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 Packages

```
> library("trioClasses")
```

2 Sample Data

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

2.1 Pedigree

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

2.2 SNPTrioExperiment

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

> 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
```

3 Methods

3.1 Holger-style Genotype Matrix

Coercion to matrix for *trio*

```
> geno <- as(ste, "matrix")
```

Or apply the aTDT method to the SNPTrioExperiment directly.

```
> aTDT(ste)

$stat
  [1]   1.000000000   0.000000000   0.000000000   8.727272727 19.565217391
  [6]           NaN   1.000000000 12.500000000 28.688311688   8.464000000
 [11]           NaN   1.000000000   1.000000000   1.000000000   1.000000000
 [16]   0.000000000   2.438127090 10.285714286   1.000000000   5.000000000
 [21]   1.000000000   1.000000000           NaN   1.000000000   1.000000000
 [26]   7.641509434   7.584269663   1.000000000   1.285714286   5.444444444
 [31]   1.384615385           NaN   0.333333333   7.934426230           NaN
 [36]   1.627306273   0.546925566   1.000000000   9.689922481   5.000000000
 [41]   1.484848485   2.000000000   2.000000000           NaN   6.259259259
 [46]   1.000000000   1.000000000   1.000000000   7.503875969   1.000000000
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 [66]   2.000000000   2.000000000 23.052980132   1.000000000 20.250000000
 [71]           NaN   2.000000000 22.729729730   1.000000000   1.000000000
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 [86]   1.000000000 21.189189189 23.052980132   1.000000000           NaN
 [91]           NaN           NaN 22.102040816   1.000000000   1.000000000
 [96]   1.000000000           NaN   1.000000000   1.000000000   1.000000000
[101]   1.000000000   1.000000000           NaN   2.000000000 28.765957447
[106]  12.448275862 30.044444444   1.000000000   1.000000000           NaN
[111]   6.255319149   1.000000000   1.636363636   1.000000000   1.000000000
[116]           NaN 11.636363636   2.000000000   1.000000000   1.333333333
[121]   3.000000000   6.211267606   1.000000000   1.000000000   8.527868852
[126]   8.032727273   1.000000000   5.000000000 11.645161290   2.000000000
[131]  24.896551724           NaN   1.000000000           NaN   1.000000000
[136]   1.000000000   1.000000000   1.000000000   0.864864865   2.000000000
[141]           NaN   1.000000000   1.000000000   2.000000000 27.586206897
[146]   1.000000000   1.000000000   5.333333333   0.333333333   5.000000000
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[156]   1.000000000   2.000000000   0.044776119   2.000000000   2.000000000
[161]   1.000000000   2.000000000   1.000000000   1.000000000           NaN
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[171]   0.000000000   4.454545455   2.000000000   4.000000000   1.000000000
[176]   1.000000000   2.000000000   0.202531646   0.201257862   2.000000000
[181]   1.000000000   2.000000000   0.831168831   6.000000000   1.000000000
[186]   1.000000000   2.000000000   0.028571429   2.000000000 22.272727273
[191]   1.000000000 24.017543860   1.000000000   7.077669903           NaN
```

