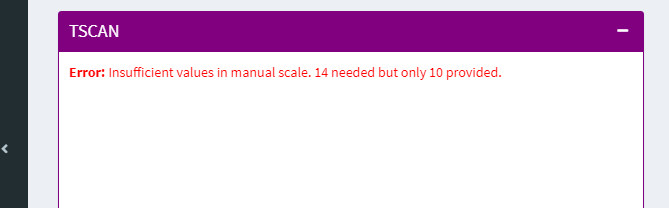
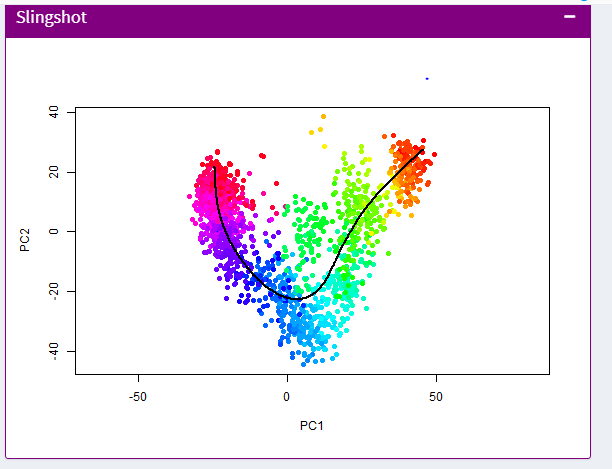
I have followed this site -<https://biocellgen-public.svi.edu.au/mig_2019_scrnaseq-workshop/public/trajectory-inference.html#slingshot>

**For TSCAN:**

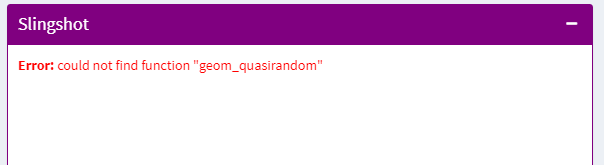
Warning: Error in : Insufficient values in manual scale. 14 needed but only 10 provided.



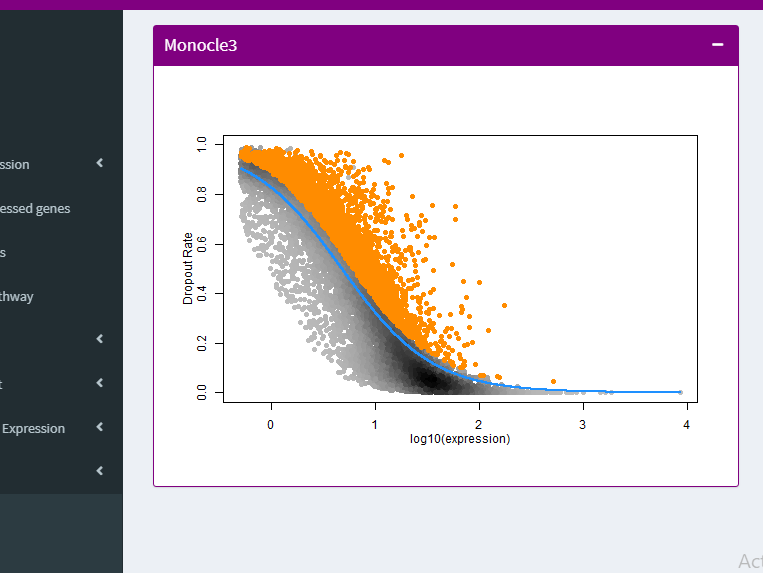
**Slingshot:**



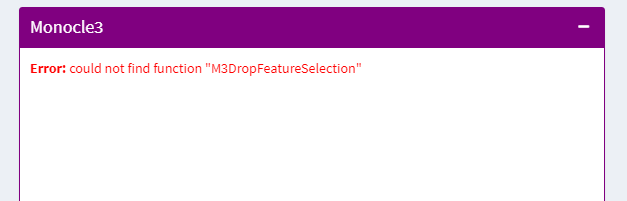
But sometimes it showed-



**Monocle2:**



But sometimes it showed-



**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

