

Description of LIAYSON

Noemi Andor

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1 Example

```
> library(liayson)
> ## Load data and map genes onto segments
> data(epg)
> data(segments)
> X=aggregateSegmentExpression(epg, segments, mingps=20, GRCh=38)
> if(is.null(X)){
+     print("BiomaRt Web service for annotation of gene locations is not available")
+     data(cnps)
+ }else{
+     head(X$eps[,1:3]); ##Aggregate expression of first three cells
+     ## Calculate number of expressed genes per cell
+     data(epg)
+     gpc = apply(epg>0, 2, sum)
+     ## Calculate copy number from expression
+     cn=segments[rownames(X$eps),"CN_Estimate"]
+     cnps = segmentExpression2CopyNumber(X$eps, gpc, cn, nCores=1)
+ }
> head(cnps[,1:3]); ##Copy number of first three cells
```

	GGACGTCTCTATCCTA-1	AGCTCTCTCCGCGTTT-1	CAGCATAACCCAGTTA-1
1:2360001-28080000	1	1	1
1:32720001-248900000	2	2	2
2:1-88940000	2	2	2
2:91820001-242040000	2	2	2
3:23580001-60260000	1	1	1
3:93840001-147160000	2	2	2

```
> outc = clusterCells(cnps, h=0.05)
```

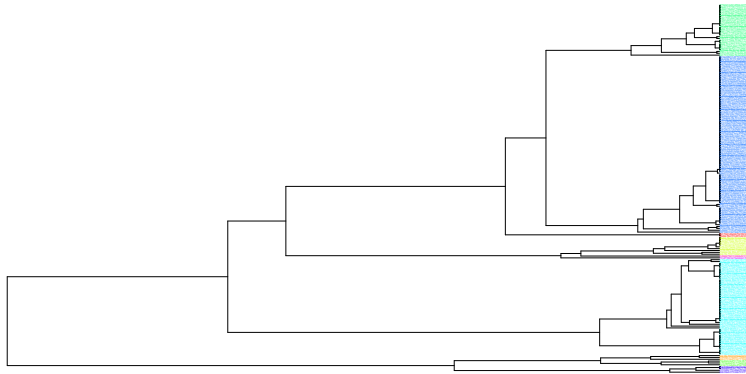


Figure 1: Cells are clustered based on their copy number