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

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

A SnpMatrix with  968 rows and  511 columns
Row names:  H_ME-DS10776_2-DS10776_2 ... H_ME-DS11313_1-DS11313_1
Col names:  chr14:54383433 ... chr14:54444750

> ped.DF

DataFrame with 4139 rows and 6 columns
          famid                        id
    <character>                <character>
1          4778          H_ME-4778_1-4778_1.2
2          4778          H_ME-4778_2-4778_2.2
3          4778          H_ME-4778_3-4778_3.2
4          4783          H_ME-4783_1-4783_1.1
5          4783          H_ME-4783_2-4783_2.1
6          4783          H_ME-4783_3-4783_3.1
7      20000492   H_ME-20000492_1-20000492_1.1
8      20000492 H_ME-20000492_2-20000492_2_a.1
9      20000492   H_ME-20000492_3-20000492_3.1
...         ...                        ...
4131    DS12332      H_ME-DS12332_1-DS12332_1
4132    DS12332      H_ME-DS12332_2-DS12332_2
4133    DS12332      H_ME-DS12332_3-DS12332_3
4134    DS99998    H_ME-DS10193_5-DS10193_5.2
4135    DS99998      H_ME-DS10193_6-DS10193_6
4136    DS99998      H_ME-DS10193_7-DS10193_7
4137    DS99999    H_ME-DS10707_4-DS10707_4.2
4138    DS99999      H_ME-DS10707_5-DS10707_5
```

```
4139     DS99999        H_ME-DS10707_6-DS10707_6
                                fid                        mid
                        <character>                <character>
1            H_ME-4778_2-4778_2.2        H_ME-4778_3-4778_3.2
2                                NA                         NA
3                                NA                         NA
4            H_ME-4783_2-4783_2.1        H_ME-4783_3-4783_3.1
5                                NA                         NA
6                                NA                         NA
7    H_ME-20000492_2-20000492_2_a.1 H_ME-20000492_3-20000492_3.1
8                                NA                         NA
9                                NA                         NA
...                             ...                        ...
4131      H_ME-DS12332_2-DS12332_2    H_ME-DS12332_3-DS12332_3
4132                             NA                         NA
4133                             NA                         NA
4134      H_ME-DS10193_6-DS10193_6    H_ME-DS10193_7-DS10193_7
4135                             NA                         NA
4136                             NA                         NA
4137                             NA                         NA
4138      H_ME-DS10707_4-DS10707_4.2   H_ME-DS10707_6-DS10707_6
4139                             NA                         NA
          sex        dx
    <numeric> <numeric>
1           1         1
2           1         0
3           2         0
4           2         1
5           1         0
6           2         1
7           2         1
8           1         0
9           2         0
...       ...       ...
4131        1         1
4132        1         0
4133        2         0
4134        2         1
4135        1         0
4136        2         0
4137        1         0
4138        1         1
4139        2         0

> gr

GRanges with 511 ranges and 0 elementMetadata cols:
              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
```

1.2 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)
```

1.3 SNPTrioExperiment

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

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

Here is the show method.

```
> ste

class: SNPTrioExperiment
dim: 511 968
exptData(0):
assays(1): geno
rownames(511): chr14:54383433 chr14:54383470 ...
  chr14:54444385 chr14:54444750
rowData values names(0):
colnames(968): H_ME-CSc175_1-CSc175_1_a.1
  H_ME-CSc175_2-CSc175_2 ... H_ME-DS11418_2-DS11418_2
  H_ME-DS11418_3-DS11418_3
colData names(28): vcfid jb_famid ... id ped
pedigree(4139): famid id fid mid sex dx
```

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

```
> getClass("SNPTrioExperiment")

Class "SNPTrioExperiment" [package "trioClasses"]

Slots:

Name:                    pedigree                    exptData
Class:                   PedClass                    SimpleList

Name:                     rowData                     colData
Class: GenomicRangesORGRangesList                    DataFrame

Name:                      assays
Class:                   SimpleList

Extends: "SummarizedExperiment"
```

