```
Today is December 8, 2012.
> rm(list = ls())
> library("trioClasses")
> data(ped)
> data(geno)
> pedigreeInfo <- within(ped.df, {
     F <- as.character(fid)</pre>
     M <- as.character(mid)</pre>
     0 <- as.character(id)</pre>
})
> pedigreeInfo <- subset(pedigreeInfo, !is.na(F) & !is.na(M) &
     !is.na(0))
> tg.ped <- Pedigree(pedigreeInfo = pedigreeInfo)</pre>
> tg.ped
This pedigree object contains 1812 complete trios.
For access to the data frame use the trios() accessor function.
> id <- offspringNames(tg.ped)</pre>
> fid <- fatherNames(tg.ped)</pre>
> mid <- motherNames(tg.ped)</pre>
> names(fid) <- names(mid) <- id
> c(length(unique(id)), length(unique(fid)), length(unique(mid)))
[1] 1812 1812 1812
    TrioSet
1
> head(geno.mat[, 1:6])
        snp1 snp2 snp3 snp4 snp5 snp6
578_01
         2
              2
                   0
                        2 2
                               2
                                    2
578_02
               0
                          0
          1
                     1
        0
              2
                   2
                       0
                             2
                                    2
578_03
        2
                  2 2 2
1539_01
             0
                                    0
1539_02
        1
             1
                     2
                          0
                               1
                                    0
        1
1539_03
> geno.trio <- genoMat(tg.ped, geno.mat)</pre>
> (tg.ped.comp <- completeTrios(tg.ped, colnames(geno.trio)))</pre>
This pedigree object contains 33 complete trios.
For access to the data frame use the trios() accessor function.
> (ts <- TrioSet(tg.ped.comp, geno = geno.trio))</pre>
TrioSet (storageMode: lockedEnvironment)
assayData: 10 features, 33 samples
  element names: geno
```

protocolData: none
phenoData: none
featureData

fvarMetadata: labelDescription

experimentData: use 'experimentData(object)'

Annotation: genome: hg19

> assayDataElement(ts, "geno")

, , F

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 1 2 2 2 0 0 0 0 0 2 2 0 2 2 2 1 0 0 0 1 2 0 1 1 0 1 2 0 1 2 1 0 0 2 2 102220111 0 2 2 5 2 1 2 1 2 1 2 1 0 0 0 1 1 1 0 0 2 2 1 2 2 0 0 202212012 2 2 2 2 0 2 2 1 1 2 1 1 1 2 2 2 2 2 1 2 2 1 1 2 2 2 1 2 1 1 2 1 1 1 1 1 2 1 2 2 1 0 1 0 10 1 2 1 0 2 2 1 2 2 2 2 2 2 0 1 1 1 2 1 0

26 27 28 29 30 31 32 33

0 1 0 0 2 1 2 2

2 1 0 0 0 1 0 2 0

3 1 1 1 2 1 1 1 1

4 0 0 1 0 0 2 1 0

5 1 2 2 2 2 1 0 2 6 2 0 2 1 1 2 0 0

7 1 1 1 0 1 1 2 2

8 0 2 1 2 1 0 0 0

9 1 0 2 1 0 0 0 0

10 1 0 0 2 0 2 2 1

, , M

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 1 0 1 2 1 2 1 2 1 1 2 0 0 0 1 1 2 2 2 2 2 0 1 1 2 0 0 2 1 2 2 1 1 1 2 0 2 0 0 2 1 1 0 1 2 0 0 2 1 0 1 0 1 1 0 2 0 2 2 2 0 1 1 1 1 1 2 2 2 2 2 1 9 0 0 2 2 1 1 1 0 0 0 2 2 2 2 2 2 1 0 1 1 0 10 2 0 1 2 2 2 2 2 1 1 2 0 1 2 1 2 1 1 1 1

26 27 28 29 30 31 32 33 0 2 2 2 2 0 2 0

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          2 2
                2
5
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      2
        2 2 0
                0
                     1
   2
      2
6
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           1
             0
                0
                  0
7
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      1
        0
           1
             2
                2
                  2
8
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           2
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9
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        1
                1
10
     2 1 1 0 1 0
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, , 0

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10 2 1 1 0 1 0 2 1 2 0
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                          0 1 2 1 1
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26 27 28 29 30 31 32 33 2 2 2 1 1 2 0 2 1 2 0 2 0 1 1 2 0 0 0 1 1

> ts <- TrioSet(tg.ped.comp)