Description of LIAYSON

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1 Example

```r
> 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. Using pre-calculated matrix of copy number states")
+ 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
```

<p>| | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>GGACGTCTCTATCCTA-1</td>
<td>AGCTCTCTCCGGTTT-1</td>
<td>CAGCATACACCAGTA-1</td>
</tr>
<tr>
<td>1:2360001-28080000</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>1:32720001-248900000</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>2:1-88940000</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>2:91820001-242040000</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>3:23580001-60260000</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>3:93840001-147160000</td>
<td>2</td>
<td>2</td>
</tr>
</tbody>
</table>
> outc = clusterCells(cnps, h=0.05)

Figure 1: Cells are clustered based on their copy number