# Description of LIAYSON

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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
```

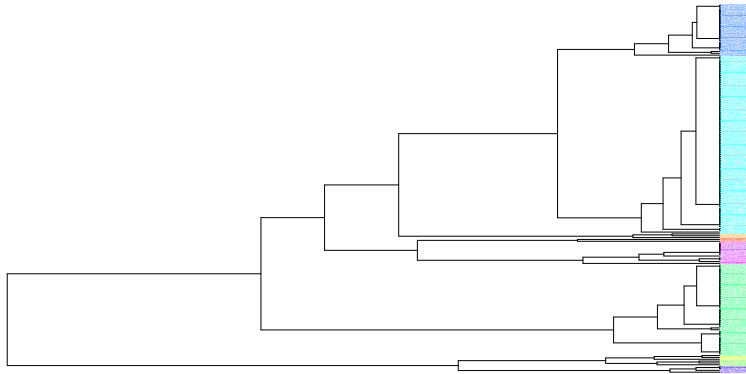|                      | GGACGTCTCTATCCTA-1 | AGCTCTCTCCGCGTTT-1 | CAGCATACACCAGTTA-1 |
|----------------------|--------------------|--------------------|--------------------|
| 1:2360001-28080000   | 1                  | 1                  | 1                  |
| 1:32720001-248900000 | 2                  | 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