1.4   PedClass

Now we investigate the pedigree slot of the SNPTrioExperiment object.

```
> 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 4139 rows and 6 columns
         famid                           id
      <factor>                     <factor>
1         4778              H_ME-4778_1-4778_1.2
2         4778              H_ME-4778_2-4778_2.2
3         4778              H_ME-4778_3-4778_3.2
4         4783              H_ME-4783_1-4783_1.1
5         4783              H_ME-4783_2-4783_2.1
6         4783              H_ME-4783_3-4783_3.1
7     20000492   H_ME-20000492_1-20000492_1.1
8     20000492 H_ME-20000492_2-20000492_2_a.1
9     20000492   H_ME-20000492_3-20000492_3.1
...        ...                          ...
4131  DS12332        H_ME-DS12332_1-DS12332_1
4132  DS12332        H_ME-DS12332_2-DS12332_2
4133  DS12332        H_ME-DS12332_3-DS12332_3
4134  DS99998        H_ME-DS10193_5-DS10193_5.2
4135  DS99998        H_ME-DS10193_6-DS10193_6
4136  DS99998        H_ME-DS10193_7-DS10193_7
4137  DS99999        H_ME-DS10707_4-DS10707_4.2
4138  DS99999        H_ME-DS10707_5-DS10707_5
4139  DS99999        H_ME-DS10707_6-DS10707_6
                               fid                             mid
                          <factor>                        <factor>
1              H_ME-4778_2-4778_2.2            H_ME-4778_3-4778_3.2
2                               NA                              NA
3                               NA                              NA
4              H_ME-4783_2-4783_2.1            H_ME-4783_3-4783_3.1
5                               NA                              NA
6                               NA                              NA
7    H_ME-20000492_2-20000492_2_a.1 H_ME-20000492_3-20000492_3.1
8                               NA                              NA
9                               NA                              NA
...                             ...                             ...
4131      H_ME-DS12332_2-DS12332_2       H_ME-DS12332_3-DS12332_3
4132                            NA                              NA
4133                            NA                              NA
4134      H_ME-DS10193_6-DS10193_6       H_ME-DS10193_7-DS10193_7
4135                            NA                              NA
4136                            NA                              NA
4137                            NA                              NA
4138      H_ME-DS10707_4-DS10707_4.2     H_ME-DS10707_6-DS10707_6
4139                            NA                              NA
         sex       dx
    <factor> <factor>
1          1        1
2          1        0
3          2        0
4          2        1
5          1        0
6          2        1
```

```
7          2        1
8          1        0
9          2        0
...        ...      ...
4131       1        1
4132       1        0
4133       2        0
4134       2        1
4135       1        0
4136       2        0
4137       1        0
4138       1        1
4139       2        0
```

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 "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:  H_ME-CSc175_1-CSc175_1_a.1 ... H_ME-DS11418_3-DS11418_3
Col names:  chr14:54383433 ... chr14:54444750
```

1.6   RowData

```
> rowData(ste)

GRanges with 511 ranges and 0 elementMetadata cols:
                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
```

1.7 ColData

