

The R package *trioClasses* for definition of the class *FamilyExperiment*, an extension of *SummarizedExperiment*, for use in trio based analyses of genetic data.

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## 1 Packages & Data

```
> library("trioClasses")
> library("CleftCNVAssoc")
> source("~/jhsph/R/packages/CleftCNVAssoc/vignettes/curated/make-data.R")
> gr.deletion.beaty <- gr.beaty[values(gr.beaty)$numsnp >=
  10 & values(gr.beaty)$cn %in% 0:1]
> homos.beaty <- with(values(gr.deletion.beaty), cn ==
  0)
> gr.deletion.pitt <- gr.pitt[values(gr.pitt)$numsnp >=
  10 & values(gr.pitt)$cn %in% 0:1]
> homos.pitt <- with(values(gr.deletion.pitt), cn == 0)
> gr.deletion.beaty.clean <- c(unlist(reduce(split(gr.deletion.beaty,
  values(gr.deletion.beaty)$id))), unlist(reduce(split(gr.deletion.beaty[homos.beaty],
  values(gr.deletion.beaty[homos.beaty])$id))))
> gr.deletion.pitt.clean <- c(unlist(reduce(split(gr.deletion.pitt,
  values(gr.deletion.pitt)$id))), unlist(reduce(split(gr.deletion.pitt[homos.pitt],
  values(gr.deletion.pitt[homos.pitt])$id))))

> system.time(cnv.obj.beaty <- CNVMatrix(gr.deletion.beaty.clean))

   user  system elapsed 
947.051   0.132  950.419 

> system.time(cnv.obj.pitt <- CNVMatrix(gr.deletion.pitt.clean))

   user  system elapsed 
638.364   0.000  640.516 

> save(cnv.obj.beaty, cnv.obj.pitt, file = "../data/cnv.RData")
```