Today is December 9, 2012.

```
> rm(list = ls())
> source("~/jhsph/R/reload.R")
> library("trioClasses")
> library("trio")

> data(ped)
> pedigreeInfo <- within(ped.df, {
      F <- as.character(fid)
      M <- as.character(mid)
      O <- as.character(id)
 })
> pedigreeInfo <- subset(pedigreeInfo, !is.na(F) & !is.na(M) &
      !is.na(O))
> tg.ped <- Pedigree(pedigreeInfo = pedigreeInfo)
> tg.ped

This pedigree object contains 1812 complete trios.
For access to the data frame use the trios() accessor function.

> id <- offspringNames(tg.ped)
> fid <- fatherNames(tg.ped)
> mid <- motherNames(tg.ped)
> names(fid) <- names(mid) <- id
> c(length(unique(id)), length(unique(fid)), length(unique(mid)))

[1] 1812 1812 1812
```

1   TrioSet

```
> data(geno)
> head(geno.mat[, 1:6])

        snp1 snp2 snp3 snp4 snp5 snp6
578_01     2    2    0    2    2    1
578_02     1    0    1    0    2    2
578_03     0    2    2    0    2    2
1539_01    2    0    2    2    2    0
1539_02    1    1    2    0    1    0
1539_03    1    0    2    2    0    2

> geno.trio <- genoMat(tg.ped, geno.mat)
> (tg.ped.comp <- completeTrios(tg.ped, colnames(geno.trio)))

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))
```

```
TrioSet (storageMode: lockedEnvironment)
assayData: 10 features, 33 samples
  element names: geno
protocolData: none
phenoData: none
featureData
  featureNames: snp1 snp2 ... snp10 (10 total)
  fvarLabels: position chromosome isSnp
  fvarMetadata: labelDescription
experimentData: use 'experimentData(object)'
Annotation:
genome:  hg19

> geno <- getGeno(ts)
> (aTDT <- allelicTDT(mat.snp = t(geno), size = 10000))

      Allelic TDT

Top 5 SNPs:
      Statistic p-value
snp10    3.8571 0.04953
snp4     2.5714 0.10881
snp5     1.1429 0.28505
snp8     1.0000 0.31731
snp6     0.6923 0.40538
```