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

Samuel G. Younkin

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1   Packages & Data

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

    user    system   elapsed
1011.396     0.064 1014.927

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

   user   system elapsed
682.164    0.040 684.554

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