

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("sample")
> data("8q24-european-all.sm")
```

## 2 SummarizedExperiment

```
> se <- SummarizedExperiment(assays = SimpleList(geno = t(sm)),
  colData = col.DF, rowData = gr)
```

## 3 Pedigree

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

## 4 FamilyExperiment

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

```
class: FamilyExperiment
dim: 8951 960
exptData(0):
assays(1): geno
rownames(8951): chr8:129296000 chr8:129296113 ...
  chr8:130354703 chr8:130354790
rowData values names(0):
colnames(960): H_ME-DS10776_2-DS10776_2
  H_ME-DS10776_3-DS10776_3 ... H_ME-DS11313_3-DS11313_3
  H_ME-DS11313_1-DS11313_1
colData names(1): id
pedigree(4139): famid id fid mid sex dx
complete trios(320):
```

## 5 Methods

### 5.1 ScanTrio

```
> (ste.rare <- ste[!(MAF(ste) >= 0.01 | is.na(MAF(ste))))])
```

```
class: FamilyExperiment
dim: 6397 960
exptData(0):
assays(1): geno
rownames(6397): chr8:129296113 chr8:129296185 ...
               chr8:130354703 chr8:130354790
rowData values names(0):
colnames(960): H_ME-DS10776_2-DS10776_2
               H_ME-DS10776_3-DS10776_3 ... H_ME-DS11313_3-DS11313_3
               H_ME-DS11313_1-DS11313_1
colData names(1): id
pedigree(4139): famid id fid mid sex dx
complete trios(320):
```

```
> system.time(scan.trio <- ScanTrio(object = ste.rare,
                                   window = window, block = range(rowData(ste.rare))))
```

```
      user  system elapsed
16.497    0.232   16.753
```

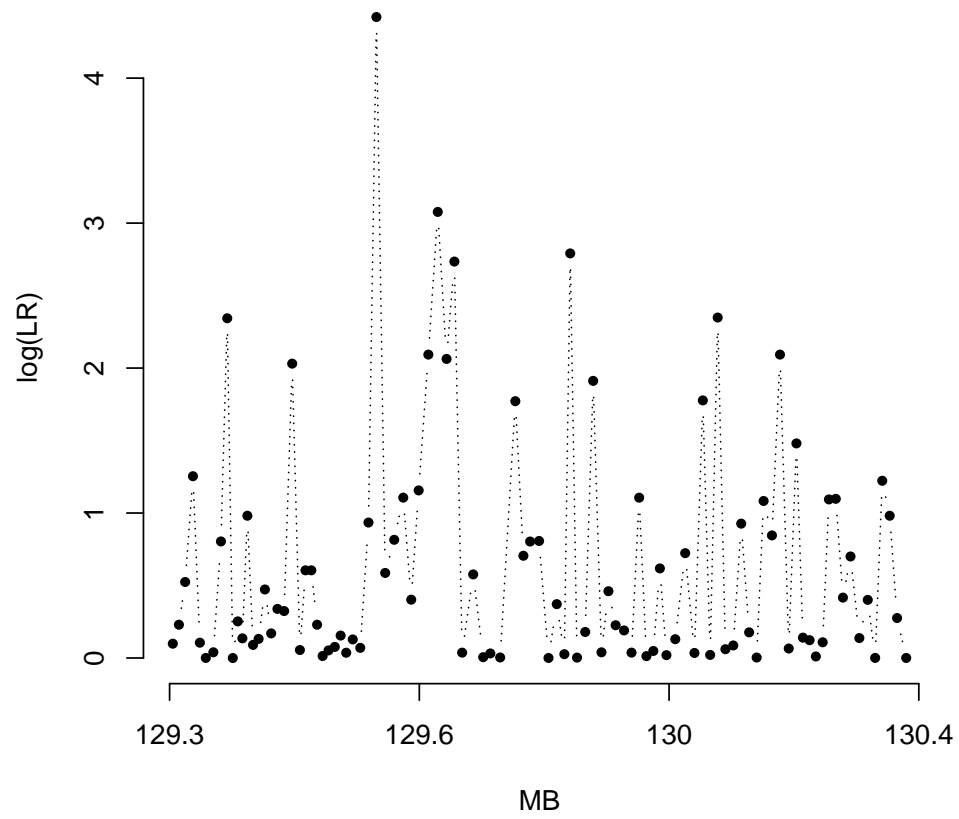
```
> scan.trio
```

DataFrame with 99 rows and 7 columns

	lr	minor.in	major.in	minor.out	major.out	mendel.in
	<numeric>	<integer>	<integer>	<integer>	<integer>	<integer>
1	1.103716	58	59	5390	5955	0
2	1.258080	46	58	5402	5956	0
3	1.689351	42	57	5406	5957	0
4	3.504761	41	62	5407	5952	0
5	1.111341	42	51	5406	5963	0
6	1.000482	73	81	5375	5933	0
7	1.040295	47	49	5401	5965	0
8	2.234714	75	67	5373	5947	0
9	10.418485	36	62	5412	5952	0
...	...	...	...	...	...	...
91	1.516825	63	59	5385	5955	0
92	2.014642	72	65	5376	5949	0
93	1.147383	44	54	5404	5960	0
94	1.493045	49	45	5399	5969	0
95	1.000654	62	68	5386	5946	0
96	3.395825	49	72	5399	5942	0
97	2.668222	34	51	5414	5963	0
98	1.317561	53	67	5395	5947	0
99	1.000407	71	78	5377	5936	0
	mendel.out					
	<integer>					

1	0
2	0
3	0
4	0
5	0
6	0
7	0
8	0
9	0
...	...
91	0
92	0
93	0
94	0
95	0
96	0
97	0
98	0
99	0

