

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 metadata column names(0):
colnames(1341): 11005_03@1008472481 11005_02@1008472482 ...
  18117_02@00070298660 18117_01@00070298681
colData names(1): id
```

3 Pedigree

```
> beaty.trios <- MinimumDistance::trios(beaty.pedigree)
> beaty.ped <- DataFrame(famid = do.call("rbind", strsplit(beaty.trios$0,
  "_"))[, 1], id = beaty.trios$0, fid = beaty.trios$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 metadata column 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, 0),
  nrow = nrow(0), ncol = ncol(0)))
> dimnames(trioStates) <- dimnames(trioAssay$0)
> table(trioStates[, 1])

000 101
446 1
```