The R package *trioClasses* for definition of the class *SNPTrioExperiment*, an extension of *SummarizedExperiment*, for use in trio based analyses of genetic data.

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1 Classes

1.1 SnpMatrix, DataFrame, GRanges

```
> class(sm)

[1] "SnpMatrix"
attr(,"package")
[1] "snpStats"

> class(ped.DF)

[1] "DataFrame"
attr(,"package")
[1] "IRanges"

> class(gr)

[1] "GRanges"
attr(,"package")
[1] "GenomicRanges"
```

1.2 SummarizedExperiment

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

1.3 SNPTrioExperiment

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

> ste

class: SNPTrioExperiment
dim: 511 968
exptData(0):
```

```
assays(1): geno
rownames(511): chr14:54383433 chr14:54383470 ...
  chr14:54444385 chr14:54444750
rowData metadata column names(0):
colnames(968): subject1 subject2 ... subject967 subject968
colData names(1): id
pedigree(968): famid id fid mid sex dx

> getClass("SNPTrioExperiment")

Class "SNPTrioExperiment" [package "trioClasses"]

Slots:

Name:                    pedigree                    exptData
Class:                   PedClass                    SimpleList

Name:                     rowData                     colData
Class: GenomicRangesORGRangesList                   DataFrame

Name:                      assays
Class:                     Assays

Extends: "SummarizedExperiment"
```

1.4 PedClass

```
> class(pedigree(ste))

[1] "PedClass"
attr(,"package")
[1] "trioClasses"

> getClass("PedClass")

Class "PedClass" [package "trioClasses"]

Slots:

Name:        rownames            nrows        listData
Class: characterORNULL           integer            list

Name:      elementType elementMetadata       metadata
Class:        character DataTableORNULL           list

Extends:
Class "DataFrame", directly
Class "DataTable", by class "DataFrame", distance 2
Class "SimpleList", by class "DataFrame", distance 2
Class "DataTableORNULL", by class "DataFrame", distance 3
Class "List", by class "DataFrame", distance 3
Class "Vector", by class "DataFrame", distance 4
Class "Annotated", by class "DataFrame", distance 5
```

```
> pedigree(ste)

PedClass with 968 rows and 6 columns
         famid          id         fid         mid         sex          dx
     <logical> <character>   <logical>   <logical>   <logical>   <logical>
1           NA    subject1          NA          NA          NA          NA
2           NA    subject2          NA          NA          NA          NA
3           NA    subject3          NA          NA          NA          NA
4           NA    subject4          NA          NA          NA          NA
5           NA    subject5          NA          NA          NA          NA
6           NA    subject6          NA          NA          NA          NA
7           NA    subject7          NA          NA          NA          NA
8           NA    subject8          NA          NA          NA          NA
9           NA    subject9          NA          NA          NA          NA
...        ...         ...         ...         ...         ...         ...
960         NA  subject960          NA          NA          NA          NA
961         NA  subject961          NA          NA          NA          NA
962         NA  subject962          NA          NA          NA          NA
963         NA  subject963          NA          NA          NA          NA
964         NA  subject964          NA          NA          NA          NA
965         NA  subject965          NA          NA          NA          NA
966         NA  subject966          NA          NA          NA          NA
967         NA  subject967          NA          NA          NA          NA
968         NA  subject968          NA          NA          NA          NA
```

1.5   geno accessor

```
> class(geno(ste))

[1] "SnpMatrix"
attr(,"package")
[1] "snpStats"

> getClass("SnpMatrix")

Class "SnpMatrix" [package "snpStats"]

Slots:

Name:    .Data
Class: matrix

Extends:
Class "matrix", from data part
Class "array", by class "matrix", distance 2
Class "mMatrix", by class "matrix", distance 2
Class "structure", by class "matrix", distance 3
Class "vector", by class "matrix", distance 4, with explicit coerce

Known Subclasses: "XSnpMatrix"

> geno(ste)
```

```
A SnpMatrix with  968 rows and  511 columns
Row names:   subject1 ... subject968
Col names:   chr14:54383433 ... chr14:54444750
```

1.6   RowData

> *rowData(ste)*

```
GRanges with 511 ranges and 0 metadata columns:
                 seqnames       ranges strand
                    <Rle>    <IRanges>  <Rle>
  chr14:54383433    chr14       [1, 1]      *
  chr14:54383470    chr14       [2, 2]      *
  chr14:54383819    chr14       [3, 3]      *
  chr14:54383945    chr14       [4, 4]      *
  chr14:54384030    chr14       [5, 5]      *
  chr14:54384232    chr14       [6, 6]      *
  chr14:54384251    chr14       [7, 7]      *
  chr14:54384291    chr14       [8, 8]      *
  chr14:54384382    chr14       [9, 9]      *
             ...      ...          ...    ...
  chr14:54443495    chr14  [503, 503]      *
  chr14:54443499    chr14  [504, 504]      *
  chr14:54443514    chr14  [505, 505]      *
  chr14:54443831    chr14  [506, 506]      *
  chr14:54443880    chr14  [507, 507]      *
  chr14:54444016    chr14  [508, 508]      *
  chr14:54444124    chr14  [509, 509]      *
  chr14:54444385    chr14  [510, 510]      *
  chr14:54444750    chr14  [511, 511]      *
  ---
  seqlengths:
   chr14
      NA
```

2   Validity

3   Methods