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")
> data("cnv", package = "trioClasses")
> data("pedigrees", package = "CleftCNVAssoc")
```

See vignette "CNVMatrix" method for description of cnv object.

2 SummarizedExperiment

```
> (se <- SummarizedExperiment(assays = SimpleList(cnv = t(cnv.obj$cnv.mat)),
     colData = DataFrame(id = rownames(cnv.obj$cnv.mat),
         row.names = rownames(cnv.obj$cnv.mat)), rowData = cnv.obj$cmp.gr))
```

```
class: SummarizedExperiment
dim: 462 8
exptData(0):
assays(1): cnv
rownames(462): comp1 comp2 ... comp461 comp462
rowData values names(0):
colnames(8): 11005_03@1008472481 11005_02@1008472482 ...
  11035_03@1008472048 11035_02@1008472050
colData names(1): id
```

3 Pedigree

```
> beaty.trios <- MinimumDistance:::trios(beaty.pedigree)
> beaty.ped <- DataFrame(famid = do.call("rbind", strsplit(beaty.trios$O,
     "_"))[, 1], id = beaty.trios$O, fid = beaty.trios$F,
     mid = beaty.trios$M, sex = NA, dx = NA)

> ped <- PedClass(beaty.ped)
```

4 FamilyExperiment

```
> (fe <- FamilyExperiment(se, pedigree = ped))
```

```
class: FamilyExperiment
dim: 462 8
exptData(0):
assays(1): cnv
rownames(462): comp1 comp2 ... comp461 comp462
rowData values names(0):
colnames(8): 11005_03@1008472481 11005_02@1008472482 ...
  11035_03@1008472048 11035_02@1008472050
colData names(1): id
pedigree(2082): famid id fid mid sex dx
complete trios(2):
```

```
> trioAssay <- trioClasses:::TrioAssay(fe, type = "cnv")
> trioStates <- with(trioAssay, matrix(paste0(F, M, O),
     nrow = nrow(O), ncol = ncol(O)))
> dimnames(trioStates) <- dimnames(trioAssay$O)
```

```
> table.list <- apply(trioStates, 2, "table")
> head(table.list)
```

```
$comp1

000 100
  1   1

$comp2

000 101
  1   1

$comp3

000 100
  1   1

$comp4

000 100
  1   1

$comp5

000 100
  1   1

$comp6

000
  2
```

Now, I need a function that acts on tables.

```
> trans.vec <- as(lapply(table.list, trioClasses:::trans.tab),
     "numeric")
> head(table.list[which(trans.vec <= 0.05/length(trans.vec))])

named list()

> reduce(cnv.obj$cmp.gr[which(trans.vec <= 0.05/length(trans.vec))])

GRanges with 0 ranges and 0 elementMetadata cols:
   seqnames    ranges strand
      <Rle> <IRanges>  <Rle>
  ---
  seqlengths:
           chr1   chr1_random ...          chrY          chrM
      247249719       1663265 ...      57772954         16571
```