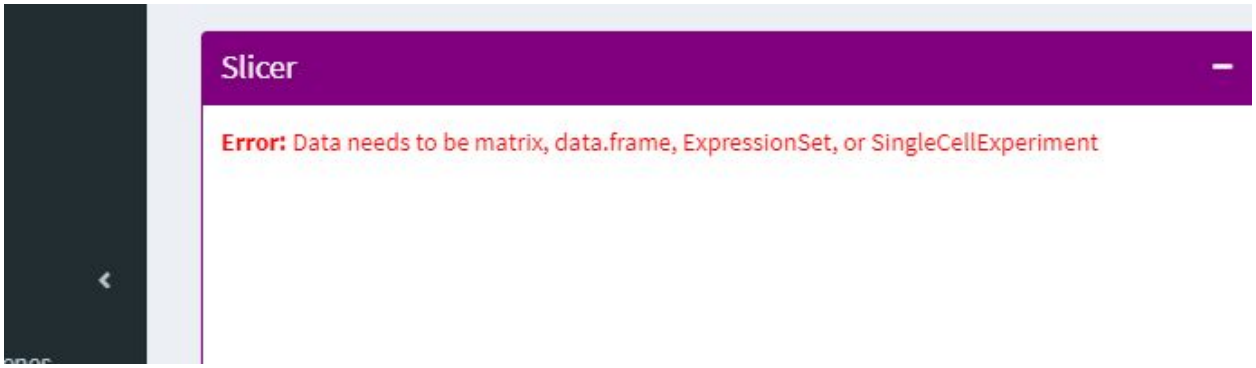
Component

Error: Error: argument cellData must be a matrix (either sparse from the Matrix package or dense)