```
> save(scan.trio, file = "../data/scan-trio.RData")
```



## 5.2 Holger-style Genotype Matrix

Coercion to matrix for *trio*

```
> geno <- as(ste, "matrix")  
> aTDT(geno[, 1:5])
```

Or apply the aTDT method to the FamilyExperiment directly.

```
> aTDT(ste[1:5])
```

## A Count of Transmission of Variants (*TransCount()*)

### A.1 Window

```
> window <- gr[100] + 10000
> window2 <- gr[100] + 1000
> block <- range(rowData(ste))

> TransCount(ste, window)
```

### A.2 Not in window, but in block

```
> TransCount(ste, setdiff(block, window))
```

### A.3 In the whole block

```
> TransCount(ste, block)
```

### A.4 In both windows

```
> TransCount(ste, GRangesList(window, window2))
```

### A.5 Not “In both windows,” but in block

```
> TransCount(ste, GRangesList(setdiff(block, window), setdiff(block,
  window2)))
```

## B Count of Transmission of Rare Variants (*TransCount()*)

### B.1 In both windows

### B.2 Not “In both windows,” but in block

## C Classes

### C.1 SnpMatrix, DataFrame, GRanges

The four key ingredients are the SNP matrix, the pedigree information as a DataFrame, position of the SNPs given by a GRanges object, and covariate data given as a DataFrame.

```
> sm
> ped.DF
> gr
```

### C.2 SummarizedExperiment

We combine three of the key ingredients when we create the SummarizedExperiment object.

```
> se <- SummarizedExperiment(assays = SimpleList(geno = t(sm)),
  colData = col.DF, rowData = gr)
```

### C.3 FamilyExperiment

Now, we include the pedigree information as an object of class `PedClass`. We keep `PedClass` independent of `FamilyExperiment` for flexibility.

```
> ped <- PedClass(ped.DF)
> ste <- FamilyExperiment(se, pedigree = ped)
```

Here is the show method.

```
> ste
```

And now we verify that it is indeed an extension of `SummarizedExperiment`.

```
> getClass("FamilyExperiment")
```

### C.4 PedClass

Now we investigate the pedigree slot of the `FamilyExperiment` object.

```
> class(pedigree(ste))
> getClass("PedClass")
> pedigree(ste)
```

### C.5 geno accessor

```
> class(geno(ste))
> getClass("SnpMatrix")
> geno(ste)
```

### C.6 RowData

```
> rowData(ste)
```

### C.7 ColData

## D Validity