

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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```
> library("trioClasses")
> library("snpStats")
> library("vcf2R")

> data("BMP4-european-all.sm")
> data("ped")

> gr <- GRanges(seqnames = paste0("snv", 1:nrow(sm)), ranges = IRanges(start = 1:nrow(sm),
  width = 1))
> df <- DataFrame(dx = rep(1, ncol(sm)), sex = rep(1, ncol(sm)),
  row.names = colnames(sm))
> se <- SummarizedExperiment(assays = SimpleList(geno = sm),
  colData = df, rowData = gr)

> ste <- new("SNPTrioExperiment", se, pedigree = ped.df)

> ste

class: SNPTrioExperiment
dim: 968 511
exptData(0):
assays(1): geno
rownames: NULL
rowData metadata column names(0):
colnames(511): chr14:54383433 chr14:54383470 ...
  chr14:54444385 chr14:54444750
colData names(2): dx sex
pedigree(4998): FAMID ID FID MID SEX DX

> class(geno(ste))

[1] "SnpMatrix"
attr(,"package")
[1] "snpStats"
```