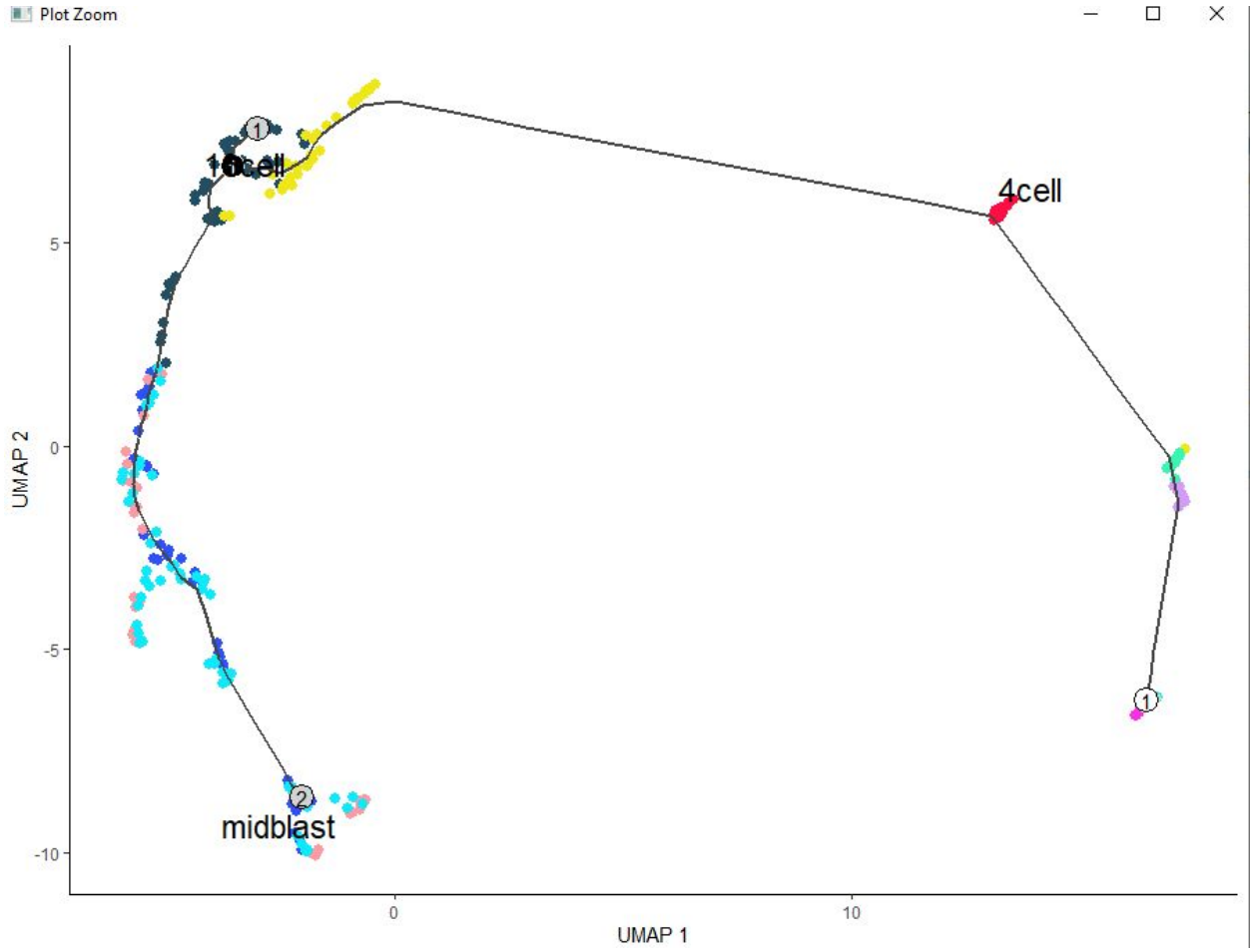
Monocle Psedutime

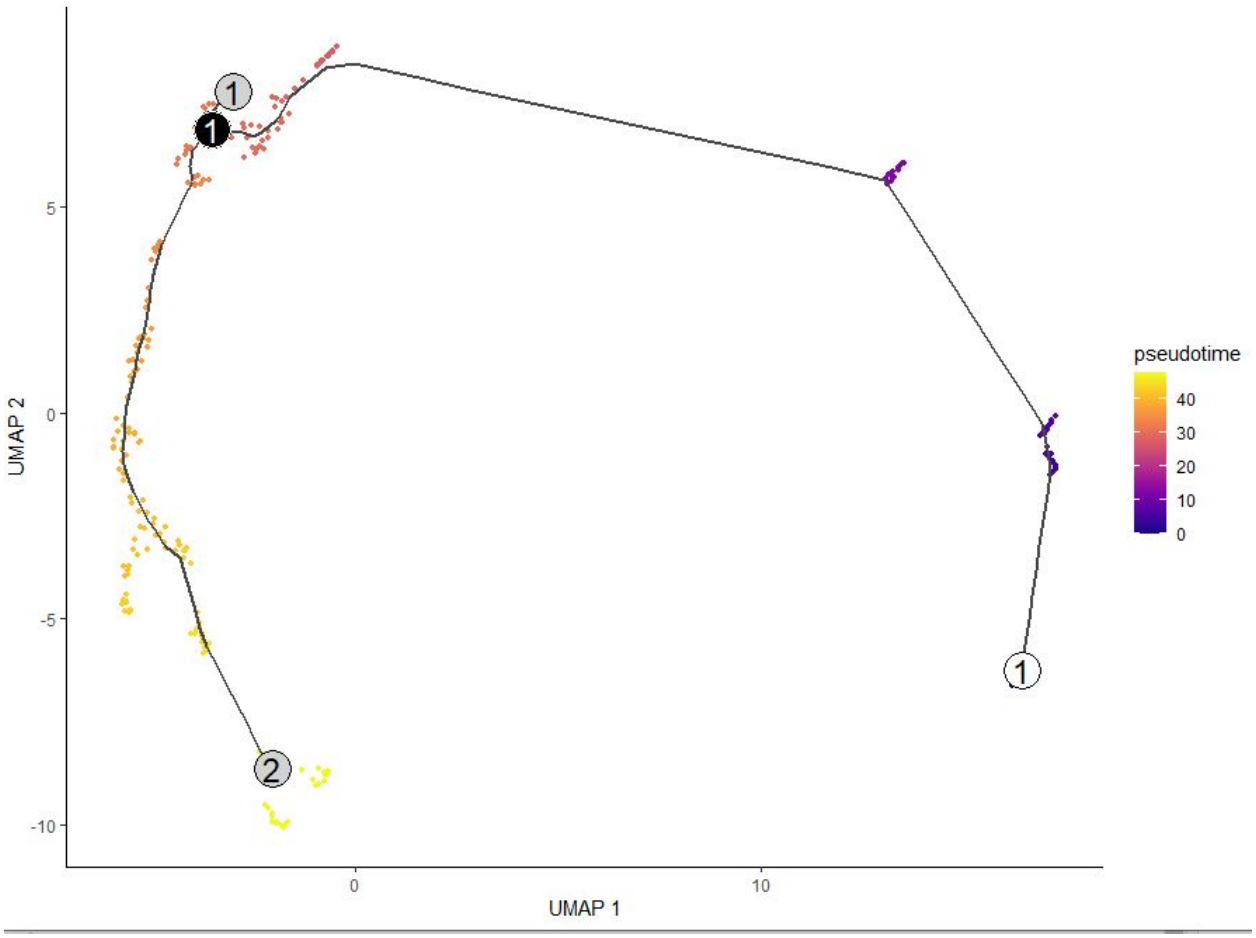
Error: Error: argument cellData must be a matrix (either sparse from the Matrix package or dense)

