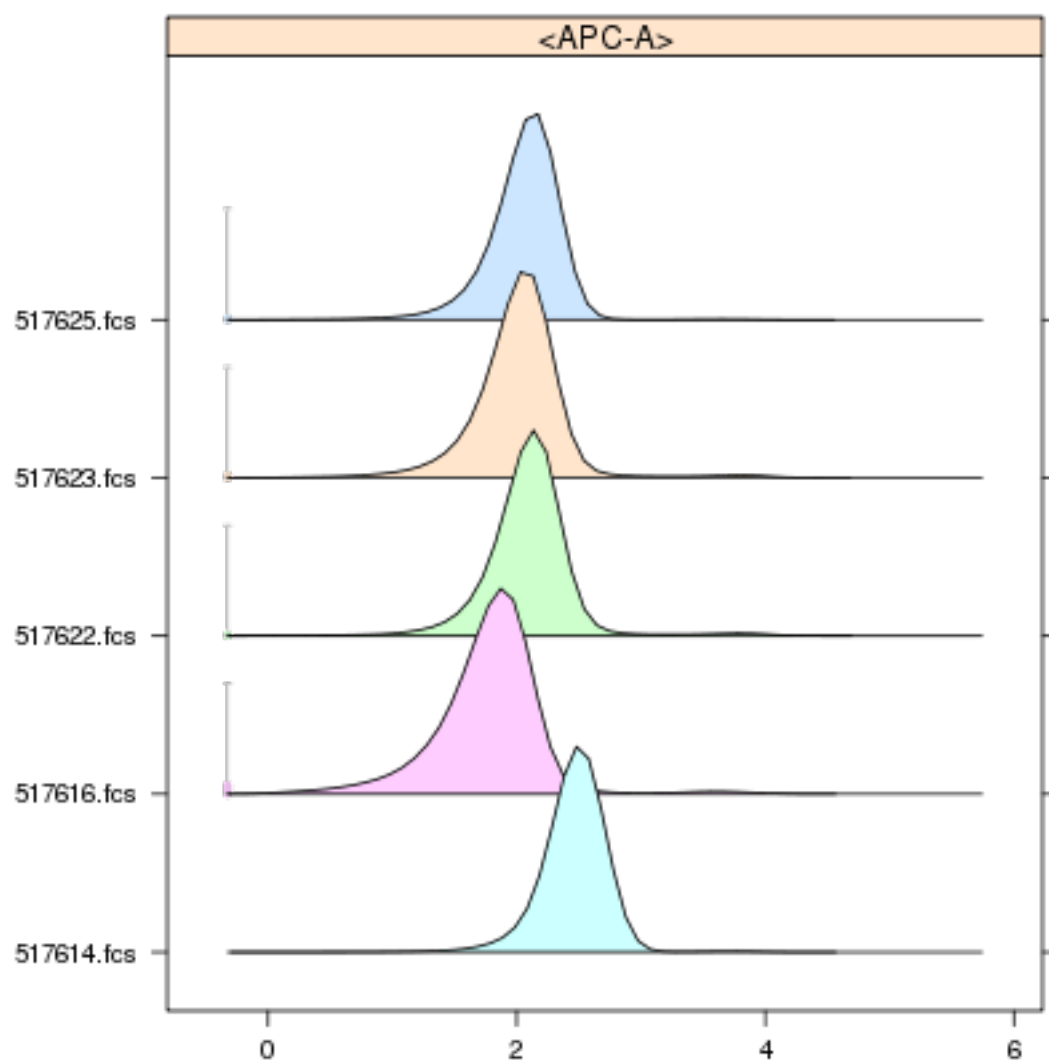# Normalization of GatingSet (C parser)

rglab.org

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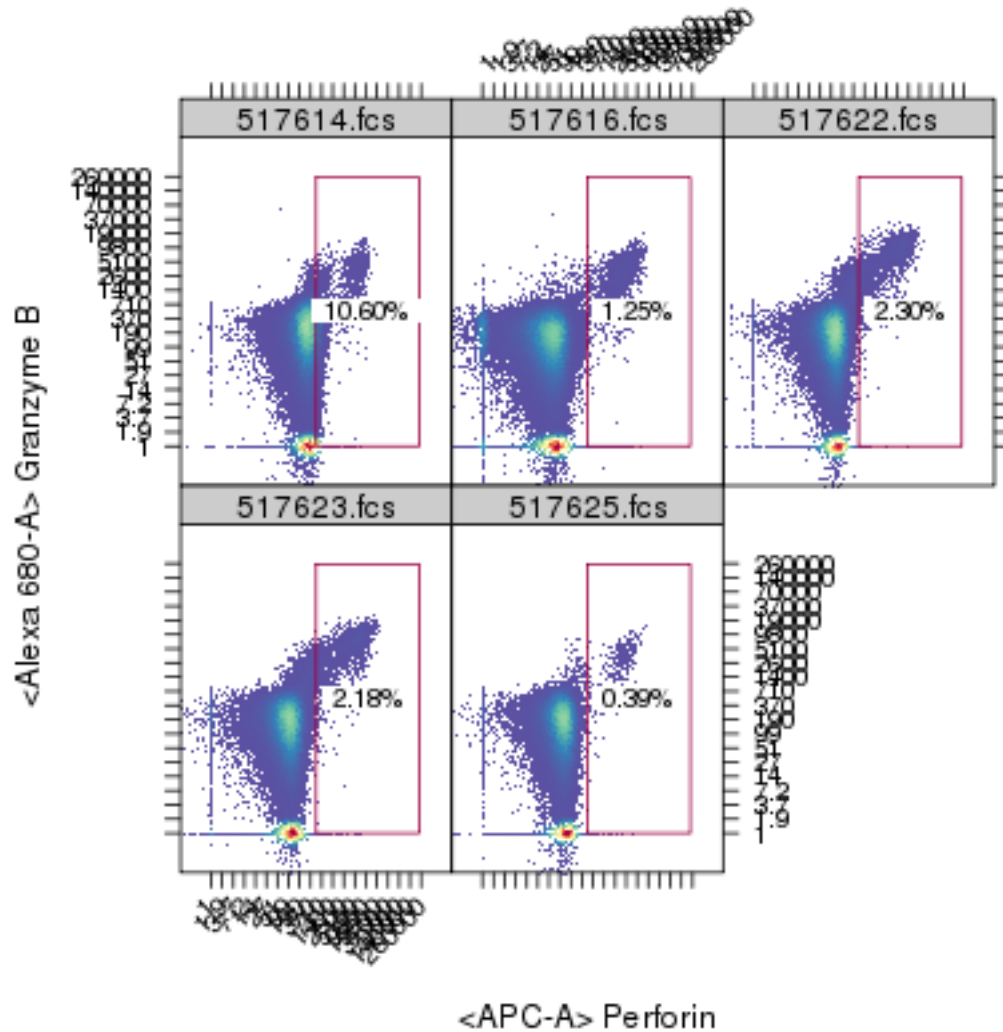
```r
# parse workspace
datapath <- "~/rglab/workspace/flowStats/data/FCSRAWDATA"
ws <- openWorkspace(file.path(datapath, "XML/080 Batch 1057 M.xml"))