```
> colData(ste)
```

```
DataFrame with 968 rows and 28 columns
                                                vcfid      jb_famid
                                          <character>   <character>
H_ME-CSc175_1-CSc175_1_a.1 H_ME-CSc175_1-CSc175_1_a.1       CSc175
H_ME-CSc175_2-CSc175_2           H_ME-CSc175_2-CSc175_2       CSc175
H_ME-CSc175_3-CSc175_3           H_ME-CSc175_3-CSc175_3       CSc175
H_ME-DS10776_1-DS10776_1     H_ME-DS10776_1-DS10776_1      DS10776
H_ME-DS10776_2-DS10776_2     H_ME-DS10776_2-DS10776_2      DS10776
H_ME-DS10776_3-DS10776_3     H_ME-DS10776_3-DS10776_3      DS10776
H_ME-DS10777_1-DS10777_1     H_ME-DS10777_1-DS10777_1      DS10777
H_ME-DS10777_2-DS10777_2     H_ME-DS10777_2-DS10777_2      DS10777
H_ME-DS10777_3-DS10777_3     H_ME-DS10777_3-DS10777_3      DS10777
...                                               ...          ...
H_ME-DS11399_3-DS11399_3     H_ME-DS11399_3-DS11399_3      DS11399
H_ME-DS11408_2-DS11408_2     H_ME-DS11408_2-DS11408_2      DS11408
H_ME-DS11408_3-DS11408_3     H_ME-DS11408_3-DS11408_3      DS11408
H_ME-DS11411_1-DS11411_1     H_ME-DS11411_1-DS11411_1      DS11411
H_ME-DS11411_2-DS11411_2     H_ME-DS11411_2-DS11411_2      DS11411
H_ME-DS11411_3-DS11411_3     H_ME-DS11411_3-DS11411_3      DS11411
H_ME-DS11418_1-DS11418_1     H_ME-DS11418_1-DS11418_1      DS11418
H_ME-DS11418_2-DS11418_2     H_ME-DS11418_2-DS11418_2      DS11418
H_ME-DS11418_3-DS11418_3     H_ME-DS11418_3-DS11418_3      DS11418
```

	jb_indid	jb_fatherid	jb_motherid
	\<character\>	\<character\>	\<character\>
H_ME-CSc175_1-CSc175_1_a.1	CSc175_01	CSc175_02	CSc175_03
H_ME-CSc175_2-CSc175_2	CSc175_02	0	0
H_ME-CSc175_3-CSc175_3	CSc175_03	0	0
H_ME-DS10776_1-DS10776_1	DS10776_01	DS10776_02	DS10776_03
H_ME-DS10776_2-DS10776_2	DS10776_02	0	0
H_ME-DS10776_3-DS10776_3	DS10776_03	0	0
H_ME-DS10777_1-DS10777_1	DS10777_01	DS10777_02	DS10777_03
H_ME-DS10777_2-DS10777_2	DS10777_02	0	0
H_ME-DS10777_3-DS10777_3	DS10777_03	0	0
...	...	...	...
H_ME-DS11399_3-DS11399_3	DS11399_03	0	0
H_ME-DS11408_2-DS11408_2	DS11408_02	0	0
H_ME-DS11408_3-DS11408_3	DS11408_03	0	0
H_ME-DS11411_1-DS11411_1	DS11411_01	DS11411_02	DS11411_03
H_ME-DS11411_2-DS11411_2	DS11411_02	0	0
H_ME-DS11411_3-DS11411_3	DS11411_03	0	0
H_ME-DS11418_1-DS11418_1	DS11418_01	DS11418_02	DS11418_03
H_ME-DS11418_2-DS11418_2	DS11418_02	0	0
H_ME-DS11418_3-DS11418_3	DS11418_03	0	0

	jb_gender	jb_affection	ts_famid
	\<numeric\>	\<numeric\>	\<character\>
H_ME-CSc175_1-CSc175_1_a.1	2	1	CSc175
H_ME-CSc175_2-CSc175_2	1	0	CSc175
H_ME-CSc175_3-CSc175_3	2	0	CSc175
H_ME-DS10776_1-DS10776_1	2	1	DS10776
H_ME-DS10776_2-DS10776_2	1	1	DS10776
H_ME-DS10776_3-DS10776_3	2	0	DS10776
H_ME-DS10777_1-DS10777_1	2	1	DS10777
H_ME-DS10777_2-DS10777_2	1	0	DS10777
H_ME-DS10777_3-DS10777_3	2	0	DS10777
...	...	...	...
H_ME-DS11399_3-DS11399_3	2	0	DS11399
H_ME-DS11408_2-DS11408_2	1	0	DS11408
H_ME-DS11408_3-DS11408_3	2	0	DS11408
H_ME-DS11411_1-DS11411_1	1	1	DS11411
H_ME-DS11411_2-DS11411_2	1	0	DS11411
H_ME-DS11411_3-DS11411_3	2	0	DS11411
H_ME-DS11418_1-DS11418_1	1	1	DS11418
H_ME-DS11418_2-DS11418_2	1	0	DS11418
H_ME-DS11418_3-DS11418_3	2	0	DS11418

	ts_indid	ts_sampleid	ts_fatherid
	\<character\>	\<character\>	\<character\>
H_ME-CSc175_1-CSc175_1_a.1	CSc175_1	CSc175_1_a.1	CSc175_2
H_ME-CSc175_2-CSc175_2	CSc175_2	CSc175_2_a.3	NA
H_ME-CSc175_3-CSc175_3	CSc175_3	CSc175_3	NA
H_ME-DS10776_1-DS10776_1	DS10776_1	DS10776_1	DS10776_2
H_ME-DS10776_2-DS10776_2	DS10776_2	DS10776_2	NA
H_ME-DS10776_3-DS10776_3	DS10776_3	DS10776_3	NA
H_ME-DS10777_1-DS10777_1	DS10777_1	DS10777_1	DS10777_2

