

Description of LIAYSON

Noemi Andor

December 12, 2018

1 Example

```
> library(liayson)
> ## Load data and map genes onto segments
> data(epg)
> data(segments)
> X=aggregateSegmentExpression(epg, segments, mingps=20, GRCh=38)

[1] ">= 20 genes expressed in 36 segments for 200 cells"

> head(X$eps[,1:3]); ##Aggregate expression of first three cells
```

	GGACGTCTCTATCCTA-1	AGCTCTCTCCGCGTTT-1	CAGCATACACCAGTTA-1
1:2360001-28080000	0.5071770	0.3827751	0.1913876
1:32720001-248900000	0.7212614	0.5564598	0.3072228
2:1-88940000	0.8058824	0.5558824	0.3411765
2:91820001-242040000	0.6964657	0.5322245	0.3659044
3:23580001-60260000	0.4837209	0.3860465	0.2139535
3:93840001-147160000	0.5737705	0.4426230	0.2131148

```
> ## 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)

[1] "After a-priori probabilities @ minRP >= 1: 0% copy numbers inferred"
[1] "No association rule mining was performed."
[1] "After posteriori probabilities: 100% copy numbers inferred"

> 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)
```

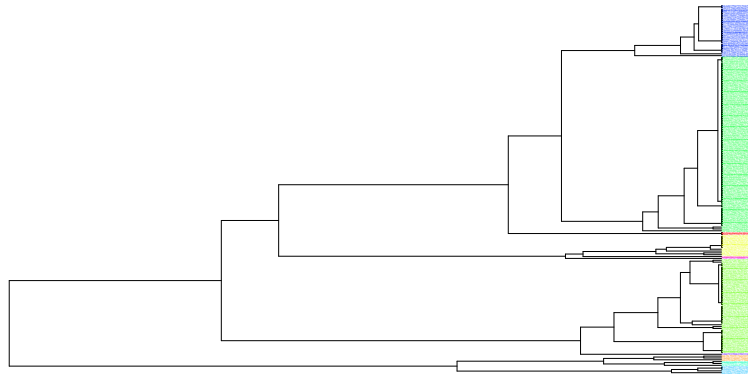


Figure 1: Cells are clustered based on their copy number