

Classes *SNPExperiment* and *CNVExperiment*: Derivatives of
SummarizedExperiment for use with genotype and intensity data
in package *trioClasses*

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```
> library("trioClasses")
> library("vcf2R")
> data(targets)
> data("BMP4-european-all.sm")
> df <- DataFrame(dx = rep(1, 10), sex = rep(1, 10), row.names = paste0("sub",
  1:10))
> class(df)

[1] "DataFrame"
attr(,"package")
[1] "IRanges"

> class(sm)

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

> logR <- matrix(runif(130), nrow = 13, ncol = 10)
> baf <- matrix(runif(130), nrow = 13, ncol = 10)

> (snpEx <- new("SNPTrioExperiment", pedigree = new("PedClass",
  ped.df), assays = SimpleList(geno = sm[1:13, 1:10],
  logR = logR, baf = baf), colData = df, rowData = targets.gr))

class: SNPTrioExperiment
dim: 13 10
exptData(0):
assays(3): geno logR baf
rownames(13): IRF6 MAFB ... FGFR2 PTCH1
rowData values names(0):
colnames(10): sub1 sub2 ... sub9 sub10
colData names(2): dx sex

> class(snpEx@pedigree)

[1] "PedClass"
attr(,"package")
[1] "trioClasses"
```

```

> class(geno(snpEx))

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

> class(logR(snpEx))

[1] "matrix"

> class(baf(snpEx))

[1] "matrix"

> pedigree(snpEx)

An object of class "PedClass"
Slot "pedigree":
  pedid   id  fid  mid sex dx
1      1 sub1   0   0  1  1
2      1 sub2   0   0  2  1
3      1 sub3 sub1 sub2  2  1
4      2 sub4   0   0  1  1
5      2 sub5   0   0  2  1
6      2 sub6 sub4 sub5  2  1
7      3 sub7   0   0  1  1
8      3 sub8   0   0  2  1
9      3 sub9 sub7 sub8  2  1
10     4 sub10  0   0  1  1

> completeTrios(snpEx)

  pedid   id  fid  mid sex dx
3      1 sub3 sub1 sub2  2  1
6      2 sub6 sub4 sub5  2  1
9      3 sub9 sub7 sub8  2  1

```