```
H_ME-DS10777_2-DS10777_2        DS10777_2     DS10777_2           NA
H_ME-DS10777_3-DS10777_3        DS10777_3     DS10777_3           NA
...                                   ...           ...          ...
H_ME-DS11399_3-DS11399_3        DS11399_3     DS11399_3           NA
H_ME-DS11408_2-DS11408_2        DS11408_2     DS11408_2           NA
H_ME-DS11408_3-DS11408_3        DS11408_3     DS11408_3           NA
H_ME-DS11411_1-DS11411_1        DS11411_1     DS11411_1    DS11411_2
H_ME-DS11411_2-DS11411_2        DS11411_2     DS11411_2           NA
H_ME-DS11411_3-DS11411_3        DS11411_3     DS11411_3           NA
H_ME-DS11418_1-DS11418_1        DS11418_1     DS11418_1    DS11418_2
H_ME-DS11418_2-DS11418_2        DS11418_2     DS11418_2           NA
H_ME-DS11418_3-DS11418_3        DS11418_3     DS11418_3           NA
                               ts_motherid   ts_gender    ts_pheno
                               <character> <character> <character>
H_ME-CSc175_1-CSc175_1_a.1        CSc175_3      Female         CLP
H_ME-CSc175_2-CSc175_2                  NA        Male          NA
H_ME-CSc175_3-CSc175_3                  NA      Female          NA
H_ME-DS10776_1-DS10776_1        DS10776_3      Female          CL
H_ME-DS10776_2-DS10776_2                NA        Male          CL
H_ME-DS10776_3-DS10776_3                NA      Female          NA
H_ME-DS10777_1-DS10777_1        DS10777_3      Female          CL
H_ME-DS10777_2-DS10777_2                NA        Male          NA
H_ME-DS10777_3-DS10777_3                NA      Female          NA
...                                   ...         ...         ...
H_ME-DS11399_3-DS11399_3                NA      Female          NA
H_ME-DS11408_2-DS11408_2                NA        Male          NA
H_ME-DS11408_3-DS11408_3                NA      Female          NA
H_ME-DS11411_1-DS11411_1        DS11411_3        Male          CL
H_ME-DS11411_2-DS11411_2                NA        Male          NA
H_ME-DS11411_3-DS11411_3                NA      Female          NA
H_ME-DS11418_1-DS11418_1        DS11418_3        Male         CLP
H_ME-DS11418_2-DS11418_2                NA        Male          NA
H_ME-DS11418_3-DS11418_3                NA      Female          NA
                                    dna   ethnicity        race
                               <numeric> <character> <character>
H_ME-CSc175_1-CSc175_1_a.1            1    european       white
H_ME-CSc175_2-CSc175_2               1    european       white
H_ME-CSc175_3-CSc175_3               1    european       white
H_ME-DS10776_1-DS10776_1             1    european       White
H_ME-DS10776_2-DS10776_2             1    european       White
H_ME-DS10776_3-DS10776_3             1    european       White
H_ME-DS10777_1-DS10777_1             1    european       White
H_ME-DS10777_2-DS10777_2             1    european       White
H_ME-DS10777_3-DS10777_3             1    european       White
...                                 ...         ...         ...
H_ME-DS11399_3-DS11399_3             1    european   Caucasian
H_ME-DS11408_2-DS11408_2             1    european   Caucasian
H_ME-DS11408_3-DS11408_3             1    european   Caucasian
H_ME-DS11411_1-DS11411_1             1    european   Caucasian
H_ME-DS11411_2-DS11411_2             1    european   Caucasian
H_ME-DS11411_3-DS11411_3             1    european   Caucasian
```