```
[196]  6.313131313          NaN  1.000000000  8.000000000  2.000000000
[201]  1.000000000  1.000000000 20.250000000          NaN  4.000000000
[206]  1.000000000  3.000000000          NaN  0.000000000  1.000000000
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[221]  1.000000000  3.555555556  5.063291139  1.000000000  1.000000000
[226]          NaN  1.000000000  4.000000000  2.000000000  0.333333333
[231]  0.003076923 10.039215686  2.000000000          NaN  1.923076923
[236]  8.852631579  2.000000000 10.285714286  7.142857143  4.454545455
[241]  1.000000000  7.578947368  1.000000000 20.547169811  1.000000000
[246]  1.000000000 16.941176471  1.000000000  1.000000000  3.350769231
[251]  2.000000000  1.000000000  1.000000000  1.000000000          NaN
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[266]  6.326797386  2.000000000  4.454545455  1.000000000  2.000000000
[271]  1.000000000  1.000000000  1.000000000          NaN  5.444444444
[276] 13.714285714  1.000000000  1.000000000  2.000000000 32.970149254
[281]  1.000000000  3.571428571  0.265573770  3.000000000  1.000000000
[286]  1.000000000  1.000000000 16.000000000          NaN          NaN
[291]  0.003367003  6.250000000  3.571428571  1.000000000  2.000000000
[296]  9.941176471  2.000000000 12.565217391  0.213333333  1.000000000
[301] 24.028571429  1.000000000  1.000000000          NaN  0.123287671
[306]  1.000000000  1.000000000  2.000000000  3.524271845  1.000000000
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[316] 13.500000000  2.000000000  2.000000000  2.000000000  3.000000000
[321]  0.013422819  0.030927835  5.555555556  9.800000000  2.000000000
[326]  2.000000000 18.132075472  7.200000000 12.565217391  2.000000000
[331]  1.285714286 10.703703704  1.000000000  1.000000000  1.000000000
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[341]  2.000000000  3.000000000  2.000000000          NaN 11.250000000
[346]          NaN  2.000000000  1.000000000  0.000000000          NaN
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[381]          NaN 25.600000000          NaN 12.755102041  0.666666667
[386] 14.411764706  2.000000000 16.643564356  1.000000000  4.500000000
[391]          NaN  2.000000000  2.000000000  1.000000000  4.000000000
[396]  1.182481752 11.560000000  1.000000000  4.500000000  1.000000000
[401]  2.000000000  6.545454545  4.500000000  2.000000000  1.000000000
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[416]  1.000000000  2.000000000  5.000000000          NaN  1.000000000
[421]  1.000000000  0.333333333          NaN          NaN  1.000000000
[426]          NaN          NaN 12.736842105  1.000000000  2.000000000
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[441]          NaN 42.050000000  2.000000000 40.913513514          NaN
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```

```
[451]  1.000000000  2.000000000  3.000000000          NaN  1.000000000
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[466] 33.062500000          NaN  2.000000000          NaN  3.769230769
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```

$pval
```
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 [36] 2.020760e-01 4.595766e-01 3.173105e-01 1.852814e-03 2.534732e-02
 [41] 2.230175e-01 1.572992e-01 1.572992e-01          NaN 1.235459e-02
 [46] 3.173105e-01 3.173105e-01 3.173105e-01 6.156635e-03 3.173105e-01
 [51] 8.326452e-02 3.173105e-01 3.173105e-01 3.173105e-01 3.173105e-01
 [56] 3.173105e-01 3.173105e-01          NaN 2.904902e-02 1.572992e-01
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```

```
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[341] 1.572992e-01 8.326452e-02 1.572992e-01          NaN 7.962302e-04
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[426]          NaN          NaN 3.585225e-04 3.173105e-01 1.572992e-01
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```
[436] 5.022804e-06          NaN 8.326452e-02 3.173105e-01 2.699796e-03
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[496] 1.572992e-01 3.173105e-01 3.173105e-01 1.901276e-05          NaN
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[511] 6.499047e-08

$transMinor
  [1]   0   9   2 108   8   0   0   6  15 102   0   0   0   0   0   4
 [17] 136   1   0  30   0   0   0   0   0 110 111   1   2   1  10   0
 [33]   1 100   0 125 161   1 104   0 138   0   0   0 102   1   1   1
 [49] 107   0   0   0   0   1   0   0   0   0   4   0   1   0   0   0
 [65]   3   0   0 105   0  99   0   0 103   0   0   1 114   2   0   1
 [81] 103   0 108   1   1   0 102 105   0   0   0   0 102   0   1   0