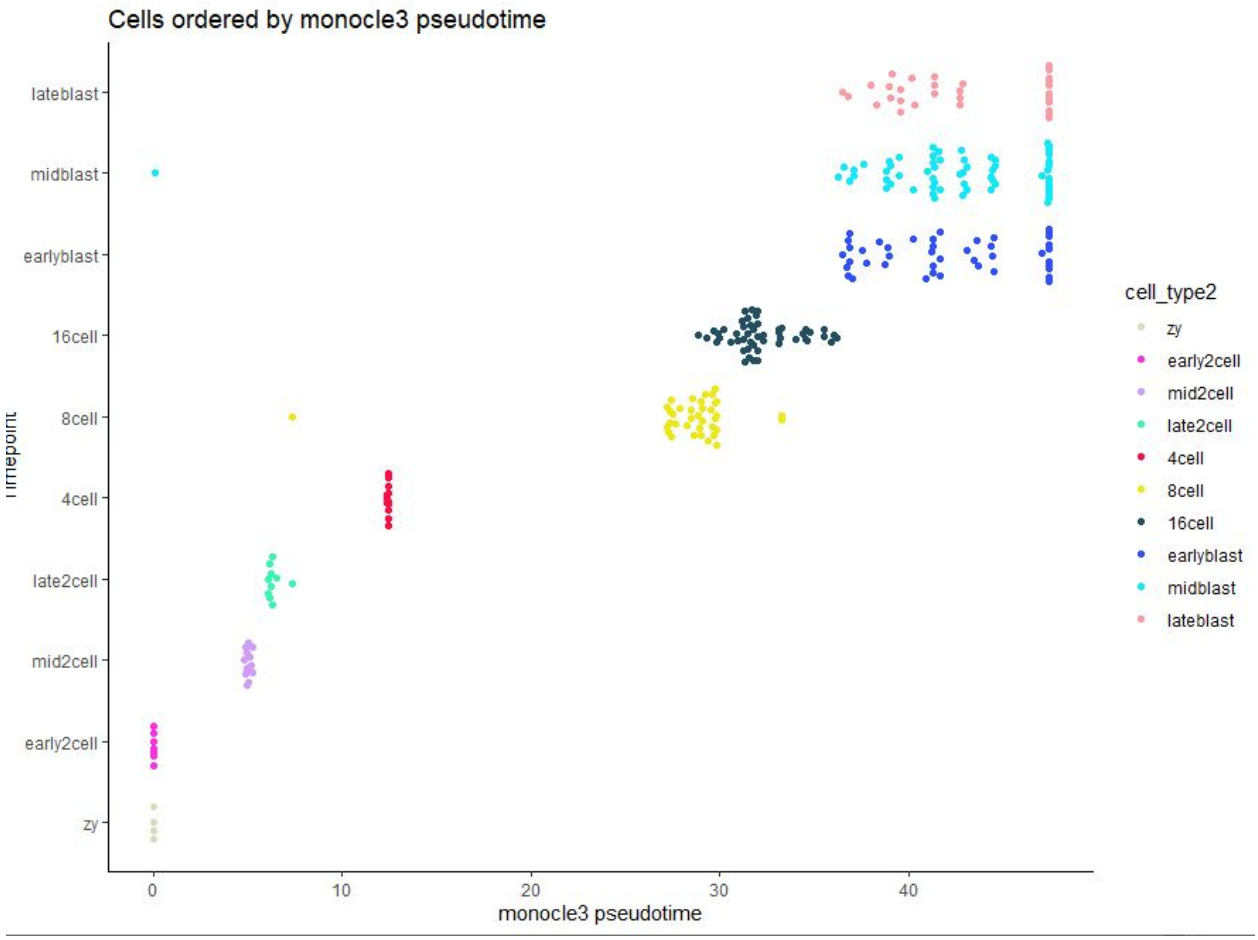
For slicer: Warning: not a recognized matrix class, coercing to 'matrix'.
Warning: Error in dataset_extract_doublematrix: Data needs to be matrix, data.frame, ExpressionSet, or SingleCellExperiment



