

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.beaty <- c(gr.deletion.beaty, gr.deletion.beaty[homos.beaty])
> 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.pitt <- c(gr.deletion.pitt, gr.deletion.pitt[homos.pitt])

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

      user      system elapsed 
1336.652    0.112 1345.292 

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

      user      system elapsed 
 907.500    0.012  912.392
```