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$cnv.mat)),
     colData = DataFrame(id = rownames(cnv$cnv.mat), row.names = rownames(cnv$cnv.mat)),
     rowData = cnv$cmp.gr))
```

```
class: SummarizedExperiment
dim: 12915 1341
exptData(0):
assays(1): cnv
rownames(12915): comp1 comp2 ... comp12914 comp12915
rowData values names(0):
colnames(1341): 11005_03@1008472481 11005_02@1008472482 ...
  18117_02@0070298660 18117_01@0070298681
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: 12915 1341
exptData(0):
assays(1): cnv
rownames(12915): comp1 comp2 ... comp12914 comp12915
rowData values names(0):
colnames(1341): 11005_03@1008472481 11005_02@1008472482 ...
  18117_02@0070298660 18117_01@0070298681
colData names(1): id
pedigree(2082): famid id fid mid sex dx
complete trios(447):
```

```
> 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

000 101
446   1

$comp2

000 011
446   1

$comp3

000 101
446   1

$comp4

000 011
446   1

$comp5

000 010
446   1

$comp6

000 010
445   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))])

$comp176

000 010 011 100 101 111
333  16  41  14  40   3

$comp177

000 010 011 100 101 110 111
306  15  55  11  53   1   6

$comp178

000 010 011 100 101 111
335  13  47   9  39   4

$comp226

000 011 100 101
418  16   1  12

$comp227

000 011 100 101
417  16   1  13

$comp276

000 011 101
395  20  32

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

GRanges with 159 ranges and 0 elementMetadata cols:
        seqnames                ranges strand
           <Rle>             <IRanges>  <Rle>
    [1]     chr1 [ 17112560,  17140083]      *
    [2]     chr1 [ 44144208,  44144762]      *
    [3]     chr1 [ 70885145,  70885657]      *
    [4]     chr1 [ 76124315,  76124567]      *
    [5]     chr1 [167495768, 167505182]      *
    [6]     chr1 [173065372, 173066743]      *
    [7]     chr1 [246638450, 246638776]      *
    [8]     chr2 [  4292914,   4294509]      *
    [9]     chr2 [ 34556561,  34571303]      *
    ...      ...                  ...    ...
  [151]    chr19   [40353627, 40354649]      *
```

```
[152]    chr20   [26241985, 26248774]      *
[153]    chr20   [54289855, 54295837]      *
[154]    chr20   [62066740, 62067654]      *
[155]    chr20   [62192612, 62192727]      *
[156]    chr21   [18249338, 18250201]      *
[157]    chr21   [22577771, 22583706]      *
[158]    chr22   [21808695, 21809273]      *
[159]    chr22   [49129839, 49130879]      *
---
seqlengths:
          chr1   chr1_random ...          chrY          chrM
     247249719       1663265 ...      57772954         16571
```