```
H_ME-DS11418_1-DS11418_1            1    european   Caucasian
H_ME-DS11418_2-DS11418_2            1    european   Caucasian
H_ME-DS11418_3-DS11418_3            1    european   Caucasian
                            population          pi      gwasid
                           <character> <character> <character>
H_ME-CSc175_1-CSc175_1_a.1        IOWA      Murray    13046_01
H_ME-CSc175_2-CSc175_2            IOWA      Murray    13046_03
H_ME-CSc175_3-CSc175_3            IOWA      Murray    13046_02
H_ME-DS10776_1-DS10776_1        TURKEY    Marazita          NA
H_ME-DS10776_2-DS10776_2        TURKEY    Marazita          NA
H_ME-DS10776_3-DS10776_3        TURKEY    Marazita          NA
H_ME-DS10777_1-DS10777_1        TURKEY    Marazita          NA
H_ME-DS10777_2-DS10777_2        TURKEY    Marazita          NA
H_ME-DS10777_3-DS10777_3        TURKEY    Marazita          NA
...                                ...         ...         ...
H_ME-DS11399_3-DS11399_3       DENMARK    Marazita          NA
H_ME-DS11408_2-DS11408_2       DENMARK    Marazita          NA
H_ME-DS11408_3-DS11408_3       DENMARK    Marazita          NA
H_ME-DS11411_1-DS11411_1       DENMARK    Marazita          NA
H_ME-DS11411_2-DS11411_2       DENMARK    Marazita          NA
H_ME-DS11411_3-DS11411_3       DENMARK    Marazita          NA
H_ME-DS11418_1-DS11418_1       DENMARK    Marazita          NA
H_ME-DS11418_2-DS11418_2       DENMARK    Marazita          NA
H_ME-DS11418_3-DS11418_3       DENMARK    Marazita          NA
                                  twin     X_merge    affected
                           <character> <character>   <numeric>
H_ME-CSc175_1-CSc175_1_a.1          NA matched (3)           1
H_ME-CSc175_2-CSc175_2              NA matched (3)           0
H_ME-CSc175_3-CSc175_3              NA matched (3)           0
H_ME-DS10776_1-DS10776_1            NA matched (3)           1
H_ME-DS10776_2-DS10776_2            NA matched (3)           1
H_ME-DS10776_3-DS10776_3            NA matched (3)           0
H_ME-DS10777_1-DS10777_1            NA matched (3)           1
H_ME-DS10777_2-DS10777_2            NA matched (3)           0
H_ME-DS10777_3-DS10777_3            NA matched (3)           0
...                                ...         ...         ...
H_ME-DS11399_3-DS11399_3            NA matched (3)           0
H_ME-DS11408_2-DS11408_2            NA matched (3)           0
H_ME-DS11408_3-DS11408_3            NA matched (3)           0
H_ME-DS11411_1-DS11411_1     Dizygotic matched (3)           1
H_ME-DS11411_2-DS11411_2            NA matched (3)           0
H_ME-DS11411_3-DS11411_3            NA matched (3)           0
H_ME-DS11418_1-DS11418_1     Dizygotic matched (3)           1
H_ME-DS11418_2-DS11418_2            NA matched (3)           0
H_ME-DS11418_3-DS11418_3            NA matched (3)           0
                                   sex                     mid
                             <numeric>             <character>
H_ME-CSc175_1-CSc175_1_a.1           2   H_ME-CSc175_3-CSc175_3
H_ME-CSc175_2-CSc175_2               1                       NA
H_ME-CSc175_3-CSc175_3               2                       NA
H_ME-DS10776_1-DS10776_1             2 H_ME-DS10776_3-DS10776_3
```