G <- parseWorkspace(ws, name = 4, path = file.path(datapath, "FCS/1057-M-080"),
    subset = c(10:11), isNcdf = TRUE)
```

```r
## before normalization
densityplot(~`<APC-A>`, getData(G[-3], 6))
```
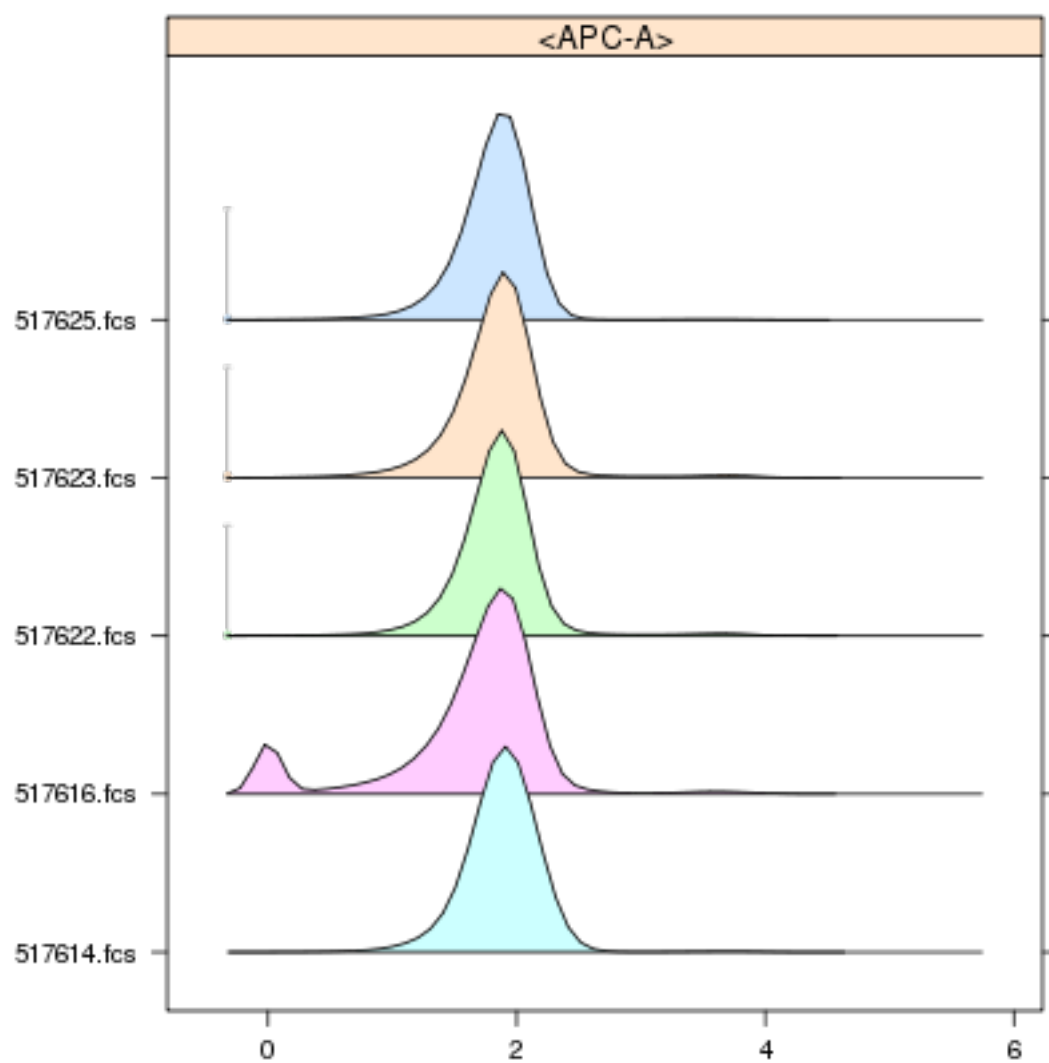
```
plotGate(G[-3], 9)
```

/S/Lv/L/3+/4+


```r
# select the gate Granzyme B+ to normalizae
skip.g <- (1:length(getNodes(G[[1]])))[-9]
# select APC to normalize
dims <- colnames(getData(G[[1]]))
skip.d <- dims[-9]
# run the normalization method
G1 <- normalize(data = G[-3], target = "517616.fcs", skipgates = skip.g, skipdims =
skip.d)
```

```r
## the plots after normalization
densityplot(~`<APC-A>`, getData(G1, 6))
```

```
plotGate(G1, 9)
```

/S/Lv/L/3+/4+