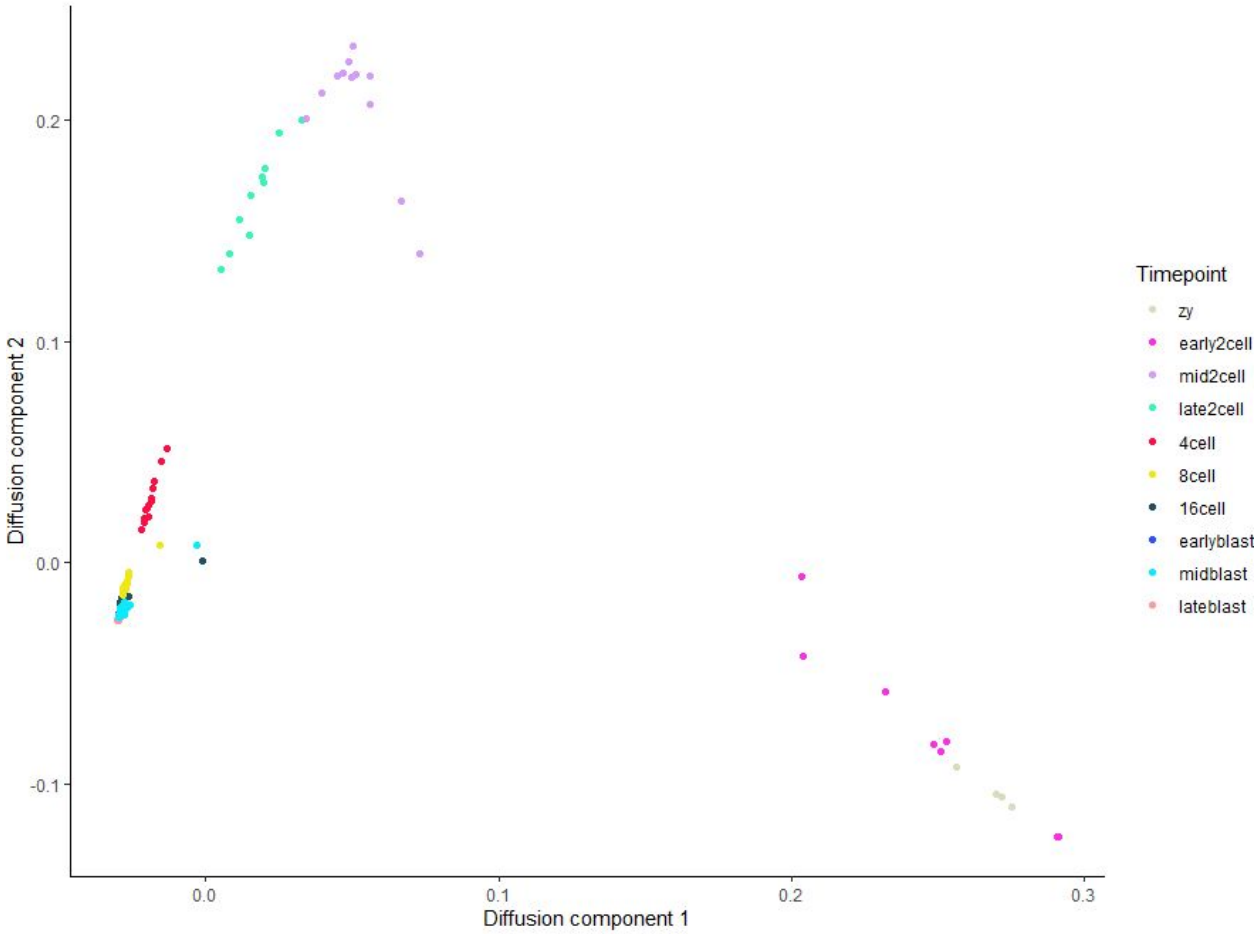
Monocle3 for Deng Data

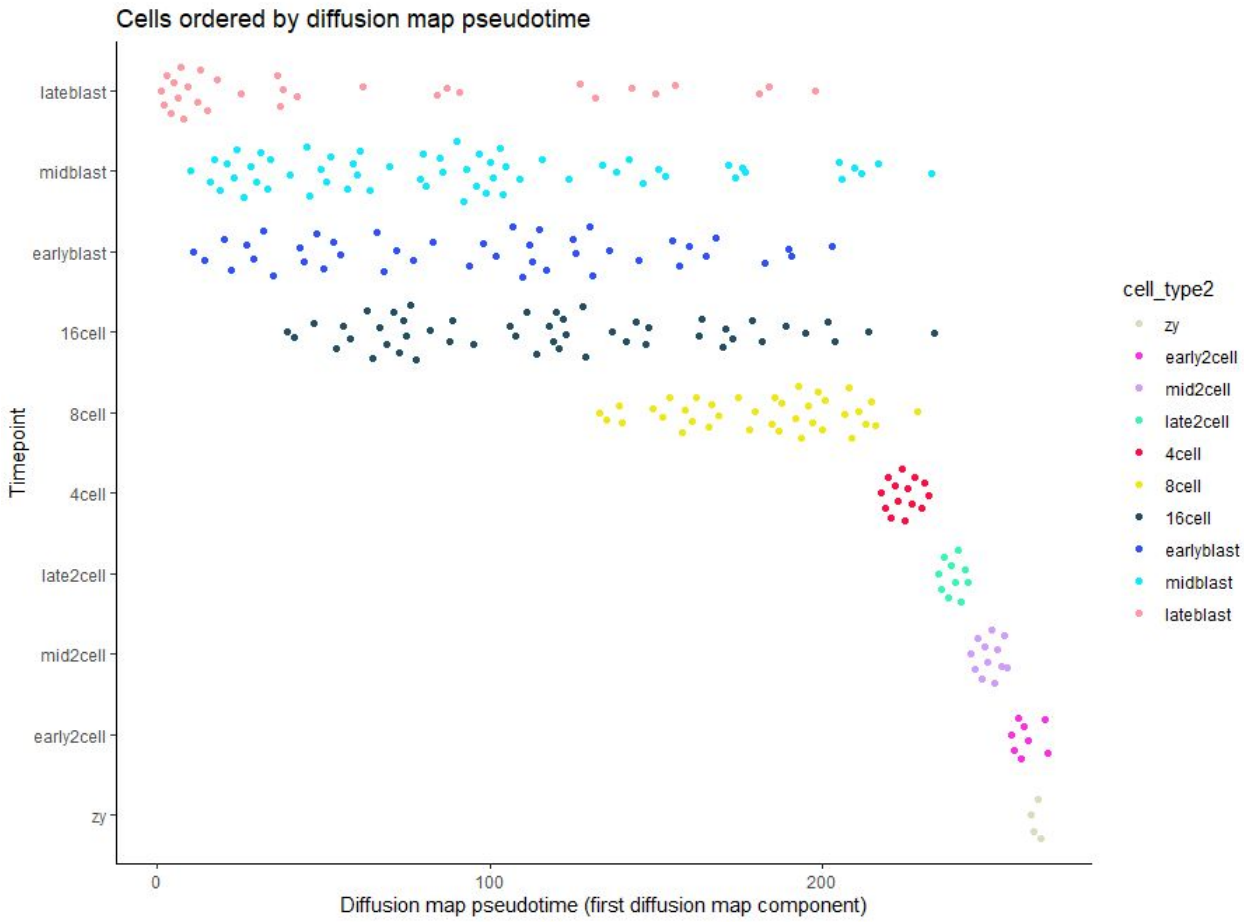



1
1
2
1
5
0
-5
-10
0
10
UMAP 1
UMAP 2
pseudotime
40
30
20
10
0



Diffusion Map:


Diffusion component 2
0.2
0.1
0.0
-0.1
0.0
0.1
0.2
0.3
Diffusion component 1
Timepoint
zy
early2cell
mid2cell
late2cell
4cell
8cell
16cell
earlyblast
midblast
lateblast


Cells ordered by diffusion map pseudotime
lateblast
midblast
earlyblast
16cell
8cell
4cell
late2cell
mid2cell
early2cell
zy
Timepoint
0
100
200
Diffusion map pseudotime (first diffusion map component)
cell_type2
zy
early2cell
mid2cell
late2cell
4cell
8cell
16cell
earlyblast
midblast
lateblast