 [97]   0   1   0   0   1   0   0   0  21   5  19   1   1   0 162   0
[113]   8   0   0   0   3   0   0   4   0 163   0   0 178 114   0   0
[129]   6   0  10   0   0   0   0   1   1   1 140   2   0   0   1   0
[145]   9   1   1   2   1   0   0   1   3   0   0   0   0 102   0   0
[161]   1   0   0   0   0   0   1   0   1 140   1   2   0   0   1   1
[177]   0 162 163   0   0   0 146   0   0   0   0 156   0  10   0  10
[193]   0  38   0  37   0   1  35   0   0   1  14   0   0   0   3   0
[209]   2   0   0   0   0   2  43   0 155 138   1 158   0   5 138   0
[225]   1   0   0   4   0   1 163  35   0   0   9  33   0   1   2   2
[241]   0 128   0  10   0   0   5   0   1 179   2   1   1   0   0 130
[257]   0   0   0   0   1   2   0   1 189 131   0   2   0   0   1   0
[273]   0   0   1  33   0   0   0  10   0   1 148   0   0   0   0   6
[289]   0   0 148   3   1   0   0   2   0   3 154   0   3   0   0   0
[305] 143   1   0   0 138   1   0   0   0   0   3   3   0   0   0   3
[321] 148 147   4   3   0   0  11   4   3   0   2   5   0   0   1   2
[337]   0 134   1   0   0   0   0   0  25   0   0   1   1   0   0   1
[353]   0   0  25   0 128   1   0   0   2  15   0  25   2   4   0   0
[369]   2  25   0   0  94 100   0   1   0   0   1   0   0   4   0  12
[385]   4  60   0  71   1   1   0   0   0   0   0 128   4   0   1   0
[401]   0  17   1   0   0   1   0   0   0   2   0  30  22   0   3   0
[417]   0   0   0   1   0   1   0   0   1   0   0   8   0   0   6   0
[433]   0  73   0   4   0   3   0  14   0  69   0 136   0   0   0   0
[449]   1   0   0   0   0   0   0   0  37   0   1   1   3   0   0   5
[465]   4   9   0   0   0   3   0   0   1   0   0   0   0   0  45   0
[481]   0   1  95   0   2   2   1   0   0   0   0   0   1   2   0
[497]   0   0  44   0   0  16   1   0   0   0   0   0  91   0  47
```

```
$transMajor
  [1]    1    9    2  156   38    0    1   26   62  148    0    1    1    1    1    4
 [17]  163   13    1   50    1    1    0    1    1  155  156    0    5    8   16    0
 [33]    2  144    0  146  148    0  154    5  159    2    2    0  141    0    0    0
 [49]  151    1    3    1    1    0    1    1    1    0   13    2    1    1    0    2
 [65]    0    2    2   46    1   45    0    2   45    1    1    3  161    3    0    0
 [81]   47    1  154    1    4    1   46   46    1    0    0    0   45    1    0    1
 [97]    0    0    1    1    3    1    0    2   73   24   71    0    0    0  120    1
[113]   14    1    1    0   19    2    1    8    3  121    1    1  127  161    1    5
[129]   25    2   48    0    1    0    1    0    0    0  156    0    0    1    3    2
[145]   49    0    0   10    2    5    1    0    0    1    0    1    2   99    2    2
[161]    0    2    1    1    0    2    0    0   10  153    1    9    2    4    0    0
[177]    2  154  155    2    1    2  162    6    1    1    2  159    2   45    1   47
[193]    1   65    0   62    0    0   63    2    1    3   50    0    4    1    0    0
[209]    2    1    1    2    0    6   69    4  164  168    0  155    1   13  178    1
[225]    0    0    1   12    2    2  162   67    2    0    4   62    2   13   12    9
[241]    1  176    1   43    1    1   29    1    0  146    6    0    0    1    0  180
[257]    2    1    1    1    0   13    1    0  143  175    2    9    1    2    0    1
[273]    1    0    8    9    1    1    2   57    1    6  157    3    1    1    1   30
[289]    0    0  149   13    6    1    2   15    2   20  146    1   32    1    1    0
[305]  149    0    1    2  171    0    2    2    1    1   12   21    2    2    2    0
[321]  150  144   14   17    2    2   42   16   20    2    5   22    1    1    0    8
[337]    1  177    0    1    2    3    2    0   55    0    2    0    1    0    1    0
[353]    1    2   55    2  179    0    1    1    4   42    1   53    1   36    2    0
[369]    1   56    1    0  121   94    1    0    0    1    0    1    0   36    0   37
[385]    2   25    2   30    0    7    0    2    2    1    4  146   21    1    7    1
[401]    2    5    7    2    1    5    3    1    1   10    1   57   29    1    1    1
[417]    2    5    0    0    1    2    0    0    0    0    0   30    1    2    0    2
[433]    1   14    3   31    0    9    1    2    0   11    2   49    0    0    1    2
[449]    4    1    1    2    3    0    1    2    8    2    0    0   24    2    0   13
[465]    3   55    0    2    0   10    3    1    1    1    2    2    1    4   13    1
[481]    1    0   20    1    8    5    0    1    1    1    1    2    5    0    7    2
[497]    1    1   12    0    1   87    0    1    1    0    1    1   65    1  116
```

