

Today is December 9, 2012.

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

> data(ped)
> head(ped.df)
```

	id	mid	fid	Population	PI	Ethnicity
578_01	578_01	578_03	578_02	PHILIPPINES	Murray	filipino
578_02	578_02	<NA>	<NA>	PHILIPPINES	Murray	filipino
578_03	578_03	<NA>	<NA>	PHILIPPINES	Murray	filipino
1539_01	1539_01	1539_03	1539_02	IOWA	Murray	european
1539_02	1539_02	<NA>	<NA>	IOWA	Murray	european
1539_03	1539_03	<NA>	<NA>	IOWA	Murray	european

```
> pedigreeInfo <- within(ped.df, {
  F <- as.character(fid)
  M <- as.character(mid)
  O <- as.character(id)
})
> 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.

## 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