

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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March 29, 2013

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: 4288 1339
exptData(0):
assays(1): cnv
rownames(4288): comp1 comp2 ... comp4287 comp4288
rowData metadata column names(0):
colnames(1339): 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$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: 4288 1339
exptData(0):
assays(1): cnv
rownames(4288): comp1 comp2 ... comp4287 comp4288
rowData metadata column names(0):
colnames(1339): 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(445):

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

$comp1

000 010
444 1

$comp2

000 010
443 2

$comp3

000 010 101
442 2 1

$comp4

000 001 010 101
441 1 2 1

$comp5

000 001 010 101
440 1 2 2

$comp6

000 001 010 100 101
438 1 3 1 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))])

$comp1994

000 001 010 011 100 101 110 111
149  7  26  57  28  71   5 102

$comp1995

000 001 010 011 100 101 110 111
116  5  30  63  38  75   9 109

$comp1996

000 001 010 011 100 101 110 111
113  5  30  64  37  74  11 111

$comp1997

000 001 010 011 100 101 110 111
109  5  30  64  39  71  12 115

$comp1998

000 001 010 011 100 101 110 111
109  5  30  64  38  72  12 115

$comp1999

000 001 010 011 100 101 110 111
108  5  30  63  38  73  12 116

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

GRanges with 2 ranges and 0 metadata columns:

	seqnames	ranges	strand
	<Rle>	<IRanges>	<Rle>
[1]	chr8	[39356825, 39469612]	*
[2]	chr8	[39476659, 39497557]	*

seqlengths:

chr1	chr1_random ...	chrY	chrM
247249719	1663265 ...	57772954	16571