3.2 Count of Transmission of Rare Variants (*TransCount()*)

3.2.1 In a block

```
> world <- range(gr)
> block <- GRanges(seqnames = "chr14", IRanges(start(gr[100]),
    width = 10000), strand = "*")

> block

GRanges with 1 range and 0 elementMetadata cols:
      seqnames                 ranges strand
         <Rle>              <IRanges>  <Rle>
  [1]    chr14 [54395802, 54405801]      *
  ---
  seqlengths:
   chr14
      NA
```

```
> TransCount(ste[MAF(ste) <= 0.01, ], block)

[1] 26
```

3.2.2   Not In the block

```
> setdiff(world, block)

GRanges with 2 ranges and 0 elementMetadata cols:
      seqnames                 ranges strand
         <Rle>              <IRanges>  <Rle>
  [1]     chr14 [54383433, 54395801]       *
  [2]     chr14 [54405802, 54444750]       *
  ---
  seqlengths:
   chr14
      NA

> TransCount(ste[MAF(ste) <= 0.01, ], setdiff(world, block))

[1] 116
```

3.2.3   In the "world"

```
> world

GRanges with 1 range and 0 elementMetadata cols:
      seqnames                 ranges strand
         <Rle>              <IRanges>  <Rle>
  [1]     chr14 [54383433, 54444750]       *
  ---
  seqlengths:
   chr14
      NA

> TransCount(ste[MAF(ste) <= 0.01, ], world)

[1] 142
```

4 Classes

4.1 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 [54383433, 54383433]        *
  chr14:54383470     chr14 [54383470, 54383470]        *
  chr14:54383819     chr14 [54383819, 54383819]        *
  chr14:54383945     chr14 [54383945, 54383945]        *
  chr14:54384030     chr14 [54384030, 54384030]        *
  chr14:54384232     chr14 [54384232, 54384232]        *
  chr14:54384251     chr14 [54384251, 54384251]        *
  chr14:54384291     chr14 [54384291, 54384291]        *
  chr14:54384382     chr14 [54384382, 54384382]        *
             ...       ...                       ...      ...
  chr14:54443495     chr14 [54443495, 54443495]        *
  chr14:54443499     chr14 [54443499, 54443499]        *
  chr14:54443514     chr14 [54443514, 54443514]        *
  chr14:54443831     chr14 [54443831, 54443831]        *
  chr14:54443880     chr14 [54443880, 54443880]        *
  chr14:54444016     chr14 [54444016, 54444016]        *
  chr14:54444124     chr14 [54444124, 54444124]        *
  chr14:54444385     chr14 [54444385, 54444385]        *
  chr14:54444750     chr14 [54444750, 54444750]        *
```

```
   ---
  seqlengths:
   chr14
      NA
```

4.2   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)
```

4.3   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"
```

4.4   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
```

4.5 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
```

4.6 RowData

```
> rowData(ste)

GRanges with 511 ranges and 0 elementMetadata cols:
                 seqnames                  ranges strand
                    <Rle>               <IRanges>  <Rle>
  chr14:54383433    chr14 [54383433, 54383433]       *
  chr14:54383470    chr14 [54383470, 54383470]       *
  chr14:54383819    chr14 [54383819, 54383819]       *
  chr14:54383945    chr14 [54383945, 54383945]       *
  chr14:54384030    chr14 [54384030, 54384030]       *
  chr14:54384232    chr14 [54384232, 54384232]       *
  chr14:54384251    chr14 [54384251, 54384251]       *
  chr14:54384291    chr14 [54384291, 54384291]       *
  chr14:54384382    chr14 [54384382, 54384382]       *
             ...      ...                     ...     ...
  chr14:54443495    chr14 [54443495, 54443495]       *
  chr14:54443499    chr14 [54443499, 54443499]       *
  chr14:54443514    chr14 [54443514, 54443514]       *
  chr14:54443831    chr14 [54443831, 54443831]       *
```

```
chr14:54443880      chr14 [54443880, 54443880]      *
chr14:54444016      chr14 [54444016, 54444016]      *
chr14:54444124      chr14 [54444124, 54444124]      *
chr14:54444385      chr14 [54444385, 54444385]      *
chr14:54444750      chr14 [54444750, 54444750]      *
---
seqlengths:
 chr14
    NA
```

4.7 ColData

5 Validity