```
H_ME-DS10776_2-DS10776_2          1                        NA
H_ME-DS10776_3-DS10776_3          2                        NA
H_ME-DS10777_1-DS10777_1          2 H_ME-DS10777_3-DS10777_3
H_ME-DS10777_2-DS10777_2          1                        NA
H_ME-DS10777_3-DS10777_3          2                        NA
...                             ...                       ...
H_ME-DS11399_3-DS11399_3          2                        NA
H_ME-DS11408_2-DS11408_2          1                        NA
H_ME-DS11408_3-DS11408_3          2                        NA
H_ME-DS11411_1-DS11411_1          1 H_ME-DS11411_3-DS11411_3
H_ME-DS11411_2-DS11411_2          1                        NA
H_ME-DS11411_3-DS11411_3          2                        NA
H_ME-DS11418_1-DS11418_1          1 H_ME-DS11418_3-DS11418_3
H_ME-DS11418_2-DS11418_2          1                        NA
H_ME-DS11418_3-DS11418_3          2                        NA
                                                          fid
                                                  <character>
H_ME-CSc175_1-CSc175_1_a.1    H_ME-CSc175_2-CSc175_2
H_ME-CSc175_2-CSc175_2                               NA
H_ME-CSc175_3-CSc175_3                               NA
H_ME-DS10776_1-DS10776_1    H_ME-DS10776_2-DS10776_2
H_ME-DS10776_2-DS10776_2                             NA
H_ME-DS10776_3-DS10776_3                             NA
H_ME-DS10777_1-DS10777_1    H_ME-DS10777_2-DS10777_2
H_ME-DS10777_2-DS10777_2                             NA
H_ME-DS10777_3-DS10777_3                             NA
...                                                 ...
H_ME-DS11399_3-DS11399_3                             NA
H_ME-DS11408_2-DS11408_2                             NA
H_ME-DS11408_3-DS11408_3                             NA
H_ME-DS11411_1-DS11411_1    H_ME-DS11411_2-DS11411_2
H_ME-DS11411_2-DS11411_2                             NA
H_ME-DS11411_3-DS11411_3                             NA
H_ME-DS11418_1-DS11418_1    H_ME-DS11418_2-DS11418_2
H_ME-DS11418_2-DS11418_2                             NA
H_ME-DS11418_3-DS11418_3                             NA
                                                       id         ped
                                               <character> <character>
H_ME-CSc175_1-CSc175_1_a.1 H_ME-CSc175_1-CSc175_1_a.1      CSc175
H_ME-CSc175_2-CSc175_2          H_ME-CSc175_2-CSc175_2      CSc175
H_ME-CSc175_3-CSc175_3          H_ME-CSc175_3-CSc175_3      CSc175
H_ME-DS10776_1-DS10776_1      H_ME-DS10776_1-DS10776_1     DS10776
H_ME-DS10776_2-DS10776_2      H_ME-DS10776_2-DS10776_2     DS10776
H_ME-DS10776_3-DS10776_3      H_ME-DS10776_3-DS10776_3     DS10776
H_ME-DS10777_1-DS10777_1      H_ME-DS10777_1-DS10777_1     DS10777
H_ME-DS10777_2-DS10777_2      H_ME-DS10777_2-DS10777_2     DS10777
H_ME-DS10777_3-DS10777_3      H_ME-DS10777_3-DS10777_3     DS10777
...                                                 ...         ...
H_ME-DS11399_3-DS11399_3      H_ME-DS11399_3-DS11399_3     DS11399
H_ME-DS11408_2-DS11408_2      H_ME-DS11408_2-DS11408_2     DS11408
H_ME-DS11408_3-DS11408_3      H_ME-DS11408_3-DS11408_3     DS11408
```

```
H_ME-DS11411_1-DS11411_1      H_ME-DS11411_1-DS11411_1      DS11411
H_ME-DS11411_2-DS11411_2      H_ME-DS11411_2-DS11411_2      DS11411
H_ME-DS11411_3-DS11411_3      H_ME-DS11411_3-DS11411_3      DS11411
H_ME-DS11418_1-DS11418_1      H_ME-DS11418_1-DS11418_1      DS11418
H_ME-DS11418_2-DS11418_2      H_ME-DS11418_2-DS11418_2      DS11418
H_ME-DS11418_3-DS11418_3      H_ME-DS11418_3-DS11418_3      DS11418
```

Now create a list of three SnpMatrices for trio analyses.

```
> GenoTrio(ste)

$O
A SnpMatrix with  320 rows and  511 columns
Row names:  H_ME-CSc175_1-CSc175_1_a.1 ... H_ME-DS11418_1-DS11418_1
Col names:  chr14:54383433 ... chr14:54444750

$F
A SnpMatrix with  320 rows and  511 columns
Row names:  H_ME-CSc175_2-CSc175_2 ... H_ME-DS11418_2-DS11418_2
Col names:  chr14:54383433 ... chr14:54444750

$M
A SnpMatrix with  320 rows and  511 columns
Row names:  H_ME-CSc175_3-CSc175_3 ... H_ME-DS11418_3-DS11418_3
Col names:  chr14:54383433 ... chr14:54444750
```

2   Validity

3   Methods